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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/340,376, filed December 14, 2001; Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed November 15, 2001; USSN 60/347,349, filed January 10, 2002; USSN 60/368,809, filed March 29, 2002; USSN 60/409,450, filed September 9, 2002; USSN 60/359,077, filed February 20, 2002; USSN 60/386,614, filed June 5, 2002; USSN 60/356,714, filed February 13, 2002; USSN 60/397,775 filed July 22, 2002; USSN 60/332,464, filed November 21, 2001; USSN 60/397,845, filed July 22, 2002; USSN 60/370,110, filed April 4, 2002; USSN 60/396,839, filed July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes. The application also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer and other diseases; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of these conditions. The invention further relates to methods for identifying and using agents and/or targets that modulate these conditions.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over

70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

5 Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

10 Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be
15 tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies
20 (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

 The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic
25 intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

 The present invention provides methods for determining the presence or absence of a
30 pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting
5 the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising at sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is
10 suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as
15 described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a
20 compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological
25 sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and
30 determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

5

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for

10 treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN:

15 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous

20 System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosén's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American

25 Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM

30 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

- (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

5 Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the

10 invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g.,

15 using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also

20 be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

25 Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin

30 cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

5 "Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

10 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over
15 a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes
20 sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

25 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison
30 algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-

scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP
5 program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

10 One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than
15 about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a
20 polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

25 A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site,
30 www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from
5 some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing
10 at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally
15 occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as
20 those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g.,
25 norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter
30 symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules

Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide.

"Secondary structure" refers to locally ordered, three dimensional structures within a

5 polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of
10 independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about
15 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages
20 (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series
25 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of
30 naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805, Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand
5 also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically
10 refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

15 A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids,
20 proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be
25 made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound
30 (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

5 A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

10 As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage
15 other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with
20 isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid,
25 protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all.
30 By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid

sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times
5 background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For
10 high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high
15 stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy
20 permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar
25 stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly
30 or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for

inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

5 Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

10 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these
15 light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild
20 conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant
25 DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies,
30 many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression
5 profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be
10 evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are
15 differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other
20 organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

25 Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer
30 sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and
5 non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are
10 applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and
15 disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not
20 necessary (e.g., where organs may be dispensable, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or
25 non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the
30 GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases,

e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have
5 been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher
10 being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development,
15 and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA).
20 Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access
30 to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or
5 absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others.
10 Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued
15 and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval
20 system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S.
25 Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with
30 navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxeavanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001)

- Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)
- Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)
- 5 Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the
- 10 Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with

15 data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another

20 tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

25 The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of

30 magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention

provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method
5 for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount
10 of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed,
15 Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line,
20 wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a
30 query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

5 The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can
10 be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal
15 comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

 The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be
20 stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different
25 samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the
30 smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus.

5 Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase
10 activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In
15 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH
20 domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.
25 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc.
30 Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by
15 removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal
20 sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion
25 into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic
30 markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,
20 moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-
5 bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-
10 positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable
15 markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

20 In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.
25

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer
30 protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other
5 components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-
10 cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of
15 purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription
20 or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than
25 about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

30 Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional
5 imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine,
10 phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the
15 scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-
20 associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally
25 be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g.,
30 WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases.

5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-
15 terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide
20 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science
30 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the
10 nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
- 30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S.
10 Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are
20 raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are
25 secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may
30 bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety.

Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein
5 which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

10 The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_D of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

15 Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide
20 expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including
25 both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and
30 among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene
5 expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to,
10 quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene
15 expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as
20 being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays
25 are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can
30 be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIAcore technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically
5 involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with
10 dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out
15 in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical
20 equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator
25 suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

30 Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or
5 heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize"
10 is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity,
15 creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques
20 Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired
25 characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical
30 library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

 Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially
15 expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

 In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

 Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

10 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes
20 are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
25 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

 Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a
30 non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5–48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

5 In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

10 In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

15 Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface
25 of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular
30 manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked
5 through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural
10 binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

15 The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and
20 washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

25 In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test
30 compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

- 5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.
- 10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

- In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
- 15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

- In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
- 20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

- 25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

- 30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al.(1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth

- 5 factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

- Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released
10 from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

- 15 Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985)
20 Anticancer Res. 5:111-130.

Invasiveness into Matrigel

- The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into
25 Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

- Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other
30 extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or
5 immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the
10 endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the
15 chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

20 Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected
25 into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction
30 (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer
Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

 The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

 Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of a polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

 Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number
5 of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999)
15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
20 the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in

5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.

10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.

15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de

20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance

25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,

30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.
10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide
15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic
20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a
25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a
30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may
5 include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated
10 activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or
15 outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and
20 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodeling, psoriasis, ischemic, heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma
bone: Ewing sarcoma, sarcomas arising from skeletal and extraskeletal connective tissues, including the peripheral nervous system (e.g., chondrosarcoma, osteosarcoma)
brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, neuroma, ganglioneuroma
- 15 breast: ductal carcinoma in situ, lobular carcinoma in situ
cervix: cancer of the cervix, vagina, or vulva
colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
- 20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastrointestinal carcinomas (e.g., cancers of the stomach, colon, or rectum)
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
- 25 head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiomylipoma, oncocytoma
leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous leukemia, thymic hyperplasia, hairy cell leukemia, malignant transformation, inappropriate activation or abnormalities of leukocytes (e.g., immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts), arthritis, inflammation, leukocytosis, lymphadenitis, lymphangitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing
- 30 liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor like conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
- 35 ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, chorioncarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
- 40 prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
- 45 skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
- 50 soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma) smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroblastoma, neuroepithelioma, extraskeletal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskeletal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotent mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma
- 55 stomach: adenocarcinoma, squamous cell carcinoma, adenocanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, chorioncarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
- 60 uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed müllerian tumors, adenosarcoma)

70 Tables 2B-2D, 76B, and 79B list accession numbers for Pkeys lacking Unigenes IDs for Tables 2A-2D, 76A, and 79A, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

75 Tables 2C-2D, 76C, and 79C list genomic positioning for Pkeys lacking Unigenes IDs and accession numbers in Tables 2A-2D, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

80 Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number
UnigenID: Unigen ID number

	Unigene Title:	Unigene gene title
	Disease:	preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), meta (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
5	Utility:	preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)
10	Pkey; ExAccn; UnigeneID; Unigene Title; Disease; Utility	
		<p>102892; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m. 104865; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL 104978; A1199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL 109424; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m. 110765; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag 110906; AA035211; Hs.17404; SOX7 SRY (sex determining reg); angio, blad; CTL 115522; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL 116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL 118695; AK000465; Hs.50081; KIAA1199 protein; colon, lung; diag 123049; BE047680; Hs.211869; dickkopf (Xenopus laevis) homolog; EWS; mAb+diag 131486; F05972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m. 133370; AF245505; Hs.72157; Adican; breast, lung, panc; diag 310016; AW449612; Hs.152475; ESTs; colon; CTL 322303; A1357412; Hs.157601; ESTs; colon, pros, fibro, breast; CTL+diag 400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m. 400297; A1127078; Hs.288361; hypothetical protein DKFZp564O; breast, blad, colon, pros; mAb 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulator; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb 400843; ; NM_003105; Homo sapiens sort; blad; s.m. 402075; ; ENSP00000251056; Plasma membra; blad, lung, headnk, cerv, meta, esoph; mAb+diag 402901; ; NM_025205; Homo sapiens hypoth; blad ; CTL 404287; ; FGENESH predicted novel CUB-do; panc, lung, colon, uter, esoph; mAb+s.m. 404682; ; ortholog of mouse polydomain p; panc; diag 404875; ; NM_022819; Homo sapiens phosph; blad; CTL+s.m. 404977; ; Insulin-like growth factor 2 (I; blad, ovar, sarc; mAb+diag 405033; ; C1002652; gij544327sp; Q04799; blad; s.m. 406400; ; kallikrein 8 (neuropsin/ovasin; ovar, uter; diag 406964; M21305; ; FGENES predicted novel secreta; angio, blad, fibro, sarc; diag 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299; glio, blad; CTL 407792; A1077715; Hs.39384; putative secreted ligand homolog; ovar, uter, cerv, panc; mAb+diag 407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag 407836; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL 407975; X89426; Hs.41716; endothelial cell-specific mole; angio, renal; diag 408243; Y00787; Hs.624; Interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag 408367; AK001178; Hs.44424; Homo sapiens orphan neurotrans; meta; mAb+s.m. 408369; R38438; Hs.118747; SLC15A2 Solute carrier family ; pros, lung, fibro, uter, glio, cerv, ovar; mAb 408380; AF123050; Hs.44532; diubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, meta; CTL 408482; NM_000676; Hs.45743; adenosine A2b receptor; lung, esoph, headnk, colon; mAb+s.m. 408562; A1436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m. 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase ; lung; mAb+s.m. 408908; BE296227; Hs.250822; serine/threonine kinase 15; blad, lung, headnk, stom, colon; s.m. 409041; AB033025; Hs.50081; Hypothetical protein, XP_05186; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag 409079; W87707; Hs.82065; interleukin 6 signal transducer; breast, pros; mAb+s.m. 409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL 409178; BE393948; Hs.50915; kallikrein 5; ovar, breast, meta; diag 409220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m. 409420; Z15008; Hs.54451; laminin, gamma 2 (niclin (100k; lung, headnk, panc, stom, cerv, esoph, blad; diag 409632; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, headnk; diag 409663; A1743750; Hs.98306; KIAA1862 protein; renal; CTL 409757; NM_001898; Hs.123114; cystatin SN; panc, stom, lung, blad; diag 409889; AW630041; Hs.56937; suppression of tumorigenicity ; colon, ovar, pros; mAb+s.m. 409893; AW247090; Hs.57101; minichromosome maintenance def; lung, cerv, blad, test, esoph; CTL+s.m. 409958; AW103364; Hs.727; Inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag 410001; AB041036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung ; diag 410055; AJ250839; Hs.58241; gene for serine/threonine prot; renal; s.m. 410153; BE311926; Hs.15830; hypothetical protein FLJ12691; renal, blad; CTL 410274; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL 410309; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m. 410407; X66839; Hs.63267; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m. 410418; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m. 411274; NM_002776; Hs.69423; kallikrein 10; colon, ovar, uter, cerv, headk, panc; diag 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m. 411773; NM_006799; Hs.72026; protease, serine, 21 (testisin; ovar; diag 411975; A916058; Hs.144583; 3'UTR of: dead ringer (Drosoph; test, colon; CTL 412078; X69699; Hs.73149; paired box gene 8; ovar; CTL 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, headnk, breast, ovar, panc, angio, test, meta; s.m. 412314; AA825247; Hs.356084; G protein-coupled receptor 27 ; ovar, uter, test; mAb+s.m. 412605; Z48804; Hs.74124; ocular albinism 1 (Nettleship; meta; s.m. 412628; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag 412709; AL022327; Hs.74518; KIAA0027 protein; glio, sarc; mAb+s.m. 412719; AW016610; Hs.816; ESTs; lung, headnk, blad, glio, cerv, sarc; s.m. 412959; D87458; Hs.75090; KIAA0282 protein; glio; CTL+s.m. 413048; M93221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb</p>

- 413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage); glio, ovar, blad, lung; diag
- 413278; BE583085; Hs.833; interferon-stimulated protein; panc, lung, blad, breast, cerv, ovar, headnk, esoph, meta; CTL+s.m.
- 413324; V00571; Hs.75294; corticotrophin releasing hormon; blad; diag
- 5 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxyg; blad, lung, meta, fibro, uter, sarc; s.m.
- 413554; AA319146; Hs.75426; secretogranin II (chromogranin); panc, glio; diag
- 413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag
- 414555; N98569; Hs.76422; phospholipase A2, group IIA (pr; pros; s.m.
- 414577; AI056548; Hs.378938; hypothetical protein FLJ20992; angio; CTL+diag
- 10 414774; X02419; Hs.77274; plasminogen activator, urokin; lung, blad, headnk, panc, stom, ovar, esoph; diag
- 414812; X7755; Hs.77367; monocline induced by gamma inta; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, meta, esoph; diag
- 414883; AA926960; Hs.348669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.
- 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
- 414991; C17898; Homo sapiens up-regulated by B; fibro, lung; mAb+diag
- 15 415138; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc, stom, lung, uter; CTL+diag
- 415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.
- 415668; AW957684; Hs.306814; Homo sapiens lysyl oxidase-like; meta; diag
- 415669; NM_005025; Hs.78589; serine (or cysteine) proteinase; lung; mAb+diag+s.m.
- 415817; U88967; Hs.78867; protein tyrosine phosphatase; lung, glio, headnk, cerv, meta, esoph, fibro; mAb+s.m.
- 20 415929; AA724373; Hs.304950; Homo sapiens mucopolip-3 (MCOI); meta; mAb
- 416091; AF285370; Hs.283082; defensin, beta 3; headnk, esoph, meta; CTL+diag
- 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient; lung, headnk, colon, uter, stom; CTL+s.m.
- 416250; AA581386; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.
- 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); ovar, uter; diag
- 25 416638; N32536; Hs.42845; solute carrier family 18 (mono); breast, panc, uter, meta; mAb+s.m.
- 416658; U03272; Hs.79432; fibrillin 2 (congenital contra; lung, ovar, uter, blad, angio, test, sarc; diag
- 416836; D54745; Hs.80247; cholecystokinin; pros, EWS, glio; diag
- 416857; AA188775; Hs.292453; FGENSEH predicted TM containin; glio; mAb+s.m.
- 416965; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb
- 30 417034; NM_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag
- 417079; U65590; Hs.81134; interleukin 1 receptor antagon; blad, lung, headnk, cerv, esoph; diag
- 417166; AA431323; Hs.42146; Paired box protein Pax-3; meta, sarc; CTL
- 417389; BE260964; Hs.82045; midkine (neurite growth-promot; ovar, lung, blad, uter, cerv, panc, stom, meta, test, colon, sarc; mAb+diag
- 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyc; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb
- 35 417771; AA804698; Hs.82547; retinoic acid receptor respond; blad, cerv, panc, pros, ovar; mAb
- 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL
- 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag
- 417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.
- 418007; M13509; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, meta; mAb+diag+s.m.
- 40 418030; BE207573; Hs.83321; neuromedin B; glio, panc; diag
- 418064; BE387287; Hs.83384; S100 calcium-binding protein; meta; diag
- 418281; U09550; Hs.1154; oviductal glycoprotein 1, 120k; uter, ovar; CTL+diag
- 418478; U38945; Hs.1174; cyclin-dependent kinase inhibit lung, blad, ovar, headnk, panc, cerv, meta, sarc; s.m.
- 418506; AA084248; Hs.372651; Unknown protein for MGC:29643; angio, ovar, glio, uter, lung, blad, panc, meta, sarc; mAb+diag
- 45 418526; BE019020; Hs.85838; solute carrier family 16 (mono); lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.
- 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk; s.m.
- 418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-); lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL
- 418738; AW388633; Hs.6682; solute carrier family 7, (cat; angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.
- 418830; BE513731; Hs.348874; hypothetical protein MGC4816; lung; CTL
- 50 418867; D31771; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
- 418870; AF147204; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad, renal; mAb+s.m.
- 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; renal, lower uter, lung; CTL
- 419121; AA374372; Hs.89626; parathyroid hormone-like hormo; lung, esoph, headnk, blad; diag
- 419171; NM_002846; Hs.89655; protein tyrosine phosphatase; lung; mAb+s.m.
- 55 419172; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.
- 419183; U60669; Hs.89663; cytochrome P450, subfamily X0; blad, lung, headnk, panc; CTL+s.m.
- 419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag
- 419235; AW470411; Hs.288433; neurotrophin; panc, fibro, headnk, lung; mAb+diag
- 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.
- 419508; AW997938; Hs.90786; ATP-binding cassette, sub-fam; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.
- 60 419558; U29615; Hs.91093; chitinase 1 (chitobiosidase); lung, fibro, test; mAb+diag
- 419704; AA429104; Hs.45057; ESTs; glio; CTL+s.m.
- 419723; AL120193; Hs.339810; longevity assurance (LAG1, S.; glio; mAb+diag
- 419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, meta, sarc; CTL+s.m.
- 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-IRNA; fibro, stom, blad, esoph, uter; diag
- 65 420159; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 ft; blad, stom; mAb
- 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; lung, meta, sarc; s.m.
- 420370; Y13645; Hs.97234; uroplakin 2; blad; mAb
- 420440; NM_002407; Hs.97644; mammaglobin 2; ovar, uter, cerv; diag
- 70 420602; AF060877; Hs.99236; regulator of G-protein signal; headnk, glio, cerv, meta; CTL+s.m.
- 420610; AI683183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL
- 420737; U88096; Hs.99899; CD70; tumor necrosis factor; renal; mAb+s.m.
- 420876; AA918426; Hs.177744; FGENSE predicted novel protein; panc, blad; s.m.
- 421066; AU076725; Hs.101408; branched chain aminotransferase; blad, lung; CTL+s.m.
- 75 421110; AJ250717; Hs.1355; calhepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag
- 421340; F07783; Hs.1369; decay accelerating factor for; angio, panc, stom; diag
- 421379; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, meta, esoph; diag
- 421471; U90545; Hs.327179; solute carrier family 17 (sodi; renal; mAb+s.m.
- 421474; U76362; Hs.104637; solute carrier family 1 (gluta; lung; mAb+s.m.
- 80 421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
- 421552; AF026692; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag
- 421563; NM_006433; Hs.105806; granulysin; fibro; diag
- 421574; AJ000152; Hs.105924; defensin, beta 2; headnk, lung; CTL+diag
- 421582; AJ910275; Hs.350470; trefoil factor 1 (breast cance; breast, panc, lung, omuc; diag

- 421659; NM_014459; Hs.106511; protocadherin 17; fibro; mAb
- 421763; BE314828; Hs.107911; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
- 421817; AF146074; Hs.108660; ATP-binding cassette, sub-fam1; lung, cerv, headnk, blad; mAb+s.m.
- 421829; AB018330; Hs.108708; calcium/calmodulin-dependent p; pros; s.m.
- 5 422048; NM_012445; Hs.288126; spondin 2, extracellular matr; panc, pros, sarc; diag
- 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase; ; pros; s.m.
- 422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag
- 422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag
- 10 422192; AA305159; Hs.113019; fls485; mela; s.m.
- 422260; AA315993; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag
- 422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag
- 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45); lung, blad, test, cerv, headnk, esoph; s.m.
- 422330; D30783; Hs.115263; epiregulin; panc, colon, blad; mAb+diag
- 15 422397; AJ223366; Hs.116051; MYEOV Myeloma overexpressed ge; panc, stom, colon, esoph, renal, blad; CTL+s.m.
- 422424; A186431; Hs.296638; prostate differentiation factor; blad, panc, pros, angio, colon, stom, lung, mela; diag
- 422578; AF239668; Hs.1545; caudal type homeo box transcript; colon; CTL
- 422627; BE336857; Hs.118787; transforming growth factor, beta; colon, renal, sarc; mAb+diag
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.
- 20 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; blad, cer, lung, uter, angio, stom, test; s.m.
- 422867; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag
- 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell; ovar, blad, panc, lung, headnk, colon, stom; CTL+s.m.
- 423161; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.
- 423184; NM_004428; Hs.1624; ephrin-A1; pros, panc, renal, colon; mAb+s.m.
- 25 423242; AL039402; Hs.125783; DEME-6 protein; breast, renal, ovar, pros, colon; CTL
- 423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb
- 423583; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
- 423634; AW959908; Hs.1690; heparin-binding growth factor; lung, blad, headnk, panc; diag
- 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (m; blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.
- 30 423936; U77629; Hs.135639; achaete-scute complex (Drosoph; colon, stom, ovar; CTL
- 423961; D13666; Hs.136348; perostin (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag
- 424008; R02740; Hs.137555; putative chemokine receptor; G; blad, headnk, stom, cerv, esoph; mAb+s.m.
- 424048; AF027868; Hs.138202; serine (or cysteine) proteinase; headnk, lung, cerv; diag
- 424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.
- 35 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.
- 424411; NM_005209; Hs.146549; crystallin, beta A2; panc, sarc; s.m.
- 424502; AF242388; Hs.149585; lensgn; lung; s.m.
- 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
- 424620; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
- 424687; J05070; Hs.151738; matrix metalloproteinase 9 (ge; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag
- 40 424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.
- 424825; AF207089; Hs.153357; procollagen-llysine, 2-oxogluta; mela; CTL+s.m.
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a); ovar, blad, lung, headnk, panc, stom; s.m.
- 424917; A1636208; Hs.96901; hypothetical protein FLJ23049; fibro, uter, ovar; CTL
- 424943; AU077260; Hs.153924; death-associated protein kinase; fibro; s.m.
- 45 425009; X58288; Hs.154151; protein tyrosine phosphatase; ; renal, fibro; mAb+s.m.
- 425071; NM_013989; Hs.154424; delodinsase, iodolthyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag
- 425115; R44664; Hs.123956; downstream of: G protein-coup; gli; mAb+s.m.
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.
- 50 425263; NM_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.
- 425322; U63630; Hs.155637; protein kinase, DNA-activated; lung, headnk; s.m.
- 425535; AB007937; Hs.158287; syndecan 3; mela, gli; mAb+s.m.
- 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, headnk, cerv, esoph, blad; mAb
- 425721; AC002115; Hs.159309; uropiaidin 1A; blad; mAb
- 55 425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag
- 425734; AF056208; Hs.159396; peptidylglycine alpha-amidating; lung; s.m.
- 425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag
- 425842; A1587490; Hs.159623; NK-2 (Drosophila) homolog B; panc, gli; s.m.
- 425852; AK001504; Hs.159651; death receptor 6, TNF superfam; blad, lung, headnk; mAb+s.m.
- 60 425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb
- 425998; AU076629; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.
- 426028; NM_001110; Hs.172028; a disintegrin and metalloprote; blad; mAb+diag
- 426215; AW963419; Hs.155223; stanniocalcin 2; breast, lung, renal, colon, ovar, uter; mAb+diag
- 426227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.
- 65 426322; J05068; Hs.2012; transcobalamin I (vitamin B12; panc, blad, stom; diag
- 426344; H41821; Hs.322469; transcriptional activator of t; gli; CTL+s.m.
- 426427; M86699; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.
- 426451; A1908165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.
- 426514; BE816833; Hs.170195; bone morphogenetic protein 7 (; ovar, colon, blad, lung, cerv; mAb+diag
- 70 426600; NM_003378; Hs.171014; VGF nerve growth factor induc; mela, sarc; diag
- 426761; A1015709; Hs.172089; PORIMIN Pro-oncosis receptor t; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.
- 426812; AF105365; Hs.172613; solute carrier family 12 (pot; renal; mAb+s.m.
- 426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL
- 427239; BE270447; Hs.356512; ubiquitin carrier protein; lung, blad, test, mela, sarc; CTL+s.m.
- 75 427335; AA448542; Hs.278444; G antigen 7B; lung, headnk, blad, mela, esoph, sarc; CTL
- 427343; A1880044; Hs.176977; protein kinase C binding prote; gli; CTL+s.m.
- 427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.
- 427923; AW274357; Hs.301406; FGENSEH predicted 11 TM prote; mela; mAb
- 80 427969; NM_001963; Hs.2230; epidermal growth factor (beta; panc; mAb+diag
- 428093; AW594506; Hs.104830; ESTs; ovar, panc; CTL
- 428179; A1127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.
- 428187; A1687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.
- 428242; H55709; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, leuk, lung; diag

- 428296; NM_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+s.m.
 428330; L22524; Hs.2258; matrix metalloproteinase 7 (ma; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+s.m.
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag
 428392; H10233; Hs.2265; secretory granule, neuroendocr; panc; diag
 5 428450; NM_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; s.m.
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; s.m.
 428484; AF104032; Hs.184601; solute carrier family 7 (catio; lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela; mAb+s.m.
 428486; AW583497; Hs.184604; pancreatic polypeptide; panc; diag
 10 428505; AL035481; Hs.2281; chromogranin B (secretogranin; panc, lung; diag
 428513; BE220806; Hs.184697; plectin C1; mela, panc, breast stom, headnk; mAb
 428579; NM_005758; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosoph; blad, ovar, pros, lung, stom, test; CTL+s.m.
 428698; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, panc, stom, headnk, ovar, EWS; mAb
 15 428748; AW593206; Hs.98785; Ksp37 protein; lung, sarc; diag
 428758; AA433988; Hs.98502; CA125 antigen; much 16; ovar, cerv, lung, panc, stom, renal; diag
 428778; AK000530; Hs.193326; fibroblast growth factor recep; ovar; mAb+s.m.
 428953; AA306610; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag
 428969; AF120274; Hs.194689; artemin; lung, cerv; diag
 20 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG; stom, panc, colon, ovar, fibro; mAb+s.m.
 429149; AW193360; Hs.197962; Homolog of mouse ADP-ribosylat; glio; mAb+s.m.
 429211; AF052683; Hs.198249; gap junction protein, beta 5 (; lung, blad, headnk, cerv, esoph, stom, mela; mAb+s.m.
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad, glio; mAb+s.m.
 25 429353; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros; mAb+s.m.
 429547; AW009166; Hs.99376; FGENESH predicted novel secret; panc, headnk, lung, ovar; diag
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate l; lung, fibro; mAb+diag
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; s.m.
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin; leio; mAb+s.m.
 30 430147; R60704; Hs.234434; hairy/enhancer-of-split relate; glio; s.m.
 430178; AW449612; Hs.152475; 3'UTR of: achaete-scute complex; colon, stom, ovar; CTL
 430377; NM_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL
 430413; AW84182; Hs.241392; small inducible cytokine A5 (R; fibro, esoph, mela; diag
 430486; BE062109; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv, esoph; mAb+s.m.
 35 430822; AJ005371; Hs.248017; glyceraldehyde-3-phosphate dehy; mela, sarc; s.m.
 431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey; ovar, uter; diag
 431462; AW583672; Hs.256311; granin-like neuroendocrine pep; panc, lung, glio, test; diag
 431515; NM_012152; Hs.258583; EDG-7 (endothelial different; ovar, pros, lung, blad; mAb+s.m.
 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+s.m.
 40 431629; AJ077025; Hs.265827; Interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag
 431630; NM_002204; Hs.265829; Integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+s.m.
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadher; fibro, ovar, uter; mAb
 431840; AA534808; Hs.2860; POU domain, class 5, transcrip; test, renal, blad; CTL
 431846; BE019924; Hs.271580; uroplakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag
 45 432101; AI918950; Hs.123642; EphA3; pros, panc, EWS sarc; s.m.
 432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+s.m.
 432196; AW300888; Hs.273230; hypothetical protein FLJ10830; renal; CTL
 432201; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung; mAb+diag+s.m.
 50 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis; renal; CTL
 432586; AJ224741; Hs.278461; maltrin 3; panc, breast, sarc; diag
 432606; NM_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL
 432829; W60377; Hs.57772; ESTs; blad; CTL+s.m.
 432874; W94322; Hs.279651; melanoma inhibitory activity; panc, stom, mela, sarc; diag
 55 432990; AL036071; Hs.279899; tumor necrosis factor receptor; pros, renal; mAb+s.m.
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; colon, breast, lung, blad, cerv, uter, test, mela; s.m.
 433447; U29195; Hs.3281; neuronal pentraxin II; mela, esoph, colon, renal; diag
 433848; AF095719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; s.m.
 433867; AK000596; Hs.3618; hippocalcin-like 1; renal; CTL
 60 434206; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung, stom; CTL+s.m.
 434276; AF123659; Hs.93605; leucine zipper, putative tumor; mela; s.m.
 434293; NM_004445; Hs.3796; EphB6; blad, pros; s.m.
 435013; H91923; Hs.110024; NM_020142; Homo sapiens NADH; renal, lung, sarc; CTL
 435472; AW972330; Hs.283022; triggering receptor expressed; glio; mAb
 65 435505; AF200492; Hs.211238; Interleukin-1 homolog 1; lung, headnk; diag
 436456; AW292677; Hs.248122; melanin-concentrating hormone; mela, glio; mAb+s.m.
 436480; AJ271643; Hs.87469; putative acid-sensing ion chan; glio; mAb+s.m.
 436481; AA379597; Hs.6199; HSPC150 protein similar to ubi; lung, blad, colon, ovar, uter, headnk, test; s.m.
 436576; AI458213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+s.m.
 70 436608; AA628980; Hs.192371; down syndrome critical region; blad, lung, sarc; CTL+s.m.
 436895; AF037335; Hs.5338; carbonic anhydrase XI; breast, renal, ovar, glio; mAb+s.m.
 436961; AW375974; Hs.156704; ESTs; lung, panc, renal, uter, colon; CTL
 436982; AB018305; Hs.6378; spondin 1, (I-spondin) extrace; ovar, fibro; diag
 437016; AU076916; Hs.5398; guanine monophosphate synthetas; lung, blad, cerv, esoph, colon, headnk; s.m.
 75 437044; AL035864; Hs.69517; differentially expressed in Fa; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL
 437789; AI581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL
 437852; BE001836; Hs.256897; putative GPCR; blad, lung; mAb+s.m.
 438380; T06430; Hs.6194; chondroitin sulfate proteoglyc; glio, mela; diag
 438549; BE386801; Hs.21858; trinitrotoide repeat containin; mela, sarc; CTL+diag
 80 439018; AW300887; Hs.26638; membrane-spanning 4-domains, s; uter, stom, pros, fibro; mAb
 439223; AW238299; Hs.250618; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb
 439477; W69813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+s.m.
 439569; AW602166; Hs.222399; CEGP1 protein; breast, pros, blad; diag
 439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+s.m.

- 439738; BE246502; Hs.9598; sema domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing; blad, ovar, lung, headnk, test; s.m.
 440065; W03476; Hs.266331; Homo sapiens Fc receptor homol; mela; diag
 440304; BE159984; Hs.125395; hepatitis A virus cellular rec; renal, colon, blad; mAb+s.m.
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glio, ovar, uter, renal, hepC; mAb+diag
 440872; AF083811; Hs.7345; MAD1 (mitotic arrest deficient); mela; s.m.
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog; lung, blad, headnk, test, mela, esoph; s.m.
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane p; ovar, uter, mAb
 442275; AW449467; Hs.54795; Homo sapiens secretoglobulin, fa; fibro; diag
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; fibro, ovar, uter; CTL
 443105; X98753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag
 443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
 443324; R44013; Hs.164225; ESTs; fibro; mAb+diag
 443426; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL
 443595; AF169312; Hs.9613; PPAR(gamma) angiotensin relat; renal; diag
 443846; AI085198; Hs.164226; Thrombospondin 1; angio, panc, uter; diag
 443859; NM_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag
 443987; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.
 444006; BE395085; Hs.334762; type I transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb
 444090; S69115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag
 444371; BE540274; Hs.239; forkhead box M1; lung, headnk, blad, glio, test, mela; s.m.
 444381; BE387335; Hs.283713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, test, mela, esoph, sarc; CTL+diag
 444488; AW192879; Hs.355660; ancient conserved domain prota; renal; mAb+s.m.
 444527; NM_005408; Hs.11383; small inducible cytokine subfa; fibro, esoph; diag
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk, cerv; mAb+diag
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph; CTL+s.m.
 445417; AK001058; Hs.12680; a disintegrin-like and metallo; panc, headnk, stom, lung, esoph, sarc, colon; diag
 445537; AJ245871; Hs.12844; EGF-like domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag
 445891; AW391342; Hs.199460; DPCR1 protein; stom, panc, esoph, omuc, esoph; mAb
 445895; D29954; Hs.13421; KIAA0056 protein; pros; CTL
 446051; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
 446163; AA026880; Hs.25252; prolactin receptor; breast, cerv, uter; mAb+s.m.
 446341; AL040763; Hs.310735; FGENSEH prediction similar to; mela; mAb+s.m.
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag
 446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.
 446921; AB012113; Hs.16530; small inducible cytokine subfa; breast, panc, headnk, lung, fibro, mela; diag
 447033; AJ357412; Hs.157601; Predicted gene: Eos cloned; se; colon, pros, fibro, breast, ovar, lung, panc, sarc; CTL+diag
 447072; D61594; Hs.17279; tyrosylprotein sulfotransferas; glio, panc; CTL+s.m.
 447131; NM_004585; Hs.17466; retinoic acid receptor respond; renal, breast, stom, lung, mela, ovar; mAb+s.m.
 447208; BE315291; Hs.237971; hypothetical protein MGC5627; esoph, stom, colon; CTL+diag
 447269; NM_004861; Hs.17958; cerebroside (3'-phosphoadenyly; renal; CTL
 447342; AI199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, blad, pros, lung, stom, ovar; CTL
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.
 448243; AW369771; Hs.367688; Integrin, beta 8; ovar, uter, lung, stom, headnk, glio, panc; mAb+s.m.
 448610; NM_006157; Hs.21602; nel (chicken)-like 1; mela, sarc; diag
 448733; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.
 448844; AI581519; Hs.177164; FGENSEH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.
 449032; AA045573; Hs.22900; nuclear factor (erythroid-deri; colon, test, stom; CTL+s.m.
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glu; panc, ovar, uter, glio, headnk, lung, sarc; mAb
 449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.
 449720; AA311162; Hs.288708; hypothetical protein FLJ21562; colon; CTL
 449722; BE280074; Hs.23960; cyclin B1; headnk, blad, lung, panc, angio, test, mela, esoph; s.m.
 450001; NM_001044; Hs.408; solute carrier family 6 (neuro; renal; mAb+s.m.
 450375; AA009647; Hs.352537; a disintegrin and metalloprota; breast, ovar, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.
 450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL
 450701; H39960; Hs.288467; hypothetical protein XP_098151; lung, headnk, panc, breast, stom, ovar, esoph, colon, sarc; mAb+diag
 450726; AW204600; Hs.355462; HUMPSFBA Human pulmonary surf; fibro, lung; s.m.
 450931; N25156; Hs.25648; tumor necrosis factor receptor; lung, renal; mAb+s.m.
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; blad, lung, ovar, panc; diag
 451310; AW250651; Hs.26213; Human DNA sequence from clone; colon, panc; CTL
 451527; AF022813; Hs.265618; transmembrane 4 superfamily ms; renal; mAb
 451537; R56631; Hs.26550; retinoid X receptor, gamma; mela; CTL+s.m.
 451668; Z43948; Hs.326444; cartilage acidic protein 1; blad, ovar, lung; mAb+diag
 451939; U80456; Hs.27311; single-minded (Drosophila) hom; pros; CTL
 451979; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
 451988; AF263928; Hs.27410; papillomavirus regulatory fact; renal; CTL
 452017; AF109302; Hs.27495; prostate cancer associated pro; pros; s.m.
 452097; AB002364; Hs.27916; a disintegrin-like and metallo; ovar; mAb+s.m.+diag
 452190; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast, stom, panc; mAb
 452194; AI694413; Hs.373599; olfactory receptor, family 2; ; stom, panc, renal, colon, mela, fibro; mAb+s.m.
 452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast, headnk, panc, stom, lung, esoph, fibro; diag
 452401; NM_007116; Hs.29352; tumor necrosis factor, alpha-k; blad, breast, panc, headnk, stom, lung, leuk, renal, esoph; diag
 452431; U88879; Hs.29499; toll-like receptor 3; renal, hepC; mAb
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung, headnk, ovar, stom, uter, panc; mAb
 452838; U65011; Hs.30743; preferentially expressed antig; lung, ovar, breast, mela, test, esoph, renal, sarc; CTL
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag
 453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL
 453496; AA442103; Hs.33084; solute carrier family 2 (facil; renal, pros; mAb+s.m.

453837; AL138387; Hs.256126; baculoviral IAP repeat-contain; renal, mela, sarc; s.m.
 453968; AA847843; Hs.62711; High mobility group (nonhistone); lung, uter, blad, test; CTL+s.m.
 456546; AJ690321; Hs.203845; KCNK15 potassium channel, sub; ovar; mAb+s.m.
 456662; NM_002448; Hs.1494; msh (Drosophila) homeo box hom; uter, ovar; CTL
 457133; M54968; Hs.351221; v-KI-ras2 Kirsten rat sarcoma; panc; s.m.
 457489; AJ693815; Hs.127179; cryptic gene; panc, pros, lung; diag
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein; lung, cerv, headnk; mAb+diag
 458079; AI796870; Hs.381220; Homo sapiens similar to RIKEN; mela, fibro, sarc; mAb
 458627; AW088642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

TABLE 2B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
402901	8894222	Minus	175426-175667
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

Table 3A provides preferred disease indications and preferred utilities for about 2709 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number
 UnigenelD: Unigene ID number
 Unigene Title: Unigene gene title
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenelD; Unigene Title; Disease; Utility

100125; R02740; Hs.137555; putative chemokine receptor; G; blad; mAb+s.m.
 100131; D12485; Hs.11951; ectonucleotide pyrophosphatase; breast; mAb
 100147; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc; mAb+diag
 100241; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; blad; mAb
 100299; D49493; Hs.2171; growth differentiation factor; EWS; diag
 100335; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 100365; AI878927; Hs.79284; mesoderm specific transcript (); colon, pros; diag
 100372; NM_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.
 100405; AW291587; Hs.82733; nidogen 2; angio; diag
 100420; D86983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, angio, leuk; diag
 100448; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G; breast; mAb+s.m.
 100452; D87742; Hs.241552; KIAA0268 protein; pros; diag
 100559; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e); lung; CTL+s.m.
 100654; A03768; Hs.184411; NM_000477; Homo sapiens albumin; pros; diag
 100655; A03758; Hs.184411; Empirically selected from AFFX; pros; diag
 100668; L05424; Hs.169610; CD44 antigen (homing function); lung, breast; mAb
 100824; AI393237; Hs.193989; runt-related transcription fac; ovar; CTL+s.m.
 100930; J04129; Hs.82269; progesterone-associated endomet; lung; diag
 101053; D54745; Hs.80247; cholecystokinin; pros, EWS; diag
 101097; BE245301; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.
 101104; AW862258; Hs.199268; neuropeptide Y receptor Y1; breast, EWS; mAb
 101192; BE247295; Hs.78452; solute carrier family 20 (phos); angio; mAb+s.m.
 101193; L20861; Hs.152213; wingless-type MMTV integration; blad, lung; diag
 101249; L18964; Hs.1904; protein kinase C, iota; ovar; s.m.

- 101261; D30857; Hs.82353; protein C receptor, endothelial; angio; mAb+s.m.
 101389; AW951430; Hs.78888; diazepam binding inhibitor (GA); pros; mAb+s.m.
 101431; BE185289; Hs.1076; small proline-rich protein 18; lung, blad; diag
 101447; M21305; ; gb:Human alpha satellite and s; angio, blad; diag
 101461; N98569; Hs.76422; phospholipase A2, group IIA (p); pros; diag
 101485; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, ovar; mAb
 101506; J02931; Hs.62192; coagulation factor III (thromb; pros; mAb
 101526; NM_002197; Hs.220529; aconitase 1, soluble; lung, colon, headnk, panc; mAb
 101543; M31168; Hs.2050; pentaxin-related gene, rapidly; angio, ovar; diag
 101545; BE246154; Hs.154210; endothelial differentiation, s; angio; mAb+s.m.
 101560; AW958272; Hs.347326; Inter cellular adhesion molecucl; angio; mAb
 101626; M57399; Hs.44; pleiotrophin (heparin binding; lung; diag
 101649; AW959908; Hs.1690; heparin-binding growth factor; lung, blad; diag
 101714; M68874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.
 101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (c; breast, pros, blad, lung; mAb+CTL
 101741; NM_003199; Hs.326188; transcription factor 4; angio; CTL+s.m.
 101748; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, cerv; mAb
 101759; M80244; Hs.184601; solute carrier family 7 (catio; lung, glio, blad, headnk; mAb+s.m.
 101791; M83822; Hs.62354; cell division cycle 4-like; pros; s.m.
 101804; M86699; Hs.169840; TTK protein kinase; ovar, lung, blad, cerv; CTL+s.m.
 101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag
 101809; M86849; Hs.323733; gap junction protein, beta 2, ; colon, blad, lung, panc, headnk; mAb
 101839; AA446644; Hs.692; GA733-2 antigen; epithelial gt; ovar, pros; mAb
 101845; U88967; Hs.78867; protein tyrosine phosphatase, ; lung, glio, headnk, cerv; mAb+s.m.
 101851; BE260964; Hs.82045; midkine (neurtle growth-promot; lung, blad, ovar, breast, panc; mAb+diag
 102009; BE245149; Hs.82643; protein tyrosine kinase 9; ovar; s.m.
 102012; BE259035; Hs.118400; singed (Drosophila)-like (sea; angio; diag
 102024; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.
 102125; NM_006456; Hs.288215; slatyltransferase; breast, lung, ovar; s.m.
 102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag
 102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 102154; U17760; Hs.75517; laminin, beta 3 (nicel (125kD; lung, blad, headnk; diag
 102178; AW178761; Hs.227948; serine (or cysteine) proteinas; blad; mAb+diag
 102187; U20325; Hs.1707; cocaine- and amphetamine-regu; breast; diag
 102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; ovar, lung, fibro; diag
 102200; AA232362; Hs.317432; branched chain aminotransferas; ovar; s.m.
 102208; U22961; Hs.184411; gb:Human mRNA clone with simil; pros; diag
 102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb
 102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.
 102297; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 102304; AF015224; Hs.46452; mammaglobin 1; breast; diag
 102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; ovar, lung, blad; diag
 102348; U37519; Hs.87539; aldehyde dehydrogenase 3 fami; lung, blad; s.m.
 102360; U40434; Hs.155981; mesothelin; ovar; diag
 102394; NM_003816; Hs.2442; a disintegrin and metalloprote; panc; s.m.
 102455; U48705; Hs.75562; discoidin domain receptor fami; breast; mAb
 102457; NM_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.
 102522; BE250944; Hs.183558; solute carrier family 1 (neut; pros; mAb
 102581; AU077228; Hs.77256; enhancer of zeste (Drosophila); blad, EWS, leuk; CTL+s.m.
 102610; U65011; Hs.30743; preferentially expressed antig; lung, ovar; CTL
 102623; AW249285; Hs.37110; melanoma antigen, family A, 9; lung, blad; mAb+CTL
 102669; U71207; Hs.29279; eyes absent (Drosophila) homot; lung, pros; CTL+s.m.
 102696; BE540274; Hs.239; forkhead box M1; lung, blad; s.m.
 102726; AB026187; Hs.374280; protocadherin 11; EWS; mAb
 102742; U79293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar; diag
 102745; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 102803; H48299; Hs.26126; claudin 10; ovar; mAb
 102829; NM_006183; Hs.80962; neurotensin; lung, ovar, headnk; diag
 102836; U94320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb
 102852; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 102898; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+s.m.
 102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.
 102917; AJ016712; Hs.287797; Integrin, beta 1 (fibronectin; angio; mAb
 102927; BE512730; Hs.65114; keratin 18; ovar; diag
 102968; AU076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.
 102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 103003; AJ910275; Hs.350470; trefol factor 1 (breast cancer; breast, panc; diag
 103021; BE001596; Hs.85266; integrin, beta 4; lung blad; mAb
 103038; M13509; Hs.83169; matrix metalloproteinase 1 (ln; angio, colon, blad, lung, leuk, ovar, headnk, fibro, panc, stom; mAb+diag+s.m.
 103037; BE018032; Hs.2894; placental growth factor, vascul; angio; diag
 103060; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, ovar, panc; mAb+diag+s.m.
 103080; AU077231; Hs.82932; cyclin D1 (PRAD1; parathyroid; breast, EWS; diag
 103095; NM_005424; Hs.78824; tyrosine kinase with Immunoglo; angio; mAb
 103111; NM_006103; Hs.2719; epididymis-specific, whey-acid; ovar, uter; diag
 103119; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag
 103206; X72755; Hs.77367; monocline induced by gamma inte; breast, lung; diag
 103210; X72925; Hs.69752; desmocollin 1; pros; mAb
 103280; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin; angio, fibro; mAb+s.m.
 103299; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; mAb+s.m.
 103312; Y12642; Hs.3185; lysosomal; lung, blad; mAb
 103365; X90908; Hs.74126; fatty acid binding protein 6, ; blad; diag

- 103408; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnk; diag
 103587; BE270266; Hs.82128; ST4 oncofetal trophoblast glyco; breast, blad, lung; mAb
 103594; AJ368680; Hs.816; SRY (sex determining region Y); lung, glio; s.m.
 103692; AW137912; Hs.227583; Homo sapiens chromosome X map; angio; mAb+s.m.
 103739; AA115173; gb:zn30d02.s1 Stragene neuro; pros; s.m.
 103767; BE244667; Hs.348996; CGI-100 protein; angio; diag
 103989; AA315993; Hs.105484; regenerating gene type IV; colon, omuc; mAb+diag
 104052; NM_002407; Hs.97644; mammaglobin 2; ovar; diag
 104115; AF183810; Hs.26102; opposite strand of: trichorh; breast; mAb
 104252; AF002246; Hs.210863; cell adhesion molecule with ho; ovar; diag
 104301; AA768491; Hs.6783; hypothetical protein FLJ22724; ovar; diag
 104308; N25117; Hs.355957; ribosomal protein S26; pros; diag
 104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 f; colon; diag
 104542; R29657; gb:F1-1179D 22 week old human; pros; diag
 104608; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb
 104659; AW969769; Hs.100343; ESTs; EWS; diag
 104660; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; uter, colon, pros; mAb
 104667; AJ239923; Hs.63931; dachshund (Drosophila) homolog; breast, pros, colon; diag
 104689; AA420450; Hs.380068; Plakophilin; lung; diag
 104691; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag
 104764; AI039243; Hs.278585; ESTs; angio; diag
 104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.
 104877; AI136635; Hs.22968; intron of VEGFR; renal; diag
 104886; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter, mAb+s.m.
 104919; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 f; breast, cerv, uter; mAb+s.m.
 104943; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar; mAb+s.m.
 104954; AW250651; Hs.26213; Human DNA sequence from clone; colon; diag
 104971; BE311926; Hs.15830; hypothetical protein FLJ12691; blad; CTL
 105012; AF081158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad; CTL
 105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.
 105039; AA907305; Hs.36475; ESTs; breast; diag
 105093; AL137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 105149; BE089288; Hs.8958; Homo sapiens cDNA FLJ12024 f; pros; diag
 105175; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb
 105263; AW388633; Hs.6682; solute carrier family 7, (cat; angio, lung, ovar, blad, panc; mAb+s.m.
 105298; BE387790; Hs.26369; hypothetical protein FLJ20287; ovar, lung; diag
 105301; AW352357; Hs.7457; MAGE1 protein; EWS; diag
 105316; AI671245; Hs.24835; hypothetical protein FLJ14594; EWS; mAb
 105328; AA234561; Hs.22862; ESTs; breast, pros; CTL+s.m.
 105330; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 105370; AF179274; Hs.22791; transmembrane protein with EGF; pros; mAb+s.m.
 105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag
 105503; AW963624; Hs.31707; ESTs, Weakly similar to YEW4_Y; pros, breast, colon; CTL+s.m.
 105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag
 105516; AK001269; Hs.30738; hypothetical protein FLJ10407; ovar; diag
 105564; BE616694; Hs.288042; hypothetical protein FLJ14299; breast; diag
 105645; AW294631; Hs.351270; ESTs; pros; diag
 105715; BE621800; Hs.29444; putative small membrane protei; colon; diag
 105743; BE245502; Hs.8598; sema domain, immunoglobulin do; breast, lung; mAb+s.m.
 105746; AW151952; Hs.46879; hypothetical protein FLJ20739; breast; CTL+s.m.
 105777; R42755; Hs.23096; ESTs; breast; diag
 105782; H09748; Hs.57987; B-cell CLL/lymphoma 11B (zinc; EWS; CTL+s.m.
 105826; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.
 105990; AI690586; Hs.29403; hypothetical protein FLJ22060; breast; diag
 106000; AW194426; Hs.20728; ESTs; breast; diag
 106012; AI240665; Hs.352537; ESTs; breast, lung; diag
 106014; AF123094; Hs.180566; mucosa associated lymphoid tis; leuk; diag
 106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag
 106066; AW274357; Hs.301406; hypothetical protein PP3501; mel; CTL+s.m.
 106111; AW875398; Hs.6451; PRO0659 protein; EWS; CTL+s.m.
 106124; H93366; Hs.7567; branched chain aminotransferase; angio; s.m.
 106155; AA425414; Hs.33287; nuclear factor I/B; breast, pros, angio; diag
 106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.
 106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 f; colon; diag
 106414; BE568205; Hs.28827; mitogen-activated protein kina; breast; s.m.
 106448; Z42061; Hs.27004; ESTs; pros; diag
 106533; AL134708; Hs.145998; ESTs; EWS; diag
 106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag
 106579; AA456135; Hs.23023; ESTs; pros; diag
 106632; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk; mAb+diag
 106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 f; ovar; diag
 106793; H94997; Hs.16450; ESTs; angio; diag
 106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL
 106908; AA881271; Hs.222024; transcription factor BMAL2; lung, blad; diag
 106990; AA280722; Hs.24758; ESTs, Weakly similar to I38022; breast; diag
 107036; AI973016; Hs.15725; hypothetical protein SBB148; pros; diag
 107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag
 107105; AW963419; Hs.155223; stannocalcin 2; breast; diag
 107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag
 107151; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; breast, colon, leuk, lung, blad; mAb+diag
 107216; D51069; Hs.211579; melanoma cell adhesion molecule; angio; diag

- 107248; AW263124; Hs.350547; nuclear receptor co-repressor; breast, colon, pros; mAb+s.m.
 107284; NM_005629; Hs.187958; solute carrier family 6 (neuro); lung; mAb+s.m.
 107385; NM_005397; Hs.16426; podocalyxin-like; angio; diag
 107901; L42612; Hs.335952; keratin 6B; breast, blad, lung; diag
 107922; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung; mAb
 107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL
 108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag
 108059; S69002; Hs.234773; Homo sapiens cDNA: FLJ22281 f; ovar; CTL+s.m.
 108153; AW519204; Hs.40808; ESTs; pros; diag
 108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 108242; AA062746; Hs.355244; gbzm03g12.s1 Stratagene come; pros; diag
 108282; AA065142; gbzm50h11.r1 Stratagene fibro; pros; diag
 108505; AA083376; gbzm09g08.s1 Stratagene hnt r; pros; diag
 108679; AA115963; Hs.323423; ESTs, Moderately similar to B; pros; diag
 108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag
 108732; AA258888; Hs.107476; ATP synthase, H⁺ transporting.; pros; s.m.
 108778; AF133123; Hs.90847; general transcription factor I; ovar; diag
 108828; AK001693; Hs.273344; DKFZP564O0463 protein; breast; diag
 108860; AA133334; Hs.816; ESTs; lung; s.m.
 109001; AI056548; Hs.72116; hypothetical protein FLJ20992; angio; CTL+diag
 109032; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 109077; AJ732617; Hs.182362; ESTs; blad; diag
 109112; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 109141; AF174600; Hs.6978; ESTs, Highly similar to AF1746; colon; CTL+s.m.
 109166; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, breast, colon, ovar, headnk, EWS; s.m.
 109220; AW958181; Hs.189998; ESTs; pros; diag
 109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag
 109292; AW975746; Hs.188662; KIAA1702 protein; breast; diag
 109454; AA232255; Hs.295232; ESTs, Moderately similar to A4; ovar; diag
 109456; AW956580; Hs.42699; ESTs; angio, panc; diag
 109514; AA234087; Hs.262346; ESTs, Weakly similar to S72482; breast; diag
 109530; AA908645; Hs.19597; KIAA1694 protein; pros; CTL+s.m.
 109648; H17800; Hs.7154; ESTs; ovar; diag
 109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag
 110009; BE075297; Hs.6614; ESTs, Weakly similar to A43932; breast, colon; diag
 110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros, EWS; diag
 110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 110240; AI668594; Hs.176588; ESTs, Weakly similar to CP4Y_H; breast; diag
 110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.
 110675; H89355; Hs.249159; adrenergic, alpha-2A-, receptor; pros; mAb+s.m.
 110728; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 110844; AT740792; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
 110915; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag
 110971; AT760098; Hs.21411; ESTs; pros; diag
 111157; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 111179; AK000136; Hs.10760; asporin (LRR class 1); breast, colon; CTL+s.m.
 111185; AJ245671; Hs.12844; EGF-like domain, multiple 6; ovar, blad; mAb+diag
 111223; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, EWS; mAb
 111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag
 111357; BE314949; Hs.87128; hypothetical protein FLJ23309; breast; diag
 111364; N94606; Hs.288969; HSCARG protein; breast; diag
 111900; AF131784; Hs.25318; Homo sapiens clone 25194 mRNA; breast; diag
 111929; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 112134; R41823; Hs.7413; ESTs; catyntenin-2; breast, EWS; diag
 112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag
 112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty; breast; s.m.
 112283; L14561; Hs.20952; ATPase, Ca⁺⁺ transporting, pla; ovar; mAb
 112287; AB033084; Hs.236463; KIAA1238 protein; breast; diag
 112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.
 113003; AW292315; Hs.7215; ESTs; EWS; diag
 113021; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 113047; AJ571940; Hs.7549; ESTs; breast, colon; diag
 113073; N39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.
 113168; AW002393; Hs.337629; gbzwu61d05.x1 NCL-OGAP_GC8 Hom; ovar; diag
 113185; H83265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag
 113230; T61430; gbzc06a03.s1 Stratagene lung; blad; diag
 113361; T79589; Hs.83325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 113374; T79525; Hs.269165; ESTs, Weakly similar to ALU1_H; leuk; diag
 113443; AW083920; Hs.16098; claudin 2; colon, panc; mAb
 113471; AJ765890; Hs.16341; MAWD binding protein; pros; diag
 113490; BE181110; Hs.173374; Homo sapiens cDNA FLJ10500 f; colon; diag
 113950; AJ287652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros; diag
 113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 114124; W57554; Hs.125019; lymphoid nuclear protein (LAF-; breast; diag
 114251; H15281; Hs.21948; ESTs; breast; diag
 114292; AI815395; Hs.184841; fatty acid desaturase 2; breast; s.m.
 114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag
 114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag
 114452; AJ369275; Hs.243010; Homo sapiens cDNA FLJ14445 f; angio; diag
 114480; BE068778; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 114540; AJ904232; Hs.75323; prohibitin; breast; diag
 114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus t; breast, pros; diag

- 114587; AF086009; Hs.296398; gb:Homo sapiens full length tnc colon; diag
 114724; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) h; ovar; CTL+s.m.
 114768; AF212848; Hs.182339; ets homologous factor; pros; breast; colon; CTL+s.m.
 114798; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.
 5 114908; AA454985; Hs.54973; cadherin-like protein VR20; pros; diag
 114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag
 114965; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb
 115060; AF052693; Hs.198249; gap junction protein, beta 5 (c); lung, blad, headnk; mAb+s.m.
 10 115221; AW365434; Hs.79741; hypothetical protein FLJ10116; ovar; diag
 115239; BE251328; Hs.73291; hypothetical protein FLJ10881; colon; diag
 115291; BE545072; Hs.122579; hypothetical protein FLJ10461; ovar; lung; CTL+s.m.
 115412; AW131168; Hs.372382; ESTs, Weakly similar to I38022; pros; diag
 115536; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon; CTL+s.m.
 15 115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.
 115875; W87707; Hs.82065; interleukin 6 signal transduce; breast; pros; mAb+s.m.
 115683; AF255910; Hs.54650; junctional adhesion molecule 2; angio, glior; mAb
 115697; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 115719; AW992405; Hs.352406; Homo sapiens, clone IMAGE:3507; pros; breast; colon; CTL+s.m.
 20 115819; AA486620; Hs.41135; endomucin-2; angio; diag
 115827; AA428000; Hs.283072; actin related protein 2/3 comp; angio; diag
 115844; AI373062; Hs.332938; hypothetical protein MGC5370; pros; diag
 115881; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 115892; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
 25 115909; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung; diag
 115947; R47479; Hs.94761; KIAA1691 protein; colon; diag
 115978; AL035864; Hs.69517; cDNA for differentially expres; lung, blad, breast, pros, ovar, headnk; CTL
 116003; BE275469; Hs.66493; Down syndrome critical region; colon; mAb
 116011; AL359053; Hs.57684; Homo sapiens mRNA full length; breast; diag
 30 116028; H59799; Hs.42644; thioredoxin-like; ovar, lung; diag
 116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 116202; BE159395; Hs.294092; ESTs; pros; diag
 116238; AV660717; Hs.47144; DKFZP586N0819 protein; ovar; diag
 116301; AW969706; Hs.293332; ESTs; EWS; diag
 35 116334; AL038450; Hs.48948; ESTs; pros; diag
 116335; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk; diag
 116393; AI972402; Hs.306051; hypothetical protein MGC2648; pros; diag
 116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.
 116401; AW893940; Hs.59698; ESTs; ovar; diag
 40 116416; AW753676; Hs.39982; ESTs; ovar; diag
 116470; AI272141; Hs.351928; SRY (sex determining region Y); colon, breast, angio, blad; diag
 116483; AI346201; Hs.76118; ubiquitin carboxyl-terminal es; angio, lung; s.m.
 116610; D80449; Hs.184841; ESTs; pros; diag
 116732; AW152225; Hs.165909; ESTs, Weakly similar to I38022; colon; diag
 45 116787; AW362955; Hs.356547; Homo sapiens cDNA FLJ14415 fis; pros, breast, colon, pros; mAb
 116962; H79677; ; gbyu76g10.s1 Soares fetal liv; pros; diag
 117027; AW085208; Hs.130093; ESTs; breast; diag
 117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; breast, colon, pros; diag
 117284; AK001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag
 50 117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung; mAb+diag
 117367; AI041793; Hs.42502; ESTs; breast; diag
 117412; N32536; Hs.42645; solute carrier family 16 (mono; breast, ovar; mAb+s.m.
 117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 117563; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk; diag
 55 117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.
 117821; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros; diag
 117884; AF189723; Hs.106778; ATPase, Ca++ transporting, typ; pros, breast, colon; mAb
 118049; N53145; ; gbyv55f09.s1 Soares fetal liv; pros; diag
 118314; N48580; Hs.46692; ESTs; blad, lung; diag
 60 118336; BE327311; Hs.47166; HT021; breast, ovar, blad, pros; CTL+s.m.
 118368; N64339; Hs.48958; gap junction protein, beta 6 (c); lung, blad; mAb
 118417; AF080229; ; gb:Human endogenous retrovirus; pros; s.m.
 118472; AL157545; Hs.173179; bromodomain end PHD finger con; breast; diag
 118511; N75620; Hs.43157; ESTs; angio; diag
 65 118901; AW292577; Hs.94445; ESTs; breast; diag
 118905; AW973708; Hs.201825; Homo sapiens cDNA FLJ13446 fis; breast; diag
 119018; AA631143; Hs.278695; Homo sapiens protein mRNA, cor; pros, pros; diag
 119036; R95872; Hs.117572; chemokine binding protein 2; breast, ovar; mAb
 119073; BE245360; Hs.45514; v-ets erythroblastosis virus E; angio, pros; CTL+s.m.
 70 119082; AF252297; Hs.91546; cytochrome P450 retinoid metab; EWS; diag
 119126; R45175; Hs.117183; ESTs; pros, breast, colon; diag
 119279; N57668; Hs.48028; EST; breast; diag
 119307; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
 119478; AI624342; Hs.179082; ESTs; breast; diag
 75 119617; AA516531; Hs.55999; NK homeobox (Drosophila), famt; pros; diag
 119743; AA947552; Hs.58088; branched chain aminotransferas; ovar; s.m.
 119771; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast; diag
 119780; NM_016625; Hs.191381; hypothetical protein; ovar, lung; CTL+s.m.
 119789; BE393948; Hs.50915; kallikrein 5; ovar; diag
 80 119845; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv; mAb+s.m.
 119940; AL050097; Hs.272531; DKFZP586B0319 protein; pros; diag
 120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, lung; diag
 120132; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 120147; AI917116; Hs.348941; hemoglobin, beta; EWS; diag

- 120206; H26735; Hs.91668; Homo sapiens clone PP1498 unkn; breast; mAb
 120242; AW969587; Hs.86366; ESTs; blad; diag
 120328; AA923278; Hs.290905; ESTs, Weakly similar to proteas; pros; s.m.
 120438; AW015242; Hs.99488; ESTs, Weakly similar to YK54_Y; ovar; diag
 120471; AA251944; Hs.104058; CG-29 protein; colon; diag
 120486; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk; diag
 120588; AA703226; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 120624; AW407987; Hs.173518; M-phase phosphoprotein homolog; breast; s.m.
 120830; AI568170; Hs.96886; ESTs; EWS; diag
 120977; AA398155; Hs.97600; ESTs; breast, ovar; diag
 121027; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 f; blad; mAb
 121231; AA814948; Hs.96343; ESTs, Weakly similar to ALUC_H; EWS; diag
 121335; AA404418; ; gbzw37e02.s1 Soares_tota_fet; angio; diag
 121362; AF050147; Hs.97932; chondromodulin I precursor; EWS; mAb
 121457; W07404; Hs.102558; hypothetical protein FLJ22055; colon; diag
 121619; AA528339; Hs.178062; ESTs, Weakly similar to phosph; EWS; s.m.
 121710; AF163474; Hs.96744; prostate androgen-regulated tr; pros; diag
 121721; AL047051; Hs.199961; ESTs, Weakly similar to ALU7_H; pros; diag
 121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag
 121748; BE536911; Hs.234545; hypothetical protein NUF2R; breast; diag
 121779; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
 121791; AA815378; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar; mAb+CTL
 121792; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
 121913; AI249368; Hs.98558; ESTs; protease inhibitor 15 (; breast, pros; s.m.
 121920; AA428300; ; gbzw18e02.s1 Soares ovary tum; ovar, uter, cerv; diag
 122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 122520; AW951324; Hs.173609; pregnancy specific beta-1-glyc; colon; diag
 122797; AJ251027; Hs.99526; odorant-binding protein 2B (OB; breast; diag
 122802; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter; mAb+s.m.
 122969; AW821252; Hs.104338; hypothetical protein; ovar; diag
 123005; AW369771; Hs.367688; Integrin, beta 8; ovar, lung, headnk, gli; mAb+s.m.
 123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc ; lung; diag
 123137; AJ073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag
 123158; AF161426; Hs.218329; hypothetical protein; breast; diag
 123160; AA488687; Hs.284235; ESTs, Weakly similar to I38022; lung; diag
 123169; AI950087; Hs.369628; gbzwq05c02.x1 NCL_CGAP_Kid12 H; ovar; diag
 123209; AW968543; Hs.203270; ESTs, Weakly similar to ALU1_H; pros; diag
 123308; C14187; Hs.157208; ESTs; EWS; diag
 123339; AW188464; Hs.101515; ESTs; ovar; diag
 123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag
 123494; AW179019; Hs.112110; mitochondrial ribosomal protein; ovar; diag
 123520; AA608550; ; gbzrae53d12.s1 Stratagene lung ; pros; s.m.
 123533; AA608751; ; gbzrae56h07.s1 Stratagene lung ; colon; diag
 123619; AA602964; Hs.366318; gbzno97c02.s1 NCL_CGAP_Py2 Hom; breast; CTL+s.m.
 123689; AA399323; Hs.285130; Homo sapiens pinch-2 protein m; ovar; diag
 123709; AA706910; Hs.112742; ESTs; breast; diag
 123829; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL
 123972; I46848; Hs.70337; immunoglobulin superfamily, me; ovar; diag
 124008; AI147155; Hs.279727; ESTs; homologue of PEM-3 (Cion; breast, angio, lung, ovar, EWS; diag
 124059; BE387335; Hs.283713; ESTs, Weakly similar to S64054; breast, colon, blad, lung; CTL+diag
 124153; AU077333; Hs.160483; erythrocyte membrane protein b; pros; mAb
 124352; AA640891; Hs.102406; ESTs; breast, pros, ovar, lung; diag
 124528; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros; mAb+s.m.
 124579; AI693815; Hs.127179; cryptic gene; panc; diag
 124777; R41933; Hs.140237; ESTs, Weakly similar to ALU1_H; pros, breast; diag
 125103; AA570056; Hs.122730; ESTs, Moderately similar to Ki; colon; mAb
 125154; W38419; ; gbzcg78e07.s1 Pancreatic islet; ovar; diag
 125250; W26524; Hs.356686; protein phosphatase 4 regulato; ovar; CTL+s.m.
 125266; W90022; Hs.186809; ESTs, Highly similar to LCT2_H; angio; diag
 125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL
 125666; AL390172; Hs.317432; Homo sapiens cDNA: FLJ21270 f; ovar; diag
 125770; AA143045; Hs.81665; v-kil Hardy-Zuckerman 4 feline; EWS; diag
 125976; AA436760; Hs.35552; gbzcv67d11.r1 Soares_tota_fet; pros; diag
 126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 126645; AA316181; Hs.61635; sbx transmembrane epithelial a; pros, breast, lung, panc, headnk, EWS; mAb+CTL
 126758; AI559444; Hs.104678; ESTs; pros, breast; mAb
 126799; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 126872; AW450979; ; gbzU1-H-B13-ela-e-12-0-U1.s1 N; blad; diag
 126892; AF121856; Hs.284291; sorting nexin 6; ovar; diag
 126960; AL390172; Hs.317432; branched chain aminotransferas; ovar; s.m.
 126966; R38438; Hs.118747; solute carrier family 15 (H+); pros; mAb
 127003; AW816515; Hs.173540; ATPase, Class V, type 10D; pros; mAb
 127221; BE062109; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv; mAb+s.m.
 127240; AJ005683; Hs.86998; nuclear factor of activated T-; pros; CTL+s.m.
 127425; AF183810; Hs.26102; trichorhinophalangeal syndrome; breast; mAb
 127479; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc; diag
 127537; AI926047; Hs.162859; ESTs; pros; diag
 127664; AA806164; Hs.116502; ESTs; EWS; diag
 128046; AA873285; Hs.357313; gbzoh68h05.s1 NCL_CGAP_Kid5 Ho; pros, breast, colon; diag
 128305; AI954968; Hs.365706; matrix Gla protein; breast; diag
 128478; AA708205; Hs.100343; ESTs; EWS; CTL+s.m.
 128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb
 128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast, CTL+s.m.

- 128510; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag
 128734; AB008390; Hs.104570; kalikrein 8 (neurosin/ovasin; ovar; diag
 128780; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, uter, panc; diag
 128797; NM_002975; Hs.105927; stem cell growth factor; lymph; EWS, leuk; diag
 128854; BE159181; Hs.168232; hypothetical protein FLJ13855; breast; diag
 128925; R67418; Hs.21851; Homo sapiens cDNA FLJ12900 fis; breast; diag
 128949; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.
 128969; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, cont; pros; diag
 129041; BE382756; Hs.169902; solute carrier family 2 (facil; lung, blad; mAb+s.m.
 129097; BE243933; Hs.108642; zinc finger protein 22 (KOX 15; ovar; CTL+s.m.
 129099; AF146074; Hs.108660; ATP-binding cassette, sub-fam; lung, blad, headnk; mAb+s.m.
 129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 129260; AF077200; Hs.279813; hypothetical protein; colon; diag
 129284; AA318224; Hs.296141; ESTs; colon; diag
 129362; U30246; Hs.110736; solute carrier family 12 (sodi; colon, breast, pros; mAb
 129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA; breast; diag
 129389; NM_012445; Hs.288126; spondin 2, extracellular mat; colon, pros; diag
 129404; AJ267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag
 129466; L42583; Hs.334309; keratin 6A; lung, blad; diag
 129482; AA188185; Hs.289043; spindlin; breast; diag
 129534; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 129571; X51630; Hs.1145; Wilms tumor 1; ovar; CTL+s.m.
 129605; AF061812; Hs.115947; keratin 16 (focal non-epidermo; lung, blad, headnk; diag
 129620; D79338; Hs.239720; CCR4-NOT transcription complex; breast, angio; diag
 129628; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk; s.m.
 129650; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 129689; AW748482; Hs.77873; 67 homolog 3; breast; diag
 129703; BE386665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag
 129720; AA156214; Hs.12152; APMCF1 protein; breast; diag
 129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.
 129869; AJ222069; Hs.13015; hypothetical protein similar t; breast; diag
 129912; AF155096; Hs.107213; hypothetical protein FLJ20585; ovar; CTL+s.m.
 129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag
 129953; AA412195; Hs.13740; ESTs; breast; diag
 129977; NM_000399; Hs.1395; early growth response 2 (Krox-; EWS; CTL+s.m.
 130010; AA301116; Hs.142838; nucleolar phosphoprotein Nopp3; ovar; diag
 130057; AF027153; Hs.324787; solute carrier family 5 (nosk; breast; mAb
 130095; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 130181; AF052119; Hs.151608; Homo sapiens clone 23622 mRNA; pros; diag
 130184; H58306; Hs.15165; retinoic acid induced 14; angio; diag
 130262; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
 130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag
 130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.
 130385; AW067800; Hs.155223; stannocalcin 2; breast, lung; mAb+diag
 130455; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 130511; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar; diag
 130558; BE564937; Hs.15984; pp21 homolog; pros; CTL+s.m.
 130577; M69241; Hs.162; insulin-like growth factor bin; ovar; diag
 130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.
 130627; BE003054; Hs.1695; matrix metalloproteinase 12 (m; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.
 130637; AA356764; Hs.17109; Integral membrane protein 2A; EWS; mAb+s.m.
 130648; AJ458165; Hs.17296; hypothetical protein MGC2376; colon; diag
 130667; BE246961; Hs.17639; Homo sapiens ubiquitin protein; breast; s.m.
 130690; AB006625; Hs.139033; paternally expressed 3; ovar; diag
 130714; AJ348274; Hs.18212; DNA segment on chromosome X (u; breast; diag
 130760; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 130800; AJ187292; Hs.19574; hypothetical protein MGC5469; colon, lung; diag
 130839; AB011169; Hs.380875; similar to S. cerevisiae SSM4; angio; diag
 130844; U76248; Hs.20191; seven in absentia (Drosophila); breast; diag
 130892; AL120837; Hs.20993; high-glucose-regulated protein; breast, CTL+s.m.
 130941; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
 130967; AA393071; Hs.182579; leucine aminopeptidase; ovar; s.m.
 130972; D81886; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 130987; BE613269; Hs.21893; hypothetical protein DKFZp761N; colon; diag
 131046; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, fibro; diag
 131080; NM_001955; Hs.2271; endothelin 1; angio; diag
 131083; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb
 131148; AW953576; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag
 131216; AI815486; Hs.243901; Homo sapiens cDNA FLJ20738 fis; colon, breast; diag
 131228; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag
 131244; AI638429; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.
 131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag
 131289; AA296696; Hs.333418; FYD domain-containing ion tra; colon; diag
 131307; NM_000025; Hs.2549; adrenergic, beta-3-, receptor; EWS; mAb
 131313; R96290; Hs.75874; ribosomal protein L44; EWS; diag
 131492; AJ452601; Hs.288869; nuclear receptor subfamily 2; pros; mAb+s.m.
 131544; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 131559; AL078599; Hs.10784; hypothetical protein FLJ20037; breast; diag
 131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast; diag
 131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.
 131643; AW410601; Hs.30026; HSPC182 protein; breast; diag
 131739; AF017986; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

- 131817; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio; s.m.
 131885; BE502341; Hs.3402; ESTs; breast; diag
 131919; T15803; Hs.272458; protein phosphatase 3 (former); pros; breast; s.m.
 131925; AF151048; Hs.183180; anaphase promoting complex sub; breast; diag
 131965; W79283; Hs.35962; ESTs; lung, ovar; diag
 131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 132050; AJ267615; Hs.38022; ESTs; angio; diag
 132173; X89426; Hs.41716; endothelial cell-specific mole; angio; diag
 132180; NM_004460; Hs.418; fibroblast activation protein; colon, panc, esoph; mAb
 132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22696 f; ovar; diag
 132349; AW975654; Hs.181286; serine protease inhibitor, Kaz; pros; blad; s.m.
 132354; BE185289; Hs.1076; small proline-rich protein 18; lung; diag
 132358; NM_003542; Hs.46423; H4 histone family, member G; pros; CTL+s.m.
 132371; AA235448; Hs.222088; PRO2000 protein; breast; diag
 132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.
 132490; NM_001290; Hs.4980; LIM domain binding 2; angio; diag
 132520; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 132528; T78736; Hs.50758; SMC4 (structural maintenance 4; ovar; CTL+s.m.
 132543; BE568452; Hs.344037; protein regulator of cytokines; colon, lung; diag
 132572; A1929659; Hs.237825; signal recognition particle 72; ovar; diag
 132592; AW603564; Hs.288850; Homo sapiens cDNA: FLJ22528 f; colon; diag
 132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag
 132632; AU076916; Hs.5398; guanine monophosphate synthetase; ovar, lung; s.m.
 132669; W38586; Hs.380933; guanine nucleotide binding protein; colon; diag
 132710; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, colon, headnk; diag
 132725; NM_006276; Hs.184167; splicing factor, arginine/serine; ovar; CTL+s.m.
 132767; BE182592; Hs.11261; small proline-rich protein 2A; lung; diag
 132791; AB029551; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.
 132837; AA370362; Hs.57958; EGF-TM7-latrophilin-related pr; angio; diag
 132856; NM_001448; Hs.58367; glypican 4; breast, colon, pros; mAb
 132888; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.
 132902; A1936442; Hs.59838; hypothetical protein FLJ10808; colon; diag
 132939; AB009284; Hs.61152; exostoses (multiple)-like 2; ovar; diag
 132964; AJ362575; Hs.303171; ESTs; pros; diag
 132967; AA316181; Hs.61635; six transmembrane epithelial a; pros, pros; mAb+CTL
 132990; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung; CTL+s.m.
 132994; AA112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.
 133006; AW978436; Hs.62515; KIAA0494 gene product; colon; diag
 133015; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactose; breast, colon, pros; s.m.
 133016; A439688; Hs.6289; hypothetical protein FLJ20885; breast; diag
 133061; AJ188431; Hs.296636; prostate differentiation factor; angio, pros, blad; diag
 133063; A1654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
 133070; U92649; Hs.380138; a disintegrin and metalloprote; leuk; diag
 133179; U81699; Hs.66731; homeo box B13; pros; CTL+s.m.
 133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.
 133260; AA403045; Hs.6906; Homo sapiens cDNA: FLJ23197 f; angio; diag
 133272; NM_002776; Hs.69423; kallikrein 10; colon, ovar; diag
 133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb
 133321; T79526; Hs.179516; integral type I protein; breast; diag
 133391; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, blad, lung; diag
 133415; X69699; Hs.73149; paired box gene 8; ovar; CTL
 133477; AW502935; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.
 133579; X75346; Hs.75074; mitogen-activated protein kina; pros; diag
 133626; AW836130; Hs.75277; hypothetical protein FLJ13910; pros; diag
 133736; D49958; Hs.75819; glycoprotein M6A; pros; mAb
 133829; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; ovar; diag
 133860; S78296; Hs.76888; hypothetical protein MGC12702; blad; diag
 133944; AW068578; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 133975; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc; CTL+diag
 133978; AJ908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.
 134100; AA460085; Hs.171075; replication factor C (activator; pros; diag
 134110; U41060; Hs.79136; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb
 134169; AJ690916; Hs.178137; transducer of ERBB2, 1; breast; CTL+s.m.
 134219; NM_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.
 134319; BE304999; Hs.285764; fumarate hydratase; colon; s.m.
 134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag
 134348; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 134374; N22687; Hs.8236; ESTs; pros; diag
 134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.
 134401; A1916662; Hs.211577; kinesin 1 (kinesin receptor); pros, breast; mAb+s.m.
 134405; AW079903; Hs.82772; collagen, type XI, alpha 1; breast, lung, ovar, headnk; CTL
 134470; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.
 134520; BE091005; Hs.349506; activated RNA polymerase II tr; ovar; s.m.
 134529; AW411479; Hs.848; FK506-binding protein 4 (55kD); breast; diag
 134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.
 134654; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 134666; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.
 134691; AW382987; Hs.88474; prostaglandin-endoperoxide syn; ovar; s.m.
 134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag
 134731; D89377; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 134786; T29618; Hs.89640; TEK tyrosine kinase, endothel; angio; s.m.
 134824; S78723; Hs.298623; 5-hydroxytryptamine (serotonin); blad; mAb
 134856; BE281128; Hs.8030; TONDU; blad; CTL+s.m.

- 134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 134924; BE294029; Hs.279903; Ras homolog enriched in brain; breast; mAb
 134972; AL033527; Hs.169252; v-myc avian myelocytomatosis v; ovar; CTL+s.m.
 134975; R50333; Hs.92186; Leman coiled-coil protein; breast; diag
 134989; AW968058; Hs.92391; nudix (nucleoside diphosphate); colon; diag
 135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 135117; W52493; Hs.94694; Homo sapiens cDNA FLJ10561 fis; breast; diag
 135166; AA135867; Hs.280858; ESTs, Highly similar to A35661; pros; diag
 135235; AW298244; Hs.266195; ESTs; angio; diag
 135242; AI583187; Hs.9700; cyclin E1; ovar; CTL+s.m.
 135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.
 135255; Y13645; Hs.97234; uropod 2; blad; mAb
 135309; AI564123; Hs.355689; ADP-ribosylation factor-like 5; pros; diag
 135315; H81136; Hs.334604; Homo sapiens mRNA for KIAA1870; pros; diag
 135389; U05237; Hs.99872; fetal Alzheimer antigen; pros; breast, colon; CTL+s.m.
 135400; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
 300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros; breast; mAb+s.m.
 300256; AW591433; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 300318; AW444502; Hs.256982; ESTs, Weakly similar to NEL1_H; angio; CTL+diag
 300605; AI218947; Hs.152670; ESTs; pros; diag
 300921; AF146747; Hs.232165; polycythemia rubra vera 1; cat; pros; mAb+s.m.
 300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.
 301042; AI659131; Hs.366053; hypothetical protein MGC2849; pros; mAb
 301043; AI160316; Hs.149155; voltage-dependent anion channel; pros; mAb+s.m.
 301050; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung; CTL+s.m.
 301341; AA887801; Hs.208229; G protein-coupled receptor; breast, lung; mAb+s.m.
 302001; AB020711; Hs.374965; KIAA0904 protein; breast; CTL+s.m.
 302005; BE252922; Hs.123118; MAD (mothers against decapentap; pros; diag
 302067; BE542706; Hs.222399; CEGP1 protein; breast; diag
 302167; NM_006227; Hs.283007; phospholipid transfer protein; pros; mAb
 302225; NM_007231; Hs.162211; solute carrier family 6 (neuro; panc; mAb+s.m.
 302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb+s.m.
 302290; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros; breast; diag
 302372; AL117406; Hs.335891; ATP-binding cassette transport; breast; pros; mAb+s.m.
 302384; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 302410; NM_004917; Hs.218366; kallikrein 4 (protease, enamel; pros; diag
 302468; AL133561; Hs.380155; DKFZP434B061 protein; pros; diag
 302562; BE149762; Hs.48956; gap junction protein, beta 6 (l; lung, blad; mAb
 302881; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 303295; AA205625; Hs.208067; ESTs; blad; diag
 303380; AW962764; Hs.303171; olfactory receptor, family 51; pros; mAb
 303506; AA340605; Hs.105887; ESTs, Weakly similar to Homolo; pros; breast, colon; diag
 303699; BE143707; Hs.19525; hypothetical protein FLJ22794; pros; diag
 303753; AW503733; Hs.9414; KIAA1488 protein; pros; breast, colon; CTL+s.m.
 305503; AA759177; Hs.298148; ESTs, Weakly similar to KIAA05; pros; diag
 306273; AA936290; gb:ov70a01.s1 Soares_NFL_T_GBC; pros; diag
 306676; AI005603; gb:ov15c10.s1 NCI_CGAP_GC3 Homr; lung; diag
 306840; AI077477; Hs.307912; ESTs; angio; diag
 309177; AI951118; Hs.326736; Homo sapiens breast cancer ant; breast; pros; mAb+CTL
 309583; AW170035; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 309931; AW341683; Hs.343663; gb:hd13d01.x1 Soares_NFL_T_GBC; lung; mAb
 310382; AI734009; Hs.127699; KIAA1603 protein; pros; diag
 310431; AI420227; Hs.366053; ESTs, Weakly similar to A46010; pros; diag
 310573; AW292180; Hs.156142; ESTs; pros; diag
 310636; AI814373; Hs.184175; ESTs; lung; diag
 310781; AI380797; Hs.158992; ESTs; breast; diag
 310955; AI476732; Hs.263912; ESTs; breast, angio; diag
 311034; BE567130; Hs.311389; ESTs, Highly similar to NKGD_H; lung; mAb+s.m.
 311166; AI821005; Hs.118599; intron of BFF9 (GDNFRA); breast; diag
 311251; AI655662; Hs.197698; ESTs; pros; diag
 311557; AF200492; Hs.211238; Interleukin-1 homolog 1; lung; diag
 311596; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 311630; AI915444; Hs.372037; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 311877; AA084248; Hs.372651; G protein-coupled receptor 39; ovar, angio, glior; mAb+s.m.
 311911; R19175; Hs.169793; ribosomal protein L32; pros; diag
 311928; T62216; Hs.378028; ESTs; pros; diag
 312182; T94344; Hs.326263; ESTs; pros; diag
 312252; AI128388; Hs.143655; ESTs; blad; diag
 312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.
 312521; AI263307; Hs.356901; H2B histone family, member L; pros; breast, lung; diag
 312544; AA518420; Hs.352340; ESTs, Weakly similar to I38022; breast; diag
 312742; AI650363; Hs.115462; ESTs; colon; diag
 312795; AW975014; Hs.26; ferrochelatase (protoporphyrin; pros; s.m.
 312857; BE083868; Hs.126914; KIAA1430 protein; colon; pros; CTL+s.m.
 312922; AA329256; Hs.378739; ESTs, Moderately similar to eit; pros; diag
 313328; AW449211; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
 313513; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 313558; AA628517; Hs.118502; ESTs; angio; diag
 313665; AW751201; Hs.120932; ESTs; angio; diag
 313774; AI916058; Hs.144563; ESTs; colon; CTL
 313915; C18863; Hs.163443; Intron of perostin (OSF-2os); breast; diag
 313978; AI870175; Hs.13957; ESTs; angio; diag
 314078; AW129357; Hs.329700; ESTs; breast; diag

- 314097; AA648744; Hs.269493; ESTs; breast; diag
 314121; A1732083; Hs.187619; ESTs; pros; breast; diag
 314171; A1821895; Hs.193481; ESTs; pros; diag
 5 314506; AA833655; Hs.206868; Homo sapiens cDNA FLJ14056 f1s; breast; diag
 314547; AA399272; Hs.144341; ESTs; breast; diag
 314558; A1873274; Hs.370280; ESTs; breast; pros; diag
 314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 f1s; lung, blad; diag
 314691; AW207206; Hs.356952; ESTs; breast; pros; diag
 10 314785; A1538226; Hs.32976; guanine nucleotide binding pro; colon; pros; diag
 314907; AW971082; Hs.222888; ESTs; Weakly similar to TRHY_H; pros; diag
 315008; A1538613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 315033; A1493048; Hs.146133; ESTs; colon; diag
 315051; AW292425; Hs.163484; ESTs; breast, pros; blad; diag
 15 315052; AA876910; Hs.134427; ESTs; pros; breast; diag
 315196; A1367347; Hs.44898; Homo sapiens clone TCCCTA00151; breast; diag
 315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag
 315408; AW273261; Hs.216292; ESTs; pros; diag
 20 315634; AA837085; Hs.372254; ESTs; breast; pros; diag
 315720; AA292998; Hs.163900; ESTs; blad; diag
 316177; A1904982; Hs.293102; downstream of breast cancer an; breast; mAb+CTL
 316442; AA760894; Hs.125350; ESTs; pros; diag
 316580; AA938198; Hs.146123; poly(A) polymerase gamma; breast, angio; s.m.
 25 316886; AA836331; Hs.170261; ESTs; breast; diag
 316943; AW014875; Hs.137007; ESTs; blad; diag
 317079; BE159984; Hs.125395; ESTs; blad; mAb+s.m.
 317140; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 f1s; breast; diag
 317224; X73608; Hs.93029; sparcosteonecin, cwcx and ka; pros; angio; diag
 317546; BE568568; Hs.159066; ESTs; pros; CTL+s.m.
 30 317803; AW664964; Hs.128899; ESTs; breast, lung, ovar; pros; mAb+s.m.
 317881; A1827248; Hs.224398; Homo sapiens cDNA FLJ11469 f1s; breast, lung; diag
 318240; A1085377; Hs.143610; ESTs; lung; diag
 318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros; colon; CTL+s.m.
 318532; AW139377; Hs.127179; cryptic gene; panc; diag
 318744; A1793124; Hs.144479; ESTs; breast; diag
 35 318754; W21423; Hs.44222; CGI-90 protein; pros; diag
 319080; AW967646; Hs.23023; ESTs; pros; diag
 319795; AB037821; Hs.146858; protocadherin 10; pros; glio; mAb+s.m.
 320066; BE305242; Hs.16098; claudin 2; colon; panc; diag
 40 320167; AA984373; Hs.90790; Homo sapiens cDNA: FLJ22930 f1; breast; pros; diag
 320203; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar; mAb+s.m.
 320211; AL039402; Hs.125783; DEME-6 protein; breast; pros; CTL
 320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag
 320324; AF071202; Hs.139336; ATP-binding cassette, sub-fam1; pros; mAb
 45 320561; AF085808; Hs.159330; uroplakin 3; pros; blad; diag
 320590; U87058; Hs.154299; Human proteinase activated rec; pros; mAb+s.m.
 320635; N50617; Hs.80506; small nuclear ribonucleoprotein; angio lung; diag
 320736; AA315361; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 320796; AK001541; Hs.31218; secretory carrier membrane pro; pros; colon; diag
 320896; BE019924; Hs.271580; uroplakin 1B; lung, blad, ovar, headnk; mAb+diag
 50 321023; AW294316; Hs.125608; ESTs; colon; diag
 321107; A1732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL
 321412; A1674383; Hs.22891; solute carrier family 7 (cat10; pros; mAb+s.m.
 321441; AF107493; Hs.201675; Homo sapiens LUCA-15 protein m; pros; breast; diag
 55 321644; AW975944; Hs.237396; ESTs; breast; pros; diag
 321717; AW956580; Hs.42699; ESTs; angio; diag
 321906; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag
 322035; AL137517; Hs.306201; hypothetical protein DKFZp564O; breast, blad; mAb
 60 322521; AF147347; ; gb:Homo sapiens full length ln; breast; diag
 322706; AA018899; Hs.127179; cryptic gene; panc; diag
 322782; AA056060; Hs.202577; Homo sapiens cDNA FLJ12166 f1s; pros; diag
 322818; AW043782; Hs.293616; ESTs; pros; breast, angio, glio; diag
 322882; AW248508; Hs.279727; Homo sapiens cDNA FLJ14035 f1s; breast, lung, ovar, angio, blad; diag
 65 322975; C16391; ; Intron of breast cancer antigen; breast; mAb+CTL
 323168; AL120862; Hs.124165; programmed cell death 9 (PDCD9; breast; diag
 323226; AF055019; Hs.355279; Homo sapiens clone 24870 mRNA; pros; diag
 323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 323287; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 70 323332; A1829520; ; gb:w118c06.x1 NCI_CGAP_U11 Hom; breast; diag
 323335; A1655499; Hs.161712; ESTs; pros; breast; mAb
 323587; A1299709; Hs.131886; Homo sapiens cDNA: FLJ22113 f1; colon; diag
 323817; AA410943; ; NAME OMITTED ... receptor kinase; breast; mAb
 324261; BE069341; ; gb:QV3-BT0381-270100-073-c08 B; breast; diag
 75 324295; AA434579; Hs.143691; ESTs; pros; diag
 324338; AA927668; Hs.145078; regulator of differentiation (; colon; diag
 324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 f1; pros; colon; diag
 324432; AA464510; Hs.152812; ESTs; breast, lung, panc; diag
 324603; AW993522; Hs.299867; ESTs; pros; breast; diag
 80 324817; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros; diag
 324658; A1694767; Hs.129179; Homo sapiens cDNA FLJ13581 f1s; pros; diag
 324718; A1557019; Hs.118467; small nuclear protein PRAC; colon; pros; diag
 324866; A1541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag
 324871; A1890347; Hs.271923; Homo sapiens cDNA: FLJ22785 f1; colon; diag

- 324987; AJ375572; Hs.172634; ESTs; breast; diag
 325372; ; Phase 2 & 3 Exons; breast; CTL+s.m.
 325544; ; Phase 2 & 3 Exons; breast; angio; diag
 327038; ; Phase 2 & 3 Exons; lung; angio; diag
 327075; ; Phase 2 & 3 Exons; breast; lung; diag
 327414; ; Phase 2 & 3 Exons; angio; diag
 328700; ; Phase 2 & 3 Exons; breast; angio; diag
 330211; ; Phase 2 & 3 Exons; pros; CTL+s.m.
 330468; L10343; Hs.112341; protease inhibitor 3; skin-der; lung, colon, blad; diag
 330493; M27826; Hs.334372; endogenous retroviral protease; lung, colon; s.m.
 330630; NM_002902; Hs.79088; reticulocalbin 2; EF-hand calc; pros; diag
 330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.
 330790; AI660243; Hs.318545; Hu01 Chip Redos; pros; blad; diag
 330814; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast; diag
 330827; AI961486; Hs.249196; ESTs; lung, uter; diag
 330892; AF109298; Hs.118258; prostate cancer associated pro; pros; diag
 331014; AW770994; Hs.30340; hypothetical protein KIAA1165; colon; diag
 331151; R82331; Hs.121602; ESTs; pros; breast; diag
 331183; T40769; Hs.8469; ESTs; colon; diag
 331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 fis; angio; diag
 331490; AF216751; Hs.26813; CDA14; pros; diag
 331578; AJ246482; Hs.243010; ESTs; angio; diag
 331614; N92293; Hs.205832; EST; Moderately similar to ALU; breast; diag
 331811; AW885727; Hs.9914; Hu01 Chip Redos; lung; diag
 331889; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 331969; AA526911; Hs.82772; collagen; type XI; alpha 1; breast; lung; CTL
 332180; AF134160; Hs.7327; claudin 1; lung; mAb
 332247; AA669097; ; ESTs; pros; breast; diag
 332396; AW579842; Hs.380730; hypothetical protein FLJ10697; pros; diag
 332453; L42583; Hs.334309; Hu01 Chip Redos; lung; diag
 332468; AB018259; Hs.118140; KIAA0716 gene product; angio; diag
 332530; M31569; Hs.1735; inhibin; beta B (activin AB be; ovar; pros; diag
 332535; AF167706; Hs.19280; cysteine-rich repeat-containing; angio; diag
 332640; BE568452; Hs.344037; protein regulator of cytokines; blad, headnk; diag
 332645; AA284371; Hs.118064; ESTs; breast; colon; diag
 332686; X69699; Hs.73149; paired box gene 8; ovar; CTL+s.m.
 332697; X51405; Hs.75360; carboxypeptidase E; pros; diag
 332740; BE409869; Hs.286241; Homo sapiens cDNA: FLJ22698 ft; pros; diag
 332798; ; C22000007.gil12314195[emb]CAB9; pros; breast; diag
 333769; ; NM_005940; Homo sapiens matrix; breast, colon, lung; mAb+diag+s.m.
 333904; ; Chromosome 22; pros; diag
 334223; ; NM_005080; Homo sapiens X-box; pros; breast; diag
 334447; ; NM_012429; Homo sapiens SEC14; pros; diag
 335115; ; NM_006498; Homo sapiens lectin; pros; CTL+s.m.
 335809; ; NM_014509; Homo sapiens kraken; breast; CTL+s.m.
 335824; ; ENSP00000249072; DJ222E13.1 (N; breast; pros; CTL+s.m.
 335825; ; ENSP00000249072; DJ222E13.1 (N; breast; diag
 335936; ; Chromosome 22; lung; diag
 336034; ; NM_007172; Homo sapiens nucleop; breast; angio; CTL+s.m.
 336152; ; NM_014246; Homo sapiens cadherin; breast; mAb
 336366; ; C22000024.gil10645308[gb]AAG2; lung, breast; CTL+s.m.
 338008; ; NM_005940; Homo sapiens matrix; lung, breast, colon; mAb+diag+s.m.
 338033; ; Chromosome 22; lung; angio; diag
 338158; ; NM_012399; Homo sapiens phosph; lung; angio; diag
 338255; ; NM_014323; Homo sapiens zinc f; pros, breast, colon; CTL+s.m.
 400195; ; Hs.42650; NM_007057; Homo sapiens ZW10 f; lung; CTL+s.m.
 400269; ; Hs.253495; Eos Control; fibro; diag
 400285; ; Eos Control; lung; diag
 400287; S39329; Hs.181350; kallikrein 2, prostatic; pros; diag
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; pros, colon, EWS; mAb
 400294; N95796; Hs.278695; Homo sapiens protein mRNA, ex; pros, pros; mAb
 400295; W72838; Hs.348419; AI905687; IL-BT095-190199-019 B; breast; diag
 400298; AA032279; Hs.61635; sbx transmembrane epithelial a; panc, lung, headnk, stom, EWS, ovar; mAb+CTL
 400328; X87344; ; transporter 2, ATP-binding cas; lung; mAb+s.m.
 400409; AF153341; ; Homo sapiens winged helix/fork; blad; CTL+s.m.
 400419; AF084545; ; Target; lung, sarc; diag
 400440; X83957; Hs.83870; nebulin; sarc; diag
 400494; ; ENSP00000238970; CIG30 (Fragma; angio; mAb
 400517; ; lensin; stom, cerv, uter, lung, pros, colon, hepC; diag
 400651; ; ENSP00000228031; COPPER CHAPER; sarc; s.m.
 400665; ; NM_002425; Homo sapiens matrix; lung; mAb+diag+s.m.
 400773; ; NM_003105; Homo sapiens sort; blad; mAb
 400844; ; NM_003105; Homo sapiens sort; blad; s.m.
 400846; ; sortilin-related receptor, L/D; blad; mAb+s.m.
 400881; ; NM_025080; Homo sapiens hypoth; ovar; diag
 401093; ; C12000586.gil16330167[db]BAA8; blad, lung; CTL+s.m.
 401234; ; mitogen-activated protein kinase; angio; diag
 401424; ; NM_001172; Homo sapiens arginas; pros; s.m.
 401486; ; C40000647.gil4758508[ref]NP_00; headnk; mAb
 401704; ; NM_021195; Homo sapiens claudin; test; mAb
 401732; ; NM_001176; Homo sapiens Rho GD; panc; diag
 401747; ; Homo sapiens keratin 17 (KRT17; blad, lung, headnk, metz; diag

401760;; Target Exon; blad, lung, headnk, esoph; diag
 401780;; NM_005557*:Homo sapiens kerat; lung, blad, headnk, esoph, melar; diag
 401781;; Target Exon; lung, blad, headnk, esoph, cerv; diag
 401785;; NM_002275*:Homo sapiens kerat; lung; diag
 401797;; Target Exon; sarc; diag
 401994;; Target Exon; lung; diag
 402145;; Target Exon; test; CTL+s.m.
 402199;; Target Exon; test; CTL+s.m.
 402230;; Fgenesh predicted: CYTOCHROME; blad; diag
 402239;; Target Exon; blad; diag
 402260;; NM_001436*:Homo sapiens fibril; blad; CTL+s.m.
 402265;; Target Exon; lung; diag
 402305;; C19000735:g[4508027]ref[NP_0; blad; CTL+s.m.
 402420;; C1000823:g[10432400]emb[CAC1; lung; diag
 402424;; NM_024901*:Homo sapiens hypothe; blad; CTL+s.m.
 402447;; C1000201:g[204416]gb[AA02627; esoph; mAb
 402474;; NM_004079*:Homo sapiens catheps; lung, colon, stom, fibro; diag
 402550;; Target Exon; fibro; diag
 402604;; Target Exon; glio; diag
 402605;; Target Exon; glio; diag
 402606;; NM_024626*:Homo sapiens hypothe; ovar, breast; mAb
 402680;; Target Exon; test; mAb
 402777;; C1002652:g[544327]sp[Q04799]; blad; diag
 402860;; ENSP00000239210:DJ50024.4 (nov; melar; CTL+s.m.
 402888;; Target Exon; sarc; diag
 402992;; Target Exon; sarc; diag
 402994;; NM_002463*:Homo sapiens myxovi; esoph; diag
 403046;; NM_005656*:Homo sapiens transm; pros; mAb
 403047;; NM_005656*:Homo sapiens transm; pros, blad, colon; mAb
 403071;; NM_003319*:Homo sapiens tlin; sarc; diag
 403088;; NM_003319*:Homo sapiens tlin; sarc; diag
 403171;; C2001472:g[5809678]gb[AAB416; test; diag
 403328;; Target Exon; melar; diag
 403329;; unnamed protein product [Homo; lung; diag
 403381;; ENSP00000231844*:Ecotropl vir; blad; CTL+s.m.
 403409;; NM_005929*:Homo sapiens antigen; melar; mAb
 403433;; NM_001622*:Homo sapiens alpha-2; hepC; diag
 403478;; NM_022342*:Homo sapiens kinesin; lung; CTL+s.m.
 403715;; Target Exon; lung; diag
 403740;; NM_001076*:Homo sapiens UDP gt; pros, hepC; s.m.
 403776;; ENSP00000226542*:Small inducib; panc; diag
 403903;; C5001632:g[10645308]gb[AAG21; blad; CTL+s.m.
 404029;; NM_018936*:Homo sapiens protoc; glio; mAb
 404049;; NM_018937*:Homo sapiens protoc; glio; mAb
 404210;; NM_005938*:Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag
 404240;; NM_018950*:Homo sapiens major h; fibro; mAb
 404253;; NM_021058*:Homo sapiens H2B h; lung; CTL+s.m.
 404286;; C6001909:g[704441]db[BAA1890; panc; diag
 404298;; C6001238:g[121715]sp[P26697]; lung; s.m.
 404403;; Target Exon; blad; diag
 404440;; NM_021048*:Homo sapiens melanom; lung, blad; mAb+CTL
 404866;; ENSP00000251112*:Sodium/potass; panc; s.m.
 404877;; NM_005365*:Homo sapiens melanom; lung, blad; CTL+s.m.
 404927;; Target Exon; lung, headnk; diag
 404996;; Target Exon; lung, headnk, esoph; diag
 405001;; Interleukin enhancer binding f; sarc; diag
 405025;; Homo sapiens bona morphogenet; angio; diag
 405121;; mitogen-activated protein kinase; angio, renat; s.m.
 405238;; Target Exon; glio; diag
 405239;; oxidative 3 alpha hydroxysteroid; glio; s.m.
 405451;; Homo sapiens glutaminyl-peptid; melar; s.m.
 405545;; Target Exon; cerv; mAb
 405546;; NM_018833*:Homo sapiens transp; cerv; mAb
 405547;; NM_018833*:Homo sapiens transp; cerv, melar; mAb
 405646;; C12000200:g[4557225]ref[NP_00; lung; diag
 405704;; NM_001844*:Homo sapiens collag; sarc; diag
 405770;; NM_002362*:Homo sapiens melanom; lung, esoph; mAb+CTL
 405849;; Target Exon; panc; diag
 405932;; C15000305:g[3806122]gb[AAC691; blad, lung, headnk, cerv; CTL+s.m.
 406081;; Target Exon; blad; diag
 406137;; NM_000179*:Homo sapiens mulS; lung; CTL+s.m.
 406173;; ENSP00000250148*:Growth hormon; panc; CTL+s.m.
 406348;; Target Exon; breast; CTL+s.m.
 406360;; Target Exon; lung, headnk; diag
 406399;; NM_003122*:Homo sapiens serine; blad; diag
 406434;; NM_030579*:Homo sapiens cytoch; blad; diag
 406457;; Target Exon; lung, headnk, blad; diag
 406506;; Target Exon; angio; diag
 406547;; Target Exon; test; diag
 406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.
 406671; AA129547; Hs.285754; mel proto-oncogene (hepatocytar; panc; mAb
 406672; M26041; Hs.198253; major histocompatibility compl; fibro; mAb
 406685; M18728; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung; mAb+CTL

- 406687; M31126; Hs.352054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.
 406690; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL
 406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag
 406850; A1624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.
 406906; Z25424; ; gb:Hsapiens protein-serine/th; blad, lung; s.m.
 406937; U14622; ; gb:Human transketolase-like pr; test; s.m.
 406967; M24349; ; gb:Human parathyroid hormone-t; lung; CTL+s.m.
 406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag
 407013; U35637; Hs.83870; gb:human nebulin mRNA, partial; sarc; diag
 407034; U84540; ; gb:Human dystrobrevin isoform ; glio; diag
 407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag
 407118; AA156790; Hs.262036; ESTs, Weakly similar to ZZZ2_H; pros; diag
 407122; H20276; Hs.31742; ESTs; pros; diag
 407137; T97307; ; gb:ye53h05.s1 Soares fetal liv; lung, blad, ovar, pros, panc, headnk; diag
 407168; R45175; Hs.117183; ESTs; pros, breast, colon; diag
 407178; AA195651; Hs.352312; AP-2 beta transcription factor; breast; CTL+s.m.
 407202; N58172; Hs.109370; ESTs; pros; diag
 407216; N91773; Hs.348385; lysyl oxidase; panc; diag
 407242; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung, ovar, cerv; mAb
 407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag
 407245; X90568; Hs.172004; tlin; sarc; diag
 407251; U67611; Mm.29182; transaldolase 1; pros; s.m.
 407262; AA659037; Hs.163780; ESTs; angio; CTL+s.m.
 407276; A1951118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 407289; AA135159; Hs.203349; Homo sapiens cDNA FLJ12149 fis; lung; diag
 407366; AF026942; Hs.17518; gb:Homo sapiens c1g33 mRNA, pa; ovar, hepC, stom, mela, esoph; diag
 407581; R48402; Hs.173508; P3ECSL; blad; CTL+s.m.
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb
 407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.
 407710; AW022727; Hs.23616; ESTs; test; diag
 407720; AB037776; Hs.38002; KIAA1355 protein; lung; mAb
 407746; AK001962; Hs.38114; hypothetical protein FLJ11100; lung; diag
 407756; AA116021; Hs.38260; ubiquitin specific protease 18; panc, lung, esoph, fibro, mela; CTL+s.m.
 407758; D50915; Hs.38365; KIAA0125 gene product; lung; diag
 407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.
 407782; AA608956; Hs.112619; ESTs, Moderately similar to PU; lung; diag
 407786; AA687538; Hs.38972; tetraspan 1; pros, colon, uter, stom, ovar, cerv; mAb
 407788; BE614982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag
 407818; AL021838; Hs.40154; jumonji (mouse) homolog; test; CTL+s.m.
 407824; AA147884; Hs.9812; Homo sapiens cDNA FLJ14388 fis; sarc; diag
 407839; AA045144; Hs.161666; ESTs; blad, headnk; mAb
 407846; AA426202; Hs.40403; Cbp/p300-interacting transact; mela; diag
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homo; colon, stom, renal, breast, ovar, uter, cerv; diag
 407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag
 407872; AB039723; Hs.40735; frizzled (Drosophila) homolog ; ovar; mAb
 407881; AW072003; Hs.40968; heparan sulfate (glucosamine) ; panc; s.m.
 407910; AA650274; Hs.41296; fibronectin leucine rich trans; fibro; mAb
 407944; R34008; Hs.239727; desmocollin 2; lung, headnk, esoph; mAb
 407949; W21874; Hs.247057; ESTs, Weakly similar to 210926; fibro, blad; diag
 407962; A1133530; Hs.62930; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL
 408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag
 408045; AW138959; Hs.245123; ESTs; breast ; diag
 408056; AA312329; Hs.42331; ephrin-A4; ovar; diag
 408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag
 408081; AW451597; Hs.187409; Intron of basic-helix-loop-hel; ovar, glio; diag
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; breast, lung, stom; s.m.
 408122; A1432652; Hs.42824; hypothetical protein FLJ10718; lung; diag
 408209; NM_004454; Hs.43697; ets variant gene 5 (ets-relate; mela; CTL+s.m.
 408296; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D; panc, renal, colon; mAb
 408353; BE439838; Hs.44298; mitochondrial ribosomal protel; lung; diag
 408430; S79876; Hs.44926; dipeptidylpeptidase IV (CD26 ; pros; mAb
 408522; A1541214; Hs.46320; Small proline-rich protein SPR; lung, blad, headnk, eosoph, cerv; diag
 408561; A1308037; Hs.84120; hypothetical protein MGC13016; mela; CTL+s.m.
 408570; AL046406; Hs.103483; KIAA1798 protein; angio; CTL+s.m.
 408572; AA055611; Hs.226568; ESTs, Moderately similar to AL; lung; diag
 408591; AF015224; Hs.46452; mammaglobin 1; breast, cerv; diag
 408611; NM_004367; Hs.46468; chemokine (C-C motif) receptor; mela; mAb
 408633; AW963372; Hs.222088; PRO2000 protein; blad, lung, headnk, pros; diag
 408660; AA525775; Hs.89040; ESTs, Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; test; diag
 408758; NM_003686; Hs.47504; exonuclease 1; mela; CTL+s.m.
 408770; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 408771; AW732573; Hs.47584; potassium voltage-gated channel; lung; mAb
 408780; D31797; Hs.652; tumor necrosis factor (ligand); leuk; diag
 408795; AW749126; Hs.170345; hypothetical protein FLJ13710; ovar; diag
 408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag
 408833; AW612232; Hs.254835; ESTs; pros; diag
 408877; AA479033; Hs.130315; ESTs, Weakly similar to A47582; breast; diag
 408915; NM_016651; Hs.48950; hepatocellular carcinoma novel ; panc, sarc; diag
 408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

- 408952; BE388436; Hs.44317; SRY (sex determining region Y); mela; diag
 408992; AA059325; Hs.30114; guanine nucleotide binding pro; lung; diag
 408996; AI979168; Hs.82226; glycoprotein (transmembrane) n; mela; mAb+s.m.
 409012; AL117435; Hs.49725; DKFZP434I216 protein; sarc; CTL+s.m.
 409038; T97490; Hs.50002; small inducible cytokine subfa; mela; diag
 409051; AA080912; gbzm04d03.r1 Stratagene hNT n; pros; s.m.
 409077; AA063037; Hs.66803; ESTs; lung; diag
 409093; BE243834; Hs.50441; CGI-04 protein; lung; diag
 409123; AA063403; gbzm04d12.s1 Stratagene corne; pros; s.m.
 409142; AL136877; Hs.50758; SMC4 (structural maintenance o; ovar, lung, mela; diag
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag
 409200; AL042914; Hs.51039; KIAA0076 gene product; sarc; CTL+s.m.
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB; fibro, blad, ovar; diag
 409228; R16811; Hs.22010; ESTs, Weakly similar to 210926; lung; mAb
 409231; AA446644; Hs.692; GA733-2 antigen; epithelial gl; pros, ovar, breast, uter, panc, colon, stom; mAb
 409243; AB037761; Hs.51743; KIAA1340 protein; test; diag
 409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.
 409264; NM_014937; Hs.52463; KIAA0966 protein; mela; CTL+s.m.
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-ii; breast, ovar, lung, panc, uter; mAb
 409327; L41162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarc; CTL+s.m.
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; mela; CTL+s.m.
 409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.
 409348; AI401535; Hs.146090; ESTs; renal, glio; diag
 409361; NM_005582; Hs.54416; sine oculis homeobox (Drosophi; blad, lung, pros; CTL+s.m.
 409389; AB007979; Hs.301281; Homo sapiens mRNA, chromosome 1; glio; diag
 409395; U46745; Hs.336678; dystrobrein, alpha; glio; diag
 409402; AF208234; Hs.695; cystatin B (stefin B); blad; diag
 409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 fi; mela; diag
 409421; AA199883; Hs.67624; ESTs; test; diag
 409430; R21945; Hs.346735; splicing factor, arginine/ser; mela; diag
 409432; D49372; Hs.54460; small inducible cytokine subfa; stom, esoph; diag
 409433; AA074382; Hs.135255; ESTs; glio, sarc; diag
 409509; AL036923; Hs.322710; ESTs; angio; diag
 409512; AW979187; Hs.293591; melanoma differentiation assoc; mela, esoph; CTL+s.m.
 409542; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 409582; R27430; Hs.271565; ESTs; lung; diag
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, mela, sarc; CTL+s.m.
 409633; AW449822; Hs.65200; ESTs; sarc; diag
 409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renal; diag
 409638; AW450420; Hs.21335; ESTs; glio; diag
 409670; AI368109; Hs.381163; KIAA1856 protein; test; CTL+s.m.
 409703; NM_006187; Hs.56009; 2'-5'-oligoadenylate synthetas; panc, esoph, mela; s.m.
 409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag
 409719; AI769160; Hs.108681; Homo sapiens brain tumor assoc; lung; diag
 409731; AA125985; Hs.56145; thymosin, beta, identified in; pros, sarc; CTL+s.m.
 409745; AA077391; gb:7B14E12 Chromosome 7 Fetal; ovar, renal; CTL+s.m.
 409935; AW511413; Hs.187393; ESTs; lung; diag
 409958; NM_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb
 409968; R27687; Hs.334334; transcription factor AP-2 alphi; mela; diag
 410006; AW732308; Hs.57783; eukaryotic translation initiat; test; diag
 410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag
 410044; BE566742; Hs.58169; highly expressed in cancer, rt; blad; diag
 410048; W76467; Hs.343874; proline oxidase homolog; test; s.m.
 410076; T05387; Hs.7991; ESTs; lung, pros; diag
 410079; U94362; Hs.380757; glycogenin 2; mela; diag
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; pros; diag
 410102; AW248508; Hs.279727; ESTs; homologue of PEM-3 [Clon; ovar, breast, blad, lung, angio, sarc; diag
 410174; AA306007; Hs.59461; DKFZP434C245 protein; mela; diag
 410240; AL157424; Hs.61289; synaptotagmin 2; angio; diag
 410247; AF181721; Hs.61345; RU2S; ovar; CTL+s.m.
 410268; AA316181; Hs.61635; six transmembrane epithelial a; panc, pros, EWS; mAb+CTL
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; mela; diag
 410310; J02931; Hs.62192; coagulation factor III (Thromb; pros, panc; mAb
 410361; BE391804; Hs.62661; guanylate binding protein 1, f; mela, esoph, hepC, fibro, uter; diag
 410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag
 410480; R97457; Hs.63984; cadherin 13, H-cadherin (heart; angio; mAb
 410491; AA465131; Hs.64001; Homo sapiens clone 25218 mRNA; mela, esoph; diag
 410530; M25809; Hs.64173; ATPase, H transporting, lysoso; ovar; mAb
 410553; AW016824; Hs.272068; hypothetical protein MGC14128; blad, lung; diag
 410555; U92649; Hs.380136; a disintegrin and metalloprote; leuk, lung; mAb
 410561; BE540255; Hs.6994; Homo sapiens cDNA: FLJ22044 fi; lung; diag
 410568; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 fi; panc; diag
 410600; AW575742; Hs.351676; ESTs, Moderately similar to S6; mela; mAb+s.m.
 410621; AA194329; Hs.172004; titin; sarc; diag
 410681; AW246890; Hs.65425; calbindin 1, (28kD); lung; diag
 410687; U24389; Hs.65436; lysyl oxidase-like 1; panc; diag
 410733; D84284; Hs.66052; CD38 antigen (p45); pros; mAb+CTL
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; panc; mAb
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.
 410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag
 410870; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1; leuk; diag

- 410889; X91662; Hs.66744; twist (Drosophila) homolog (ac; sarc; CTL+s.m.
 410929; H47233; Hs.30643; ESTs; ovar; test; diag
 411078; A1222020; Hs.182364; CooaCrisp; pros; glio; breast; diag
 411089; AA456454; Hs.214291; cell division cycle 2-like 1 (c; lung; fibro; CTL+s.m.
 411243; AB039886; Hs.69319; CA11; esoph; diag
 411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 f5; blad; diag
 411257; AA628967; Hs.115274; Indian hedgehog protein (IHH); ovar; diag
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centro; lung; blad; headnk; CTL+s.m.
 411296; BE207307; Hs.10114; growth suppressor 1; sarc; diag
 411358; R47479; Hs.94761; KIAA1691 protein; mela;renal; sarc; mAb
 411388; X72925; Hs.69752; desmocollin 1; headnk; mela; mAb
 411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMEN; ovar; diag
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); panc; pros; stom; breast; uter; cerv; ovar; mAb
 411573; AB029000; Hs.70823; KIAA1077 protein; panc; headnk; lung; stom; diag
 411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag
 411732; U47924; Hs.71642; guanine nucleotide binding prot; lung; diag
 411768; NM_013371; Hs.71979; Interleukin 19; ovar; uter; cerv; diag
 411789; AF245505; Hs.72157; Adican; breast; panc; lung; stom; headnk; ovar; uter; esoph; sarc; diag
 411825; AK000334; Hs.352415; solute carrier family 39 (zinc; colon; ovar; mAb
 411828; AW161449; Hs.72290; wingless-type MMTV integration; ovar; diag
 411869; W20027; Hs.23439; ESTs; angio; diag
 411874; AA096108; Hs.20403; ESTs; blad; diag
 411880; AW872477; ; gbhm30f03.x1 NCL_CGAP_Thy4 Ho; blad; diag
 411945; AL033527; Hs.92137; L-myc-2 protein (MYCL2); blad; ovar; CTL+s.m.
 412006; AW451618; Hs.380683; ESTs; sarc; diag
 412026; AA383618; Hs.73073; testis-specific ankyrin motif ; test; diag
 412045; AA099802; Hs.83883; transmembrane, prostate androg; pros; mAb+s.m.
 412099; U64198; Hs.73165; Interleukin 12 receptor, beta ; leuk; mela; mAb
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc; fibro; diag
 412115; AK001763; Hs.73239; hypothetical protein FLJ10901; lung; blad; CTL+s.m.
 412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb
 412133; U83460; Hs.380728; solute carrier family 31 (copp; pros; mAb
 412228; AW503785; Hs.73792; complement component (3d/Epste; mela; mAb
 412247; AF022375; Hs.73793; vascular endothelial growth fa; renal; glio; blad; colon; diag
 412265; AA101325; Hs.86154; hypothetical protein FLJ12457; test; CTL+s.m.
 412326; R07566; Hs.73817; small inducible cytokine A3 (h; pros; leuk; diag
 412351; AL135960; Hs.73828; T-cell acute lymphocytic leuke; angio; CTL+s.m.
 412420; AL035668; Hs.73853; bone morphogenetic protein 2; blad; glio; lung; stom; angio; diag
 412448; L12964; Hs.73895; tumor necrosis factor receptor; leuk; mAb
 412471; M63193; Hs.73946; endothelial cell growth factor; cerv; mela; esoph; diag
 412490; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 f1; mela; diag
 412519; AA196241; Hs.73980; troponin T1, skeletal, slow; sarc; diag
 412530; AA766268; Hs.266273; hypothetical protein FLJ13346; blad; lung; diag
 412564; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag
 412580; AA113262; Hs.17901; similar to CABLES (Homo sapien; diag
 412610; X90908; Hs.74126; fatty acid binding protein 6; ; blad; diag
 412661; N32860; Hs.24611; ESTs, Weakly similar to I54374; blad; CTL+s.m.
 412715; NM_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.
 412723; AA648459; Hs.335951; hypothetical protein AF301222; lung; blad; headnk; colon; stom; uter; diag
 412755; BE144306; Hs.179891; ESTs, Weakly similar to P4HA_H; angio; s.m.
 412811; H06382; Hs.349705; ESTs; lung; diag
 412817; AL037159; Hs.74819; proteasome (prosome, macropain; lung; s.m.
 412843; AF007655; Hs.74624; protein tyrosine phosphatase, ; pros; mAb
 412856; BE386745; Hs.74631; basigin (OK blood group); mela; mAb
 412926; A1879076; Hs.75061; macrophage myristoylated elan; mela; CTL+s.m.
 412939; AW411491; Hs.75069; eukaryotic translation elongat; mela; renal; diag
 412970; AB026436; Hs.177534; dual specificity phosphatase 1; breast; mela; s.m.
 412986; X81120; Hs.75110; cannabinoid receptor 1 (brain); glio; mAb
 413004; T35901; Hs.75117; interleukin enhancer binding f; lung; diag
 413011; AW088115; Hs.821; biglycan; lung; CTL+s.m.
 413049; NM_002151; Hs.823; hepsin (transmembrane protease; pros; mAb
 413095; AA494359; Hs.30715; potassium voltage-gated channel; panc; stom; renal; colon; mAb+s.m.
 413125; BE244589; Hs.75207; glyoxalase I; pros; s.m.
 413126; AW419203; Hs.174174; ESTs; angio; diag
 413129; AF292100; Hs.104613; RP42 homolog; lung; diag
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent; angio; CTL+s.m.
 413142; M81740; Hs.75212; ornithine decarboxylase 1; lung; s.m.
 413163; Y00815; Hs.75216; protein tyrosine phosphatase, ; pros; mAb
 413171; AA318325; Hs.75219; tyrosinase-related protein 1; mela; mAb
 413190; AA151802; Hs.40368; adaptor-related protein complex; mela; diag
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 f5; esoph; cerv; diag
 413223; A1732182; Hs.191866; ESTs; lung; diag
 413268; AL039079; Hs.75256; regulator of G-protein signal; headnk; CTL+s.m.
 413281; AA861271; Hs.22024; transcription factor BMAL2; lung; blad; headnk; panc; angio; diag
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; test; s.m.
 413328; Y15723; Hs.75295; guanylate cyclase 1, soluble, ; pros; s.m.
 413335; A1613318; Hs.48442; ESTs; ovar; diag
 413364; BE536218; Hs.137516; nidogen-like 1; lung; diag
 413372; H55532; Hs.349695; tubulin, alpha 2; test; diag
 413435; X51405; Hs.75360; carboxypeptidase E; pros; glio; panc; sarc; diag
 413436; AF238083; Hs.68061; sphingosine kinase 1; sarc; s.m.
 413472; BE242870; Hs.75379; solute carrier family 1 (glut; glio; mAb
 413566; AW604451; Hs.381153; sprouty (Drosophila) homolog 4; sarc; CTL+s.m.

- 413573; A1733859; Hs.149089; ESTs; lung; diag
 413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag
 413597; AW302885; Hs.117183; ESTs; pros; diag
 5 413623; AA825721; Hs.246973; Intron of Bicaudal D homolog 1; ovar; pros; diag
 413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb
 413711; AW291765; Hs.75486; heat shock transcription factor; rena; diag
 413753; U17760; Hs.75517; laminin, beta 3 (nlcein (125kD); lung, blad, headnk, panc, cerv, esoph, colon; diag
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag
 10 413778; AA090235; Hs.75535; myosin, light polypeptide 2, r; sarc; diag
 413794; AF234532; Hs.61638; myosin X; meta; diag
 413804; T64682; ; gbtc48b02.r1 Stratagene liver; blad; diag
 413808; J00287; Hs.350038; Homo sapiens mRNA for caldesmo; esoph; diag
 413813; M96956; Hs.75561; teratocarcinoma-derived growth; colon; diag
 15 413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.
 413842; M29383; Hs.856; interferon, gamma; leuk; diag
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; fibro, renal; mAb
 413880; A1660842; Hs.110915; interleukin 22 receptor; panc, colon; mAb+s.m.
 413924; AL119964; Hs.75616; seladin-1; pros, breast, ovar; diag
 20 413943; AW294416; Hs.144687; Homo sapiens cDNA FLJ12981 f1s; blad, lung; CTL+s.m.
 413985; A1018666; Hs.75667; synaptophysin; glio, sarc; mAb
 414004; AA737033; Hs.7155; ESTs, Moderately similar to 21; panc, meta; diag
 414020; NM_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag
 414034; U89277; Hs.305985; early development regulator 1; test; CTL+s.m.
 25 414035; Y00630; Hs.75716; serine (or cysteine) proteinases; lung, cerv, headnk, blad; s.m.
 414053; BE391635; Hs.75725; transgelin 2; blad; diag
 414061; NM_000699; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag
 414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 f1s; pros; diag
 414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 family; pros, panc, sarc; s.m.
 30 414142; AW368397; Hs.334485; hemicentin (fibulin 6); fibro, panc, sarc; diag
 414181; AA136108; Hs.184852; KIAA1553 protein; test; diag
 414166; AW888941; Hs.75789; N-myc downstream regulated; pros, renal; diag
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 f1; glio; diag
 414219; W20010; Hs.75823; ALL1-fused gene from chromosome; sarc; diag
 35 414221; AW450979; ; gb:U1-H-B13-ala-a-12-O-U1.s1 N; blad; diag
 414251; AL042306; Hs.97689; VASA protein; test; CTL+s.m.
 414259; W44633; Hs.301296; integrin, beta-like 1 (with EG; panc; diag
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; test; diag
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb
 40 414368; W70171; Hs.75939; uridine monophosphate kinase; lung; s.m.
 414386; X00442; Hs.75990; haptoglobin; ovar; diag
 414416; AW409985; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.
 414420; AA043424; Hs.76095; immediate early response 3; panc, colon; diag
 414430; A1346201; Hs.76118; ubiquitin carboxyl-terminal es; lung; s.m.
 414443; AU077268; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb
 45 414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 414477; U41635; Hs.76228; amplified in osteosarcoma; sarc; diag
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antig; meta; mAb
 414521; D28124; Hs.76307; neuroblastoma, suppression of; breast, ovar, uter, pros, blad, panc, colon, stom, fibro; diag
 50 414565; AA502972; Hs.183390; hypothetical protein FLJ13590; pros; diag
 414569; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 414575; H11257; Hs.375743; Homo sapiens clone IMAGE45193; renal; diag
 414595; AA641726; Hs.289015; hypothetical protein MGC4171; blad; diag
 414602; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb
 55 414683; S78296; Hs.76888; hypothetical protein MGC12702; blad, lung, test; diag
 414732; AW410976; Hs.77152; minichromosome maintenance def; test, blad; diag
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila); lung, blad, test; CTL+s.m.
 414776; AA155598; Hs.212839; hypothetical protein FLJ14195; angio; diag
 414786; A1248482; Hs.243010; Homo sapiens cDNA FLJ14372 f1s; angio; diag
 60 414799; A1752416; Hs.77326; insulin-like growth factor bin; renal; diag
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; lung; mAb
 414807; A1738616; Hs.77348; hydroxyprostaglandin dehydroge; blad; s.m.
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD7; lung; mAb+s.m.
 414825; X06370; Hs.77432; epidermal growth factor recept; glio, lung, renal, esoph, panc, headnk, leuk; mAb+s.m.
 65 414915; NM_002462; Hs.76391; myxovirus (influenza) resist; esoph; diag
 414918; A1219207; Hs.77222; hypothetical protein FLJ13459; blad; CTL
 414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag
 414945; BE076358; Hs.77667; lymphocyte antigen 6 complex; meta; mAb
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag
 70 414998; NM_002543; Hs.77729; oxidised low density lipoprote; fibro, ovar, panc, colon; mAb
 415003; M11437; Hs.77741; kininogen; panc; diag
 415025; AW207091; Hs.72307; ESTs; blad; diag
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Co; lung, headnk; s.m.
 415178; D80503; Hs.46692; ESTs; blad; diag
 75 415214; A1445236; Hs.125124; EphB2; colon, stom; mAb
 415314; N88802; Hs.5422; glycoprotein M6B; meta; mAb
 415457; AW081710; Hs.7359; Homo sapiens testes specific A; fibro, ovar, uter; CTL+s.m.
 415511; A1732617; Hs.182362; ESTs; blad, ovar, renal; diag
 415542; R13474; Hs.280263; ESTs, Weakly similar to I38022; blad; diag
 80 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.
 415752; BE314524; Hs.78776; putative transmembrane protei; endo, uter, breast, stom, blad, meta; mAb
 415786; AW419198; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 415787; H01463; Hs.93534; ESTs; pros; diag
 415819; AU077330; Hs.360791; transcription elongation factor; test; CTL+s.m.

- 415829; AW450198; Hs.163742; ESTs; test; diag
 415857; AA866115; Hs.127787; Homo sapiens cDNA FLJ11381 fis; lung; test; diag
 415910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb
 415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colo; test; diag
 415989; AJ267700; Hs.351201; ESTs; pros, ovar, blad, lung, headnk, panc, colon, sarc; diag
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; pros, fibro; mAb
 415999; AA172179; Hs.294029; ESTs; pros, uter; diag
 416018; AW138239; Hs.78977; proprotein convertase subtilisin; colon, panc, lung; diag
 416030; H15261; Hs.21948; ESTs; breast, fibro; diag
 416065; BE267931; Hs.78996; proliferating cell nuclear ant; blad, lung, headnk, mela; CTL+s.m.
 416111; AA033813; Hs.79018; chromatin assembly factor 1, s; lung, stom; CTL+s.m.
 416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag
 416201; AA467752; Hs.195161; ESTs; test; diag
 416208; AW291168; Hs.41295; ESTs, Weakly similar to MUC2_H; lung; diag
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calc; ovar; diag
 416225; AA577730; Hs.188684; ESTs, Weakly similar to PC4259; pros, blad; diag
 416350; AF188625; Hs.189507; phospholipase A2, group IID; test, mela, fibro; diag
 416370; N90470; Hs.203697; CD38 antigen (p45); pros, glio; mAb+CTL
 416373; AA195845; Hs.73680; ESTs, Weakly similar to S12658; sarc; diag
 416402; NM_000715; Hs.1012; complement component 4-binding; fibro; diag
 416448; L13210; Hs.79339; lectin, galactoside-binding, s; ovar, colon, stom; diag
 416498; U33532; Hs.79351; potassium channel, subfamily K; panc, stom, breast, ovar, colon; mAb
 416539; Y07909; Hs.79368; epithelial membrane protein 1; pros, headnk; diag
 416602; NM_006159; Hs.367895; Protein kinase C-binding prote; breast; diag
 416640; BE262478; Hs.13406; neuron-specific protein; mela; diag
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad, lung, headnk, cerv, panc, angio; diag
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; test; CTL+s.m.
 416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactose; angio; s.m.
 416819; U77735; Hs.80205; pim-2 oncogene; lung, test; diag
 416881; N32520; Hs.141358; ESTs; mela; diag
 416929; N20535; Hs.43265; melanotin 1; mela; diag
 416975; NM_004131; Hs.1051; granzyme B (granzyme 2, cytoto; mela; s.m.
 417003; AL038170; Hs.80756; betaine-homocysteine methyltra; blad; s.m.
 417070; Z19077; Hs.172004; ilin; sarc; diag
 417105; X60992; Hs.81226; CD6 antigen; fibro; mAb
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotei; test; CTL+s.m.
 417124; BE122762; Hs.25338; ESTs; angio; diag
 417148; AA359896; Hs.374554; hypothetical protein FLJ14902; panc; diag
 417151; AA194055; Hs.293858; ESTs; blad; diag
 417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros, sarc; diag
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.
 417237; H86385; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.
 417259; AW903838; Hs.81800; chondroitin sulfate proteoglyc; panc, breast; diag
 417275; X63578; Hs.295449; parvalbumin; blad; diag
 417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag
 417308; H60720; Hs.81892; KIAA0101 gene product; lung, headnk, blad, cerv, angio, mela, sarc; diag
 417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.
 417333; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
 417355; D13168; Hs.82002; endothelin receptor type B; glio, mela; mAb
 417365; D50683; Hs.82028; transforming growth factor, ba; fibro, angio; mAb
 417366; BE185289; Hs.1076; small proline-rich protein 18; lung, blad, headnk, panc, esoph, mela; diag
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; fibro, mela; diag
 417391; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 417400; AA663486; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 417407; AA923278; Hs.290905; ESTs, Weakly similar to protea; test, pros; s.m.
 417409; BE272508; Hs.82109; syndecan 1; blad; diag
 417412; X18896; Hs.82112; interleukin 1 receptor, type I; fibro, pros, panc; mAb
 417426; NM_002291; Hs.82124; laminin, beta 1; angio; diag
 417437; U52682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.
 417512; X76534; Hs.82226; glycoprotein (transmembrane) n; lung, mela, headnk, panc, breast; mAb
 417515; L24203; Hs.82237; ataxia-telangiectasia group D-; lung, headnk, blad; diag
 417542; J04129; Hs.82269; progestagen-associated endomet; lung, mela; diag
 417592; AA204664; Hs.182437; ESTs, Weakly similar to IS4383; test; diag
 417599; AA204688; Hs.62954; ESTs; blad, esoph; diag
 417621; AV654694; Hs.82316; interferon-induced, hepatitis; esoph; diag
 417695; BE241624; Hs.82401; CD69 antigen (p60, early T-cell; pros; mAb
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb
 417715; AW999587; Hs.86366; ESTs; blad, lung, headnk; diag
 417720; AA205625; Hs.208067; ESTs; blad, lung, esoph, headnk; diag
 417750; AJ267720; Hs.260523; synovial sarcoma, translocated; sarc; diag
 417777; AJ823763; Hs.7055; ESTs, Weakly similar to I78885; test; s.m.
 417791; AW965339; Hs.44269; ESTs; ovar, blad, lung, headnk; CTL+s.m.
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EG; panc, fibro; diag
 417805; U38545; Hs.82587; phospholipase D1, phosphatidyl; angio; s.m.
 417831; H16423; Hs.82685; CD47 antigen (Rb-related antig; ovar; mAb
 417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 fis; pros; diag
 417847; AJ521558; Hs.7331; hypothetical protein FLJ22316; ovar; diag
 417849; AW291587; Hs.82733; nidogen 2; angio, headnk; diag
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, ; panc; mAb+s.m.
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesio; mela; mAb
 417886; AA214584; ; ESTs; test, ovar; diag
 417900; BE250127; Hs.82908; CDC20 (cell division cycle 20; lung, stom, test, blad, headnk, cerv, esoph; CTL+s.m.
 417911; AA333387; Hs.82916; chaperonin containing TCP1, su; test; diag

- 417944; AU077196; Hs.82985; collagen, type V, alpha 2; sarc; diag
 417975; AA641836; Hs.30085; hypothetical protein FLJ23186; colon, stom, lung; mAb
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gamma; colon, stom, fibros; diag
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family; lung, headnk, esoph; s.m.
 418036; Z37976; Hs.83337; latent transforming growth fac; angio; diag
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag
 418067; A127958; Hs.83393; cystatin E/M; headnk, panc, blad; diag
 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS; blad; s.m.
 418113; A1272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glio, test, sarc; CTL+s.m.
 418134; AA397769; Hs.86617; ESTs; test; diag
 418140; BE613836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.
 418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.
 418216; AA662240; Hs.283099; AF15q14 protease; headnk, lung, blad; diag
 418245; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 418283; S79895; Hs.83942; cathepsin K (pseudodysostosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag
 418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibi; headnk, lung, blad; s.m.
 418338; NM_002522; Hs.84154; neuronal pentraxin I; sarc; diag
 418339; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase; cerv, lung; s.m.
 418371; M13560; Hs.84298; CD74 antigen (invariant) polypeptide; renal; mAb
 418379; AA218940; Hs.137516; fidgetin-like 1; lung; diag
 418394; AF132818; Hs.84728; Kruppel-like factor 5 (intest); panc; CTL+s.m.
 418396; A1765805; Hs.26691; SLC2A12 Solute carrier family; pros; mAb
 418397; NM_001269; Hs.84746; chromosome condensation 1; lung; diag
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag
 418406; X73501; Hs.84905; cytokeratin 20; blad, colon; diag
 418432; M14156; Hs.85112; insulin-like growth factor 1 (; pros, fibro; diag
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide; fibro; mAb
 418462; BE001596; Hs.85266; integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb
 418543; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb
 418576; AW968159; Hs.302740; Epithelial calcium channel 2, ; pros; mAb+s.m.
 418610; AW245993; Hs.32417; hypothetical protein MGC2742; pros; diag
 418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb
 418655; AA226354; Hs.111240; ESTs; pros; diag
 418661; NM_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.
 418663; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb
 418683; U90908; Hs.87241; hypothetical protein from clone; angio; CTL+s.m.
 418686; Z36830; Hs.87268; annexin A8; blad, lung; diag
 418693; A1750878; Hs.87409; thrombospondin 1; angio, panc; diag
 418696; AW959433; Hs.326290; hypothetical protein FLJ12581; test; diag
 418739; AA310964; Hs.88012; SHP2 interacting transmembrane; mela; diag
 418756; AA252254; Hs.226949; ESTs; test; diag
 418825; AA228881; Hs.22394; hypothetical protein FLJ10893; angio; diag
 418829; AA516531; Hs.55999; NK homeobox (Drosophila); famit; pros; diag
 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-fam; ovar, pros, breast, lung; diag
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate r; fibro; s.m.
 418888; AU076801; Hs.89436; cadherin 17, L1 cadherin (live; colon, stom, ovar, uter, panc; mAb+s.m.
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red b; mela, fibro; mAb
 418932; L34059; Hs.89484; cadherin 4, type 1, R-cadherin; glio; mAb
 418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag
 418968; NM_000078; Hs.89538; cholesteryl ester transfer pro; mela; diag
 418994; AA296520; Hs.89546; selectin E (endothelial adhesi; pros, angio; mAb
 419038; AW134924; Hs.68290; ESTs; pros; diag
 419073; AW372170; Hs.183918; transmembrane receptor Unc5H2; ovar, renal, blad, lung; mAb
 419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag
 419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag
 419092; J05581; Hs.89603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb
 419222; AD001528; Hs.89718; spermine synthase; pros; s.m.
 419223; X50111; Hs.1244; CD9 antigen (p24); breast, pros, ovar; mAb
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227; fibro; diag
 419261; X07876; Hs.89791; wingless-type MMTV Integration; panc; diag
 419264; AA877104; Hs.293672; ESTs, Weakly similar to ALUB_H; pros; diag
 419290; A128114; Hs.112885; spinal cord-derived growth fac; panc; diag
 419358; A1656166; Hs.7331; hypothetical protein FLJ22316; uter, ovar; diag
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag
 419440; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag
 419490; NM_008144; Hs.90708; granzyme A (granzyme 1, cytol; fibro; s.m.
 419519; A198719; Hs.176376; ESTs; mela; diag
 419551; AW582256; Hs.91011; anterior gradient 2 (Xenopus I; panc, pros, breast; diag
 419559; Y07828; Hs.91096; ring finger protein; blad, colon, stom; CTL+s.m.
 419568; AB026116; Hs.283078; HOAT4; renal; mAb
 419569; A1971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag
 419588; H87546; Hs.49768; ESTs; mela, sarc; diag
 419587; AU077005; Hs.82208; a disintegrin and metalloprote; breast, cerv, angio; mAb
 419593; AA133749; Hs.301350; FXD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb
 419721; NM_001650; Hs.315369; aquaporin 4; glio, lung, fibro; mAb
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA; blad, headnk; diag
 419749; X73608; Hs.93029; sparse/osteonectin, cwcx and ka; pros, panc, lung; diag
 419752; AA249573; Hs.152618; ESTs, Moderately similar to ZNF; lung; diag

- 5 419839; U24577; Hs.93304; phospholipase A2, group VII (p; pros; lung; diag
419870; AW403911; Hs.266175; phosphoprotein associated with; meta; diag
419875; AA853410; Hs.93557; proenkephalin; sarc; diag
10 419948; AB041035; Hs.93847; NM_016931: Homo sapiens NADPH c; angio; mAb
419956; AL137939; Hs.40096; cadherin 19, type 2; meta; mAb
419968; X04430; Hs.93913; Interleukin 6 (interferon, bet; lung, panc, esoph; diag
419981; AA897581; Hs.128773; ESTs; angio; diag
420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag
10 420062; AW411096; Hs.94785; TGF(beta)-induced transcript; test; CTL+s.m.
420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptide; fibro; mAb
420154; AI093155; Hs.95420; G antigen family C 1 protein (i; pros, test; CTL+s.m.
15 420174; AI824144; Hs.199749; ESTs; angio; CTL+s.m.
420208; BE276055; Hs.95972; silver (mouse homolog) like; meta; sarc; mAb
420209; AA256444; Hs.126485; hypothetical protein FLJ12604; angio; diag
420218; AW958037; Hs.381105; ribosomal protein L4; meta; pros; diag
420255; NM_007289; Hs.1298; membrana metallo-endopeptidase; pros; mAb
420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin; angio; fibro; mAb
20 420287; N37030; Hs.173337; ESTs; meta; sarc; diag
420281; AI623693; Hs.323494; Predicted cation efflux pump; lung, blad, ovar, panc; mAb
420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; meta; diag
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339; meta; mAb
420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide; fibro; mAb
25 420344; BE463721; Hs.97101; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb
420347; AL033539; Hs.97124; Human DNA sequence from clone; test; diag
420360; U83171; Hs.97203; small inducible cytokine subfa; leuk; diag
420367; AA258090; Hs.257028; ESTs; test; diag
420376; AL137471; Hs.97266; protocadherin 18; sarc; mAb+s.m.
30 420378; NM_014143; Hs.97269; B7-H1 protein; leuk; mAb
420380; AA640891; Hs.102406; ESTs; lung; diag
420424; AB033036; Hs.97594; KIAA1210 protein; pros; diag
420462; AF050147; Hs.97932; chondromodulin I precursor; lung, EWS, sarc; mAb
420474; L09753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb
35 420544; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
420576; AA297634; Hs.54925; KIAA1859 protein; sarc; diag
420598; NM_002692; Hs.99185; polymerase (DNA directed); eps; test; CTL+s.m.
420633; NM_014581; Hs.274480; odorant-binding protein 2B (OB; breast, endo; diag
420656; AA279098; Hs.187636; ESTs; fibro; diag
40 420710; NM_007009; Hs.99875; zona pellucida binding protein; test; diag
420729; AW964897; Hs.290825; ESTs; pros; diag
420757; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
420769; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis; test; diag
420783; AI659838; Hs.99923; lectin, galactoside-binding, s; lung, blad, headnk; diag
45 420789; AI670057; Hs.199882; ESTs; renal; diag
420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag
420908; AL049974; Hs.100261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag
420923; AF097021; Hs.273321; differentially expressed in he; blad, colon; diag
50 420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, meta; diag
420981; L40904; Hs.100724; peroxisome proliferative activ; colon; mAb+s.m.
421016; AA504583; Hs.101047; transcription factor 3 (E2A lnc; test; CTL+s.m.
421044; AF061871; Hs.101302; Human DNA sequence from clone; panc; diag
421059; AI654133; Hs.358247; thyroid receptor interacting p; pros; mAb+s.m.
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-i; blad, uter; diag
55 421070; AA283185; Hs.19327; ESTs; blad; diag
421100; AW351839; Hs.124660; Homo sapiens cDNA: FLJ21763 ft; blad; diag
421133; AA814971; Hs.26410; ESTs; lung; diag
421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 fis; BPH; diag
421155; H87879; Hs.102267; lysyl oxidase; headnk, panc, renal, sarc; diag
60 421218; NM_000499; Hs.72912; cytochrome P450, subfamily I (i; blad, angio; diag
421233; AA209534; Hs.284243; tetraspan NET-6 protein; pros, breast, ovar; mAb
421241; X91817; Hs.102866; transketolase-like 1; test; s.m.
421302; T34462; Hs.103291; neuritin; uter, endo; diag
65 421305; BE397354; Hs.324830; diptheria toxin resistance pro; ovar; diag
421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, lung, angio, test, sarc; diag
421341; AJ243212; Hs.279611; deleted in malignant brain tumor; lung; diag
421350; AW301608; Hs.278188; ESTs, Moderately similar to I5; test; diag
421373; AA808229; Hs.222088; ESTs; blad; diag
421433; AI829192; Hs.22380; ESTs; pros; diag
70 421451; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
421458; NM_003654; Hs.104576; carbohydrate (keratan sulfate); sarc; s.m.
421478; AI683243; Hs.97258; ESTs, Moderately similar to S2; ovar, blad, renal, uter; diag
421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag
421502; AF111856; Hs.106039; solute carrier family 34 (sodt; ovar, fibro; mAb
75 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.
421508; NM_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, meta; CTL+s.m.
421535; AB002359; Hs.105478; phosphoribosylformylglycanimid; test; s.m.
421537; BE383488; Hs.105547; neural proliferation, differen; pros; diag
421566; NM_000399; Hs.1395; early growth response 2 (Krox-; pros; CTL+s.m.
80 421579; NM_002975; Hs.105927; stem cell growth factor; lymph; sarc; mAb
421633; AF121860; Hs.106260; sorting nexin 10; meta; diag
421650; AA781795; Hs.343800; ESTs; meta; diag
421666; AL035250; Hs.1408; endothelin 3; meta; diag
421727; Y13153; Hs.107318; kynurenine 3-monooxygenase (ky; breast; s.m.

- 421773; W59233; Hs.112457; ESTs; meta, esoph, sarc; diag
 421777; BE562088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag
 421779; AJ878159; Hs.108219; wingless-type MMTV integration; colon, ovar; diag
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase; fibro; s.m.
 5 421814; L12350; Hs.108623; thrombospondin 2; panc; diag
 421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 421887; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 421896; N52293; Hs.45107; ESTs; pros; diag
 10 421917; AB028943; Hs.109445; KIAA1020 protein; test; diag
 421920; BE551245; Hs.1438; gamma-aminobutyric acid (GABA); sarc; mAb
 421924; BE514514; Hs.109606; coronin, actin-binding protein; fibro; diag
 421948; L42583; Hs.334309; keratin 6A; lung, headnk, blad, esoph, cerv, meta; diag
 421952; AA300900; Hs.98849; dynein light chain 2B (DNL2B); fibro; diag
 15 421991; NM_014918; Hs.110486; KIAA0950 protein; panc; diag
 421996; AW583807; Hs.1460; glucagon; panc; diag
 422002; X70070; Hs.110642; neurotensin receptor 1 (high a; colon; mAb
 422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.
 20 422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glio; mAb
 422087; X58968; Hs.111301; matrix metalloproteinase 2 (ge; sarc; diag
 422089; AA523172; Hs.103135; ESTs; Weakly similar to SFR4_H; pros; diag
 422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.
 422095; AB68872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.
 422099; AA156022; Hs.111518; hypothetical protein; angio; CTL+s.m.
 25 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.
 422110; AI376736; Hs.121555; secreted protein, acidic, cyst; panc; diag
 422119; AJ277829; Hs.111862; KIAA0590 gene product; blad; diag
 422134; AW179019; Hs.112110; mitochondrial ribosomal prote; lung; diag
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.
 30 422163; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 422164; NM_014312; Hs.112377; cortic al thymocyte receptor (l; blad; mAb+s.m.
 422168; AA586894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, meta, esoph, sarc, cerv; CTL+s.m.
 422170; AJ791949; Hs.112432; anti-Mullerian hormone; uter, blad; diag
 422173; BE385828; Hs.250619; phorbol-like protein MDS019; meta; diag
 35 422247; U18244; Hs.113502; solute carrier family 1 (high; blad; mAb
 422278; AF072873; Hs.114218; fritzled (Drosophila) homolog; ovar, headnk, blad, cerv, lung, panc, stom; mAb
 422309; U79745; Hs.114924; solute carrier family 16 (mono; meta; mAb+s.m.
 422311; AF073515; Hs.114948; cytokine receptor-like factor; lung, fibro; diag
 422355; AW403724; Hs.300697; coagulation factor VII (serum; fibro; diag
 40 422363; T55979; Hs.115474; replication factor C (activator; meta, colon; diag
 422398; AI476149; Hs.334489; hypothetical protein FLJ21892; fibro; CTL+s.m.
 422406; AF025441; Hs.116208; Opa-interacting protein 5; blad, lung; diag
 422420; U03398; Hs.1524; tumor necrosis factor (ligand); colon, panc, stom, leuk; mAb
 422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb
 45 422440; NM_004812; Hs.116724; aldo-keto reductase family 1; lung, headnk; s.m.
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag
 422532; AL008726; Hs.118126; protective protein for beta-ga; renal, meta; s.m.
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea; panc, test, meta; diag
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin; panc; mAb+s.m.
 50 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase; esoph, meta; s.m.
 422603; BE242687; Hs.118651; hematopoietically expressed ho; angio; CTL+s.m.
 422633; X56832; Hs.118804; enolase 3, (beta, muscle); sarc; s.m.
 422658; AF231981; Hs.250175; homolog of yeast long chain po; pros; diag
 422689; AW856665; Hs.299797; gbr-RC3-CT0297-290100-013-d03 C; test; diag
 55 422726; U11690; Hs.1572; facio-genital dysplasia (Aarskog; test; diag
 422728; AW937826; Hs.103262; MAD (mothers against decapentap; pros; diag
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.
 422835; BE218705; Hs.121378; metallothionein-like 5, testis; breast; diag
 422871; AL031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag
 60 422887; AJ751848; Hs.49215; ESTs; sarc; CTL+s.m.
 422938; NM_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.
 422963; M79141; Hs.13234; ESTs; lung, panc; diag
 422997; BE018212; Hs.122908; DNA replication factor; test; CTL+s.m.
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase; blad, headnk, meta; mAb+diag
 65 423052; M28214; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 423189; M59371; Hs.171596; EphA2; colon, ovar; mAb
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; fibro; CTL+s.m.
 423198; M81933; Hs.1634; cell division cycle 25A; test; CTL+s.m.
 423201; NM_000163; Hs.125180; growth hormone receptor; pros; mAb
 70 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (e; lung, esoph; diag
 423271; W47225; Hs.126256; Interleukin 1, beta; blad, stom, esoph; diag
 423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag
 423354; AB011130; Hs.127438; calcium channel, voltage-depend; test, fibro; mAb
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide; pros; mAb
 75 423397; NM_001838; Hs.1652; chemokine (C-C motif) receptor; blad, meta; mAb
 423412; AF109300; Hs.351615; prostate cancer associated pro; pros; diag
 423422; AC005175; Hs.128425; NY-REN-24 antigen; glio; mAb+CTL
 423445; NM_014324; Hs.128749; alpha-methylacyl-CoA racemase; pros; s.m.
 423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.
 80 423458; AJ204212; Hs.351113; ESTs; test; CTL+s.m.
 423511; AF036328; Hs.129715; gonadotropin-releasing hormone; lung; diag
 423515; AA327017; Hs.176594; ESTs; ovar; diag
 423541; AA296922; Hs.129778; serine protease inhibitor, Kaz; colon, panc; diag
 423575; C18863; Hs.163443; Intron of perlestin (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

- 423605; AF047826; Hs.129887; cadherin 19, type 2; meta; mAb
 423642; AW452650; Hs.157148; hypothetical protein MGC13204; lung; diag
 423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc); lung; diag
 423685; BE350494; Hs.49753; ureal autoantigen with coiled; panc, uter, colon; CTL+s.m.
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag
 423739; AA398155; Hs.97600; ESTs; breast, ovar, panc; diag
 423761; NM_006184; Hs.132576; paired box gene 9; headnk; CTL+s.m.
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag
 423778; Y09267; Hs.132821; flavin containing monooxygenase; fibro; s.m.
 423779; AW071837; Hs.67971; TRANSCRIPTION FACTOR HES-5; gli; diag
 423787; AJ295745; Hs.236204; nuclear pore complex protein; test; esoph; diag
 423798; AF047033; Hs.132904; solute carrier family 4, sodiu; angio; mAb
 423799; AW026300; Hs.132905; 19A24 protein; meta; mAb
 423849; AL157425; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag
 423887; AL080207; Hs.134585; DKFZP434G232 protein; headnk, lung; diag
 423899; NM_001427; Hs.134989; engrailed homolog 2; meta; CTL+s.m.
 423905; AW579960; Hs.135150; lung type-I cell membrane-asso; test; mAb
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, me; test; diag
 423934; U89995; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.
 424001; W67883; Hs.137476; paternally expressed 10; breast, ovar; diag
 424012; AW368377; Hs.137559; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag
 424036; AA770688; Hs.348495; H2A histone family, member L; panc, ovar; CTL+s.m.
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, s; pros, fibro; mAb
 424078; AB006625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); test; s.m.
 424088; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag
 424125; M31669; Hs.1735; inhibin, beta B (activin AB bet; ovar, pros; diag
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag
 424153; AA451737; Hs.141496; MAGE-like 2; meta; CTL+s.m.
 424165; AW582904; Hs.142255; islet amyloid polypeptide; panc; mAb
 424212; NM_005814; Hs.143131; glycoprotein A33 (transmembran; colon, stom, ovar; mAb
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); meta, fibro; diag
 424244; AV647184; Hs.143601; hypothetical protein hCLA-iso; blad; diag
 424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag
 424264; D80400; Hs.239388; Human DNA sequence from clone; blad; mAb
 424308; AW975531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag
 424310; AA338648; Hs.50334; testes development-related NYD; fibro; diag
 424332; AA338919; Hs.101615; ESTs; pros; diag
 424339; BE257148; Hs.145416; endoglycan; pros, lung; diag
 424343; AW956360; Hs.4748; adenylate cyclase activating p; gli, ovar, uter; mAb
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast, uter, headnk; diag
 424420; BE614743; Hs.146688; prostaglandin E synthase; lung, blad; s.m.
 424440; AA340743; Hs.133208; ESTs; sarc; diag
 424441; X14850; Hs.147097; H2A histone family, member X; lung; diag
 424450; AL137526; Hs.147472; dynein intermediate chain 2; fibro; diag
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374; fibro; diag
 424578; AK001873; Hs.150890; hypothetical protein; test; CTL+s.m.
 424581; M62062; Hs.150917; catenin (cadherin-associated p; gli, ovar, uter; mAb+s.m.
 424586; NM_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.
 424629; M90656; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.
 424635; AA420687; Hs.115459; Homo sapiens cDNA FLJ14259 fis; gli; diag
 424676; Y08565; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 424704; AI263293; Hs.152096; cytochrome P450, subfamily IIJ; renal; s.m.
 424711; NM_005795; Hs.152175; calcitonin receptor-like; angio; mAb
 424717; H03754; Hs.152213; wingless-type MMTV integration; blad, lung, headnk; diag
 424800; AL035588; Hs.153203; MyoD family inhibitor; test, pros; diag
 424806; AA382523; Hs.105689; MSTP031 protein; angio; mAb
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad, ovar, headnk, esoph, cerv, uter; diag
 424846; AU077324; Hs.1832; neuropeptide Y; pros; diag
 424897; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
 424902; NM_003866; Hs.153687; inositol polyphospho-4-phosp; panc, leuk, meta; CTL+s.m.
 424954; NM_000546; Hs.1848; tumor protein p53 (Li-Fraumeni; meta, colon; CTL+s.m.
 424971; AA479005; Hs.154036; tumor suppressing subtransfera; panc, meta; CTL+s.m.
 424998; U58515; Hs.154138; chitinase 3-like 2; gli; diag
 425023; AW856889; Hs.154210; EDG-1 (endothelial different); angio; mAb
 425048; H05468; Hs.164502; ESTs; lung, blad; diag
 425057; AA826434; Hs.1619; achaete-scute complex (Drosoph; gli, lung; CTL+s.m.
 425088; AA663372; Hs.169395; hypothetical protein FLJ12015; gli, meta; diag
 425154; NM_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.
 425200; BE255203.comp; Hs.155101; ATP synthase, H transporting, ; panc; s.m.
 425206; NM_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb
 425211; M18667; Hs.1867; progastricsin (pepsinogen C); fibro, esoph, pros; diag
 425234; AW152225; Hs.165909; ESTs, Weakly similar to I38022; lung, angio, blad, meta; diag
 425235; AA353113; Hs.105468; Homo sapiens cDNA: FLJ22743 f; angio; diag
 425237; U07695; Hs.155227; EphB4; test; mAb
 425245; AI751788; Hs.155314; KIAA0095 gene product; lung; diag
 425259; AL049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 425262; D87119; Hs.155418; GS3955 protein; meta, renal; CTL+s.m.
 425266; J00077; Hs.155421; alpha-fetoprotein; lung; diag
 425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

- 425289; AW139342; Hs.155530; Interferon, gamma-inducible pr; meta; CTL+s.m.
 425308; M97639; Hs.155585; receptor tyrosine kinase-like; pros; sarc; mAb
 425367; BE271188; Hs.155975; protein tyrosine phosphatase; ; fibro; diag
 425371; D49441; Hs.155981; mesothelin; ovar; lung; fibro; mAb
 5 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (i; lung, blad, panc, angio, test, mela, esoph; CTL+s.m.
 425427; A1652662; Hs.317432; branched chain aminotransferase; test; s.m.
 425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag
 425465; L18964; Hs.1904; protein kinase C, iota; ovar; pros; colon; s.m.
 425525; AA358883; Hs.23871; ESTs; sarc; diag
 10 425545; N98529; Hs.158295; Homo sapiens, clone MGC:12401; ; sarc; diag
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 f; fibro; CTL+s.m.
 425572; AB011078; Hs.158307; undifferentiated embryonic cel; test; CTL+s.m.
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; test; CTL+s.m.
 425606; U52112; Hs.158331; renin-binding protein; mela; diag
 15 425628; NM_004476; Hs.1915; folate hydrolase (prostate-spe; pros; s.m.
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.
 425679; X05997; Hs.159177; lipase, gastric; esoph; s.m.
 425692; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 425695; NM_005401; Hs.159238; protein tyrosine phosphatase; ; lung; mAb+s.m.
 20 425709; AA383076; Hs.159274; outer dense fibre of sperm tail; test; diag
 425710; AF030880; Hs.159275; solute carrier family, member; ; pros; mAb
 425722; A1659076; Hs.97031; hypothetical protein MGC13047; mela; diag
 425726; AF085808; Hs.159330; uroplakin 3; pros; blad; diag
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA; ; test; diag
 25 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort; test; diag
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.
 425921; NM_007231; Hs.162211; solute carrier family 6 (neuro; stom, panc; mAb
 425976; C75094; Hs.334514; NG22 protein; pros; ovar; mAb
 426027; NM_002608; Hs.1976; platelet-derived growth factor; sarc; diag
 30 426050; AF017307; Hs.166096; E74-like factor 3 (ets domain; ; ovar, blad, stom; CTL+s.m.
 426059; BE292842; Hs.166120; interferon regulatory factor 7; esoph, cerv; CTL+s.m.
 426067; AW664691; Hs.97053; ESTs; lung; diag
 426088; AF038007; Hs.166196; ATPase, Class I, type 8B, memb; blad, lung; mAb
 426094; AF034611; Hs.166206; cubilin (intrinsic factor-coba; renal; diag
 35 426116; AA868729; Hs.144694; ESTs; fibro; diag
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophi; colon, stom, panc, pros, renal, fibro, cerv; mAb
 426166; BE244537; Hs.167382; natriuretic peptide receptor A; ovar; mAb
 426168; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; diag
 426172; AA371307; Hs.125056; ESTs; pros; diag
 40 426174; AA547959; Hs.115838; Homo sapiens similar to Echinor; breast, pros, fibro; diag
 426212; S71824; Hs.167988; neural cell adhesion molecule; ; glio; mAb
 426271; AF026547; Hs.169047; chondroitin sulfate proteoglyc; glio; diag
 426274; D38122; Hs.2007; tumor necrosis factor (ligand); fibro, mela; mAb
 426300; U15979; Hs.169228; delta-like homolog (Drosophila; ovar, sarc; mAb
 45 426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; breast; mAb
 426312; AF026939; Hs.181874; interferon-induced protein wit; esoph, mela; diag
 426320; W47595; Hs.169300; transforming growth factor, be; ovar, pros, blad, panc; diag
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.
 426363; M58524; Hs.2025; transforming growth factor, be; pros; diag
 50 426370; R98288; Hs.281706; sortilin 1; sarc; diag
 426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb
 426440; BE382756; Hs.169902; solute carrier family 2 (facil; lung, panc, ovar, blad, headnk, esoph; mAb
 426462; U59111; Hs.169993; dermatan sulphate proteoglycan; sarc; diag
 55 426470; AA528794; Hs.128644; ESTs; mela; diag
 426471; M22440; Hs.170009; transforming growth factor, at; headnk, renal, panc; diag
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; panc; mAb+s.m.
 426501; AW043782; Hs.293616; ESTs; pros, breast, glio, lung, mela; mAb
 426502; Y07759; Hs.170157; myosin VA (heavy polypeptide 1; mela; diag
 60 426534; U58096; Hs.2051; testis specific protein, Y-link; test; CTL+s.m.
 426535; AU077012; Hs.170279; ESTs, Weakly similar to ubiquit; angio; diag
 426555; NM_000372; Hs.2053; tyrosinase (oculocutaneous alb; mela, sarc; mAb
 426559; AB001914; Hs.170414; paired basic amino acid cleav; hepC, breast, ovar, renal; diag
 426575; M74826; Hs.170808; glutamate decarboxylase 2 (pan; panc; s.m.
 65 426627; AF012359; Hs.195685; ESTs; test; diag
 426635; BE395109; Hs.129327; hypothetical protein MGC13057; ovar; CTL+s.m.
 426682; AV660038; Hs.2056; UDP glycosyltransferase 1 fami; blad, lung; s.m.
 426691; NM_008201; Hs.171834; PCTAIRE protein kinase 1; ovar; CTL+s.m.
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 f; angio; mAb
 70 426721; AA383588; Hs.268545; ESTs, Weakly similar to T29012; fibro; diag
 426726; AA488915; Hs.171955; trophinin associated protein (i; test; diag
 426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag
 426752; X69490; Hs.172004; titin; sarc; diag
 426759; A1590401; Hs.21213; ESTs; mela; diag
 75 426793; X89887; Hs.172350; HIR (histone cell cycle regul; pros; CTL+s.m.
 426828; NM_000020; Hs.172670; activin A receptor type II-like; angio; mAb
 426866; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.
 426897; AW976570; Hs.97387; ESTs; lung; diag
 426900; AW163564; Hs.142375; ESTs; blad, pros; mAb
 80 426935; NM_000088; Hs.172926; collagen, type I, alpha 1; test, sarc; CTL+s.m.
 426968; A1493134; Hs.349204; sclerosin; lung; diag
 426968; U07616; Hs.173034; amphiphysin (Sliff-Mann syndro; blad; mAb+CTL
 426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 f; ovar, sarc; diag
 427080; AW068287; Hs.301175; ras-related C3 botulinum toxin; mela; diag

- 427099; AB032953; Hs.173560; odd Ozten-m homolog 2 (Drosop; headnk, esoph; diag
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb
 427244; AA02400; Hs.178045; ESTs; esoph; diag
 427260; AA663848; gbaae70b06.s1 Stragene schiz; lung; diag
 427274; NM_005211; Hs.174142; colony stimulating factor 1 re; pros, sarc; mAb
 427298; AA400495; ESTs; test; diag
 427318; AF186081; Hs.175783; zinc transporter; pros; mAb
 427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb
 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin); ovar; mAb
 427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag
 427398; AW390020; Hs.20415; chromosome 21 open reading fra; pros; diag
 427427; AF077345; Hs.177936; lectin, superfamily member 1 (; breast; diag
 427441; AA412605; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.
 427461; AA531527; Hs.332040; hypothetical protein MGC13010; pros; mAb
 427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfat; sarc; diag
 427486; AA974433; Hs.362432; fibroblast growth factor 4 (hs; test; diag
 427510; Z47542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.
 427515; T79526; Hs.179516; integral type I protein; pros; diag
 427521; AW973352; ESTs; test; diag
 427528; AU077143; Hs.179565; minichromosome maintenance def; mela; CTL+s.m.
 427535; R29543; Hs.2164; pro-platelet basic protein (in; fibro; diag
 427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag
 427550; BE242818; Hs.311609; nuclear RNA helicase, DECD var; mela; CTL+s.m.
 427557; NM_002659; Hs.179657; plasminogen activator, urokin; panc, colon, stom, ovar, cerv, blad, lung, headnk, esoph; mAb
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_H; test; diag
 427583; M82962; Hs.179704; meprin A, alpha (PABA peptide; colon; mAb
 427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc, stom, colon, ovar, cerv, sarc; diag
 427615; BE410107; Hs.179817; CG4-82 protein, PSDR1; pros; diag
 427634; AI399745; Hs.18449; hypothetical protein MGC10820; mela, sarc; diag
 427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fls; sarc; diag
 427666; AI791495; Hs.180142; calmodulin-like skn protein (; breast, cerv, blad, lung, headnk, esoph; diag
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fls; test; diag
 427668; AA298760; Hs.180191; hypothetical protein FLJ14904; lung, test; diag
 427681; AB018263; Hs.284232; tumor necrosis factor receptor; ovar; mAb+s.m.
 427698; AW972594; Hs.335499; ESTs; fibro; CTL+s.m.
 427701; AA411101; Hs.243886; nuclear autoantigenic sperm pr; lung; mAb+CTL
 427715; BE245274; Hs.180428; KIAA1181 protein; pros; diag
 427719; AI393122; Hs.134726; ESTs; test, blad; diag
 427730; AW250549; Hs.180577; granuln; mela; diag
 427786; BE407863; Hs.256871; ESTs; esoph, blad; diag
 427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb
 427811; M81057; Hs.180884; carboxypeptidase B1 (tissue); breast; s.m.
 427897; NM_017413; Hs.303084; apelin; peptide ligand for APJ; angio, renal, pros; diag
 427912; AL022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb
 427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb
 427961; AW293165; Hs.143134; ESTs; lung, sarc; diag
 428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; mela; diag
 428004; AA449563; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fl; lung; diag
 428046; AW812795; Hs.337534; ESTs, Moderately similar to I3; lung, colon; diag
 428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag
 428087; AA100673; Hs.182421; troponin C2, fast; sarc; CTL+s.m.
 428141; D50402; Hs.182611; solute carrier family 11 (prot; glio; mAb
 428153; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
 428169; AI928984; Hs.182793; golgi phosphoprotein 2; pros; diag
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar, sarc; CTL+s.m.
 428183; AW969728; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
 428206; AB020643; Hs.183006; KIAA0836 protein; angio; mAb
 428221; U95781; Hs.183075; ATPase, Ca transporting, card; sarc; s.m.
 428227; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, headnk, fibro, colon, stom, cerv, leuk, renal, test, mela, esoph, hepC; diag
 428248; AI126772; Hs.40479; ESTs; sarc; diag
 428293; BE250944; Hs.183556; solute carrier family 1 (neur; pros; mAb
 428305; AA446628; Hs.2799; cartilage linking protein 1; sarc; diag
 428329; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag
 428336; AA503115; Hs.183752; microsemnoprotein, beta-; pros; diag
 428355; BE256452; Hs.2257; vitronectin (serum spreading f; colon; diag
 428398; AI249368; Hs.98558; ESTs; pros, breast; diag
 428405; Y00762; Hs.2268; cholinergic receptor, nicotin; esoph, sarc; mAb
 428423; AU076517; Hs.184276; solute carrier family 9 (sodic; ovar; CTL+s.m.
 428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA s; lung, fibro; diag
 428467; AK002121; Hs.184465; hypothetical protein FLJ11259; fibro; mAb
 428471; X57348; Hs.184510; stratifin; lung, headnk, colon, panc; diag
 428645; AA431400; Hs.98729; ESTs, Weakly similar to Z01720; lung; s.m.
 428651; AF198478; Hs.188401; annexin A10; blad, stom, panc; diag
 428667; AI375550; Hs.346868; nucleolar protein p40; homolog; fibro, uter; diag
 428722; U76456; Hs.190787; tissue inhibitor of metallopro; glio; diag
 428728; NM_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.
 428771; AB028992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.
 428784; Y12851; Hs.193470; purinergic receptor P2X, ligand; glio, mela; mAb
 428800; M57627; Hs.193717; Interleukin 10; fibro; diag
 428801; AW277121; Hs.254881; ESTs; pros; diag
 428804; AK000713; Hs.193736; hypothetical protein FLJ20708; mela; diag

- 428810; AF068236; Hs.193788; nitric oxide synthase 2A (inducible); lung; s.m.
 428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.
 428824; W23624; Hs.173059; ESTs; panc; diag
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZNF; panc, uter; diag
 428841; A1418430; Hs.104935; ESTs; renal; diag
 428848; NM_000230; Hs.194236; leptin (murine obesity homolog); sarc; diag
 428862; NM_000346; Hs.2316; SRY (sex determining region Y); pros, sarc; CTL+s.m.
 428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag
 428928; BE409838; Hs.194657; cadherin 1, type 1, E-cadherin; pros, breast, stom, blad; mAb
 428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag
 428957; NM_003881; Hs.194679; WNT1 Inducible signaling pathw; cerv; diag
 428959; AF100779; Hs.194680; WNT1 Inducible signaling pathw; sarc; diag
 428977; AK001404; Hs.194698; cyclin B2; test; CTL+s.m.
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_H; sarc; diag
 429002; AW248439; Hs.2340; junction plakoglobin; blad; CTL+s.m.
 429010; Y18198; Hs.194725; one cut domain, family member; panc; diag
 429038; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb
 429058; AF138863; Hs.35254; hypothetical protein FLB8421; esoph; diag
 429065; AJ753247; Hs.29543; Homo sapiens cDNA FLJ13103 f1; lung; diag
 429083; Y09397; Hs.227817; BCL2-related protein A1; mel; diag
 429113; D28235; Hs.196384; prostaglandin-endoperoxide syn; angio, blad, stom; s.m.
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; ovar; mAb
 429163; AA884766; ; gb:am20a10.s1 Soares_NFL_T_GBC; pros; diag
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; breast, panc, stom, lung, mel; s.m.
 429201; X03178; Hs.198246; group-specific component (viral); panc; diag
 429220; AW207206; Hs.356962; ESTs; breast, pros, BPH; diag
 429228; AJ553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag
 429259; AA420450; Hs.380088; Plakophilin; lung, headnk; diag
 429290; AF203032; Hs.198760; neurofilament, heavy polypept; pros; CTL+s.m.
 429299; AI620463; Hs.347408; hypothetical protein MGC13102; pros, cerv; diag
 429329; AA456140; Hs.99235; Homo sapiens pannexin 3 (PANX3); sarc; mAb
 429345; R11141; Hs.199695; hypothetical protein; blad; diag
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (m); headnk, breast, cerv, ovar, blad, lung, esoph, mel, sarc; mAb
 429413; NM_014058; Hs.201877; DESC1 protein; lung, blad; diag
 429415; NM_002593; Hs.202097; procollagen C-endopeptidase en; sarc; diag
 429423; AJ016712; Hs.380983; Integrin, beta 1 (fibronectin); angio; mAb
 429432; AJ678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 429441; AJ224172; Hs.204096; lipophilin B (uteroglobin fam); breast, pros, ovar; diag
 429466; M85835; Hs.12827; ESTs; glio, uter; CTL+s.m.
 429469; M54590; Hs.380791; glycine dehydrogenase (decarbox); test; s.m.
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; blad, lung, headnk, test; diag
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cyto); lung, glio, headnk, mel, sarc; diag
 429504; X99133; Hs.204238; lipocalin 2 (oncogene 24p3) (N); ovar, lung, blad; diag
 429505; AW820035; Hs.278679; a disintegrin and metalloprote; colon, leuk; mAb
 429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag
 429563; BE619413; Hs.2437; eukaryotic translation Initiat; lung; diag
 429586; T73510; Hs.209153; angiotensin-like 3; hepC; CTL+s.m.
 429597; NM_003816; Hs.2442; a disintegrin and metalloprote; panc, colon, stom, lung; mAb
 429609; AF002248; Hs.210863; cell adhesion molecule with ho; ovar, mel; diag
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; lung, blad, headnk; diag
 429655; U48959; Hs.211582; myosin, light polypeptide kin; pros; s.m.
 429655; M68874; Hs.211587; phospholipase A2, group IVA (c); angio, lung; s.m.
 429664; L20433; Hs.211588; POU domain, class 4, transcrip; sarc; CTL+s.m.
 429736; AF125304; Hs.212680; tumor necrosis factor receptor; lung; mAb
 429747; M87507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.
 429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb
 429769; NM_004917; Hs.218366; kallikrein 4 (protease, enamel; pros; s.m.
 429784; M89796; Hs.30; membrane-spanning 4-domains, s; fibro; mAb
 429823; AA459443; Hs.181400; ESTs; sarc; diag
 429859; NM_007050; Hs.225952; protein tyrosine phosphatase, ; breast; mAb+s.m.
 429918; AW873986; Hs.119383; ESTs; pros, glio; diag
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL
 429983; W92620; Hs.260855; ESTs; blad; diag
 429986; AF092047; Hs.227277; sine oculis homeobox (Drosophila); lung; CTL+s.m.
 430014; H59354; Hs.374303; actinin, alpha 4; renal; diag
 430016; NM_004738; Hs.227658; xenotropic and polytropic retr; ovar; mAb
 430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag
 430056; X97548; Hs.228059; KRAB-associated protein 1; test; CTL+s.m.
 430129; BE301708; Hs.233955; hypothetical protein FLJ20401; angio; diag
 430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb
 430144; AT732722; Hs.98927; ERGL protein; ERGL-53-like pr; pros; diag
 430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb
 430154; AW583058; Hs.234726; serine (or cysteine) proteinases; pros; diag
 430157; BE348708; Hs.278543; ESTs; blad; diag
 430168; AW968343; Hs.145582; DKFZP434I1735 protein; blad; diag
 430223; NM_002514; Hs.235935; nephroblastoma overexpressed g; mel; diag
 430226; BE245562; Hs.2551; adrenergic, beta-2-, receptor, ; pros; mAb
 430228; AW950939; Hs.6382; ESTs, Highly similar to T00391; glio; diag
 430252; AI638774; Hs.106328; testes development-related NYD; test; CTL+s.m.
 430253; AK001514; Hs.235844; hypothetical protein FLJ10652; test; CTL+s.m.
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.
 430259; BE550182; Hs.375142; Rat GEF-like protein 3, mouse h; ovar; CTL+s.m.

- 430280; AA381258; Hs.237858; Interleukin 7 receptor; mela, lung, panc, stom, esoph, headnk, fibro; mAb+s.m.
 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_H; test; diag
 430294; AI538226; Hs.32976; guanine nucleotide binding pro; pros; diag
 5 430337; M36707; Hs.239600; calmodulin-like 3; lung; diag
 430354; AA954810; Hs.239784; human homolog of Drosophila Sc; ovar; diag
 430378; Z29572; Hs.2556; tumor necrosis factor receptor; lung, fibro, breast headnk, blad, breast, colon, stom; diag
 430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; panc; diag
 10 430407; H23551; Hs.30974; ESTs; panc; diag
 430439; AL133581; Hs.380155; DKFZP434B061 protein; lung, test; diag
 430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag
 430454; AW469011; Hs.105635; ESTs; lung; diag
 430476; AA447465; Hs.2563; tachykinin, precursor 1 (subst; sarc; diag
 15 430487; D87742; Hs.241552; KIAA0268 protein; pros; diag
 430491; AL109791; Hs.241559; Homo sapiens mRNA full length; ovar; diag
 430498; X02910; Hs.241570; tumor necrosis factor (TNF sup; leuk; diag
 430508; AI015435; Hs.104637; ESTs; lung; mAb+s.m.
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.
 20 430540; AW245422; Hs.106357; Homo sapiens cDNA: FLJ22105 f; mela; mAb
 430563; AA481269; Hs.348628; ATP-binding cassette, sub-fam; lung; diag
 430594; AK000790; Hs.246885; hypothetical protein FLJ20783; mela; diag
 430634; AI860651; Hs.26685; calcyphosine; ovar; diag
 430637; BE160081; Hs.256290; S100 calcium-binding protein A; mela; diag
 25 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_H; test; diag
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope prote; test; diag
 430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb
 430678; AI458174; Hs.192855; ESTs; lung; diag
 430686; NM_001942; Hs.2633; desmoglein 1; lung, headnk, mela; mAb
 30 430691; C14187; Hs.157208; aristless-related homeobox pr; EWS, ovar, panc; diag
 430704; AW813091; Hs.335799; ESTs; stom; diag
 430770; AA765694; Hs.123296; ESTs; mela; diag
 430832; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag
 430838; N46664; Hs.169395; hypothetical protein FLJ12015; mela; CTL+s.m.
 35 430890; X54232; Hs.2699; glypican 1; glio, lung, cerv, blad, esoph; mAb
 430985; AA490232; Hs.27323; ESTs, Weakly similar to I78885; lung; mAb
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad, headnk, esoph; mAb
 431053; S40369; Hs.249141; Glutamate receptor subunit; glio; mAb
 431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag
 40 431089; BE041395; Hs.374529; ESTs, Weakly similar to unknown; blad, lung, pros, angio, fibro; diag
 431099; Y13367; Hs.249235; phosphoinositide-3-kinase, cta; pros; CTL+s.m.
 431103; M57399; Hs.44; pleiotrophin (heparin binding; sarc, mela; diag
 431124; AF284221; Hs.59506; doublesex and mab-3 related b; lung; CTL+s.m.
 45 431151; BE207083; Hs.366053; gb:ba10d10.y1 NIH_MGC_7 Homo s; pros; mAb
 431164; AA493650; Hs.94367; thyroid transcription factor 1; fibro; CTL+s.m.
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endopl; mela, pros, panc, colon, stom; mAb
 431211; M86849; Hs.323733; gap junction protein, beta 2; colon, blad, lung, panc, headnk, esoph; mAb
 431217; NM_013427; Hs.250830; Rho GTPase activating protein; pros; CTL+s.m.
 431221; AA449015; Hs.286145; SRB7 (suppressor of RNA polyme; lung; CTL+s.m.
 50 431222; X58777; Hs.273790; zona pellucida glycoprotein 3A; pros; diag
 431250; BE264649; Hs.251377; taxol resistance associated ga; esoph; diag
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences; blad, ovar, uter; diag
 431347; AI133461; Hs.251664; insulin-like growth factor 2 (; blad; mAb+diag
 431354; BE046956; Hs.251673; DNA (cytosine-5)-methyltransf; test; CTL+s.m.
 55 431360; NM_000427; Hs.251680; torc1r; mela, sarc; diag
 431362; AI874223; Hs.293560; ESTs; angio; diag
 431369; BE184455; Hs.251754; secretory leukocyte protease I; ovar, blad; diag
 431384; BE158000; Hs.334372; gb:MR2-HT0377-150200-202-e03 H; lung; diag
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag
 60 431441; U81961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb
 431448; AL137517; Hs.306201; hypothetical protein DKFZp564O; blad; mAb
 431457; NM_012211; Hs.256297; integrin, alpha 11; headnk; mAb
 431474; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 431494; AA991355; Hs.298312; hypothetical protein DKFZp434A; lung; diag
 65 431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.
 431548; AI834273; Hs.9711; novel protein; lung, angio, pros; diag
 431553; X78075; Hs.2799; cartilage linking protein 1; sarc; diag
 431579; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon; mAb
 70 431674; AA098901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag
 431728; NM_007351; Hs.268107; multimerin; angio; diag
 431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag
 431838; AF178532; Hs.271411; beta-site APP-cleaving enzyme; mela; mAb
 75 431870; AW449902; Hs.105500; ESTs; renal; diag
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alph; blad, headnk, lung, panc, cerv, stom; mAb
 431938; AA938471; Hs.54431; specific granule protein (28 k; panc; diag
 431939; AW008061; Hs.231994; ESTs; renal, colon; diag
 431941; AK000108; Hs.272227; Homo sapiens cDNA FLJ20099 fts; cerv, glio; diag
 80 431988; AW972870; Hs.291069; ESTs; ovar; diag
 431992; NM_002742; Hs.2891; protein kinase C, mu; pros, glio; s.m.
 432004; BE018302; Hs.2894; placental growth factor, vascu; renal; diag
 432015; AL157504; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 432023; AW273128; Hs.300268; EST; lung; diag

- 432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 432117; AL036195; Hs.2909; prolamine 1; test; CTL+s.m.
 432128; AA127221; Hs.66; ESTs; angio; diag
 432141; BE410964; Hs.272736; nuclear receptor binding prota; test; mAb+s.m.
 432189; AAS27941; ; gb:nh30c04.s1 NCL_CGAP_Py3 Hom; pros; diag
 432199; AI693815; Hs.127179; cryptic gene; panc; diag
 432210; AI567421; Hs.273330; Homo sapiens, clone IMAGE:3544; ovar, lung, blad; diag
 432222; AI204995; ; gb:an03c03.x1 Stratagene schiz; angio, blad, fibro; diag
 432231; AA339977; Hs.274127; CLST 11240 protein; fibro; diag
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad, lung, headnk, esoph, sarc; s.m.
 432240; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 f1; pros; diag
 432305; M62402; Hs.274313; insulin-like growth factor b1r; cerv; diag
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 f1; cerv, lung, fibro, pros; diag
 432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 n; lung, test, colon; diag
 432415; T16971; ; ESTs, Weakly similar to A43932; ovar, pros; diag
 432432; AA541323; Hs.115831; ESTs; uter, pros; diag
 432435; BE218886; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag
 432441; AW292425; Hs.163484; Intron of hepatocyte nuclear f; blad, fibro, pros; diag
 432473; AI202703; Hs.152414; ESTs; pros; diag
 432481; AW451645; Hs.151504; Intron of collagen, type XI, a; sarc; diag
 432512; NM_003284; Hs.3017; transition protein 1 (during h; test; CTL+s.m.
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUIA; fibro, ovar, uter; CTL+s.m.
 432527; AW975028; Hs.102754; ESTs; pros, uter, ovar, cerv; diag
 432542; AW083920; Hs.16098; claudin 2; colon, panc; diag
 432583; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb
 432615; AA557191; Hs.55028; ESTs, Weakly similar to I54374; pros; diag
 432621; AI298501; Hs.21192; ESTs, Weakly similar to T46428; pros; mAb
 432629; AW860548; Hs.280658; ESTs; ovar; diag
 432653; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros, lung; mAb+s.m.
 432666; AW204069; Hs.351118; ESTs, Weakly similar to unname; test; diag
 432706; NM_013230; Hs.286124; CD24 antigen (small cell lung; colon, ovar, pros; mAb+CTL
 432730; AI066520; Hs.131358; ESTs; test; diag
 432731; R31178; Hs.287820; fibronectin 1; panc, fibro; diag
 432788; AA521091; Hs.178499; Homo sapiens cDNA: FLJ23117 f1; lung, ovar, CTL+s.m.
 432800; BE391046; Hs.278962; AIM-1 protein; mela, pros; mAb
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; blad, lung, headnk; CTL+s.m.
 432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); test; mAb
 432855; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag
 432867; AW016936; Hs.233364; ESTs; stom, colon; diag
 432878; BE386490; Hs.279663; Pirin; mela; CTL+s.m.
 432887; AI926047; Hs.162859; AK056805; Homo sapiens cDNA FL; pros; diag
 432938; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 432966; AA650114; Hs.325198; ESTs; pros; diag
 433012; NM_004045; Hs.279910; ATX1 (antioxidant protein 1, y; mela; diag
 433013; AI697890; Hs.127337; axin 2 (conductin, axl); colon; CTL+s.m.
 433043; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 433068; NM_006456; Hs.288215; sialyltransferase; breast, ovar, mela; s.m.
 433078; AW015188; Hs.121575; Homo sapiens cDNA FLJ12231 f1; blad; diag
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, ; blad, lung, headnk, cerv; mAb
 433147; AF091434; Hs.43080; platelet derived growth factor; ovar, panc, fibro; diag
 433159; AB035898; Hs.150587; kinesin-like protein 2; ovar, uter, colon, blad; diag
 433170; AB037816; Hs.8982; KIAA1395; angio; diag
 433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag
 433228; F28212; Hs.14953; KIAA1491 protein; test; CTL+s.m.
 433258; AI066626; Hs.207300; ESTs, Weakly similar to ALUB_H; lung; diag
 433285; AW976944; Hs.237396; ESTs; breast, pros; diag
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.
 433323; AA805132; Hs.159142; ESTs; pros; diag
 433334; AI927208; Hs.231858; matrix metalloproteinase 28; panc; s.m.
 433336; AF017986; Hs.31386; secreted frizzled-related prot; ovar, fibro, headnk, lung, panc, blad; diag
 433364; AI075407; Hs.296083; ESTs, Moderately similar to IS; mela; diag
 433365; AF026944; Hs.293797; ESTs; blad; diag
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.
 433388; AI432672; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.
 433404; T32982; Hs.352670; Homo sapiens cDNA FLJ32054 f1; pros; diag
 433437; U20538; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio, colon; s.m.
 433444; AW975324; Hs.129816; ESTs; pros; diag
 433466; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 433485; AI493076; Hs.306098; aldo-keto reductase family 1, ; lung; s.m.
 433495; AW373784; Hs.71; alpha-2-glycoprotein 1, zinc; breast, pros; diag
 433576; BE080715; Hs.161091; ESTs; mela; diag
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene; colon; diag
 433671; AW138797; Hs.132906; 19A24 protein; fibro; mAb
 433701; AW445023; Hs.15155; ESTs; test; diag
 433724; AI827749; Hs.144924; serine/threonine protein kinase; test; CTL+s.m.
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM.; pros, ovar; diag
 433800; AI034361; Hs.135150; lung type-I cell membrane-asso; glio, lung, test; mAb
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.
 434011; AW953437; Hs.6486; clone FLB5214; pros; diag
 434105; AW952124; Hs.13094; presenilins associated rhombol; lung; diag
 434217; AW014795; Hs.23349; ESTs; angio; diag
 434262; AF121858; Hs.12169; sorting nexin 8; mela; CTL+s.m.
 434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis; test; diag
 434340; AI193043; Hs.353146; ESTs, Weakly similar to T17226; lung; diag
 434360; AW015415; Hs.127780; ESTs; lung; diag
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic re; colon, stom; diag
 434377; AW137148; Hs.306593; intron of periostin (OSF-2os); headnk; diag
 434398; AA121098; Hs.3838; serum-inducible Kinase (SNK); angio, breast; CTL+s.m.
 434411; AA632649; Hs.201372; ESTs; stom, leuk; diag
 434414; AI798376; ; gb:tr34b07.x1 NCL CGAP_Oy23 Ho; lung, test, colon; diag
 434423; NM_006769; Hs.3844; LIM domain only 4; panc; diag
 434449; AW953484; Hs.3849; hypothetical protein FLJ22041 ; sarc; diag
 434487; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb+s.m.
 434596; T59538; ; gb:trb5g12.s1 Stragene ovary; angio; s.m.
 434608; AA805443; Hs.179908; hypothetical protein FLJ22995; test; CTL+s.m.
 434609; R76593; ; gb:tr60c11.1 Soares placenta ; pros; diag
 434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350; test; diag
 434665; AA642126; Hs.74502; gb:tr60c01.s1 NCL CGAP_Lym3 Ho; panc; diag
 434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis; panc; diag
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphat; melar; s.m.
 434846; AW295389; Hs.119758; ESTs; angio; diag
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIIR; lung, blad; mAb
 434927; H46612; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag
 434973; AW449285; Hs.313536; EST; pros; diag
 435045; BE297155; Hs.143698; ESTs; test; diag
 435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb
 435066; BE261750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.
 435080; AI831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb
 435094; AI560129; Hs.289008; EST; ovar, cerv; diag
 435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, melar; CTL+s.m.
 435140; AA668123; Hs.134170; ESTs; fibro; diag
 435159; AA668879; Hs.116649; ESTs; lung; diag
 435206; AI432364; Hs.160594; ESTs; test; diag
 435243; AW292886; Hs.348932; hypothetical protein dJ434014; cerv, headnk; diag
 435292; N20514; Hs.172965; ESTs; melar; diag
 435299; AI745458; Hs.343026; ESTs, Weakly similar to T20593; fibro; diag
 435479; AF197137; Hs.155101; ATP synthase, H transporting, ; pros; s.m.
 435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag
 435563; AF210317; Hs.95497; solute carrier family 2 (facil; blad; mAb+s.m.
 435576; AF213457; Hs.44234; triggering receptor expressed ; fibro; mAb+s.m.
 435602; AF217516; Hs.283532; uncharacterized bone marrow pr; test; diag
 435615; Y15065; Hs.4975; potassium voltage-gated channel; glio; mAb
 435652; N32388; Hs.334370; uncharacterized hypothalamus pr; panc; diag
 435793; AB037734; Hs.4993; KIAA1313 protein; ovar, lung, uter; diag
 435849; BE305242; Hs.16098; claudin 2; colon, panc; diag
 435876; AW612586; Hs.160271; G protein-coupled receptor 48; pros; mAb
 435897; AF269223; Hs.128322; t-complex 11 (a murine top hom; test; diag
 435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.
 435918; AF263538; Hs.86232; growth differentiation factor ; test; diag
 435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 436032; AA150797; Hs.109276; latexin protein; panc, angio; diag
 436063; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 436120; AI248193; Hs.119860; ESTs; fibro; diag
 436199; R38946; Hs.127951; hypothetical protein FLJ14503; renal; diag
 436246; AW450963; Hs.119991; ESTs; blad; diag
 436251; BE515065; Hs.296585; nucleolar protein (KKE/D repea; colon, test, blad; CTL+s.m.
 436278; BE396290; Hs.5097; synaptogyrin 2; pros; mAb
 436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag
 436293; AI601188; Hs.308201; ESTs; blad; diag
 436302; AL355841; Hs.99330; hypothetical protein FLJ23588; lung; diag
 436315; BE390513; Hs.27935; hypothetical protein MGC4837; melar; diag
 436396; AI683487; Hs.152213; wingless-type MMTV integration; lung, headnk, pros, panc; diag
 436420; AA443966; Hs.31595; ESTs; angio; mAb
 436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag
 436511; AA721252; Hs.291502; ESTs; lung; diag
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; lung; diag
 436569; BE439539; Hs.301961; glutathione S-transferase M2 (; blad; s.m.
 436614; AW104388; Hs.149091; ESTs; melar; CTL+s.m.
 436700; AI693690; Hs.301406; hypothetical protein PP3501; melar; mAb
 436729; BE621807; Hs.351316; transmembrane 4 superfamily me; panc, colon, stom, ovar, lung, blad; mAb
 436772; AW975688; Hs.348918; metallothionein 1E (functional; angio; diag
 436775; AA731111; Hs.372225; ESTs; uter, ovar; diag
 436839; AA767346; Hs.372277; ESTs; lung; diag
 436856; AI469355; Hs.127310; ESTs; melar; diag
 436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag
 436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb
 437052; AA861697; Hs.120591; ESTs; pros; diag
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458; test; diag
 437100; AI761073; Hs.14535; Homo sapiens cDNA: FLJ22314 f; panc, renal; diag
 437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; fibro; diag
 437145; AF007216; Hs.5462; solute carrier family 4, sodiu; panc, pros, stom; mAb
 437156; AI916600; Hs.121194; Homo sapiens cDNA: FLJ21569 f; stom, renal, colon; diag
 437181; AI306615; Hs.125343; ESTs, Weakly similar to KIAA07; blad; mAb+s.m.

- 437204; AL110216; Hs.355961; ESTs, Weakly similar to I55214; lung; CTL+s.m.
 437212; AL765021; Hs.210775; ESTs; renal, uter, ovar; diag
 437224; AL117628; Hs.97808; ESTs; test; diag
 437259; AL377755; Hs.120695; ESTs; lung; diag
 437267; AW511443; Hs.258110; ESTs; BPH; diag
 437269; AA334384; Hs.149420; ESTs; angio; diag
 437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag
 437381; NM_003684; Hs.5591; MAP kinase-interacting serine; glio; CTL+s.m.
 437390; AL125859; Hs.112607; ESTs; lung; diag
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag
 437435; AA249439; Hs.27027; hypothetical protein DKFZp762H; lung; diag
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L; test; CTL+s.m.
 437478; AL390172; Hs.317432; branched chain aminotransferase; angio; s.m.
 437553; AL829935; Hs.130497; ESTs, Weakly similar to MAT8_H; blad; mAb
 437571; AA760894; Hs.125350; ESTs; pros; diag
 437623; D63880; Hs.5719; chromosome condensation-relate; test; diag
 437740; AA810265; Hs.122915; ESTs; mela; diag
 437802; AL475995; Hs.122910; ESTs; panc; diag
 437862; AW978107; Hs.5884; Homo sapiens mRNA; cDNA DKFZp5; mela; CTL+s.m.
 437908; AL082424; Hs.351043; ESTs; test; diag
 437915; AL637993; Hs.202312; Homo sapiens clone N11 Ntera2D; lung, headnk, ovar, blad, uter; diag
 437931; AL249468; Hs.124434; ESTs; blad; diag
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter, panc; mAb+s.m.
 437938; AL950087; Hs.369628; gb:wg05c02.x1 NCL_CGAP_Kd12 H; renal, ovar, uter, cerv, blad; diag
 437939; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 437960; AL669586; Hs.369312; ESTs; uter, ovar; diag
 438167; R28363; Hs.24286; chemokine binding protein 2 (C; ovar, breast, uter; mAb
 438199; AW016531; Hs.122147; hypothetical protein FLJ13189; breast; diag
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nud; mela; mAb+s.m.
 438233; W52448; Hs.56147; ESTs; pros, cerv; diag
 438274; AL918906; Hs.55080; ESTs; headnk; diag
 438403; AA806607; Hs.292206; ESTs; lung; mAb
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 438450; AL050866; Hs.65853; nodal, mouse, homolog; test; diag
 438456; AA913381; Hs.279763; ESTs; test; diag
 438552; AL245820; Hs.6314; type I transmembrane receptor; pros, ovar; diag
 438670; AL275803; Hs.123428; ESTs; fibro; CTL+s.m.
 438702; AL879064; Hs.7164; ESTs; lung; diag
 438707; L08239; Hs.5326; amino acid system N transporter; ovar; mAb
 438746; AL885815; Hs.184727; Human melanoma-associated anti; panc, blad, mela, ovar; mAb+CTL
 438817; AL023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag
 438859; AL559626; Hs.93522; Homo sapiens mRNA for KIAA1647; renal; diag
 438866; U44385; Hs.6441; tissue inhibitor of metallopro; mela; diag
 438873; AL302471; Hs.124292; Homo sapiens cDNA: FLJ23123 f; fibro; diag
 438898; AL818663; Hs.106243; ESTs; lung; diag
 438915; AA280174; Hs.355711; Williams-Beuren syndrome chrom; lung, test, mela; diag
 438929; AW195515; Hs.253177; ESTs; renal; diag
 438956; W00847; Hs.135056; Human DNA sequence from clone; lung; diag
 438966; AW979074; ; gb:EST391184 MAGE resequences.; renal; diag
 438983; AF085984; Hs.20029; proacrosin binding protein sp3; test; CTL+s.m.
 438993; AA828995; ; gb:od77b08.s1 NCL_CGAP_Ov2 Hom; ovar; mAb+s.m.
 439053; BE244588; Hs.6456; chaperonin containing TCP1, su; test; diag
 439092; AA830149; ; gb:oc44f08.s1 NCL_CGAP_GCB1 Ho; pros; diag
 439176; AL446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag
 439180; AL393742; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; mAb
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582; mela, fibro; diag
 439239; AL031540; Hs.235331; ESTs; blad; diag
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 439310; AF086120; Hs.102793; ESTs; mela; diag
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, mela; mAb+s.m.
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secreto; fibro, uter; diag
 439366; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.
 439382; BE247684; Hs.103070; ESTs; angio; diag
 439394; AA149250; Hs.56105; ESTs; lung; diag
 439410; AA632012; Hs.188746; ESTs; angio; diag
 439453; BE264974; Hs.6566; thyroid hormone receptor Inter; lung, esoph, ovar; mAb+s.m.
 439496; BE616501; Hs.32343; Homo sapiens, Similar to RIKEN; mela, esoph; diag
 439659; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, mela, colon; mAb
 439668; AL091277; Hs.302634; frizzled (Drosophila) homolog; ovar, uter; mAb
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC0048; lung, headnk, cerv; diag
 439702; AW085525; Hs.55964; ESTs; mela; diag
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung, headnk; diag
 439735; AL635386; Hs.142846; hypothetical protein; pros; diag
 439737; AL751438; Hs.41271; Homo sapiens mRNA full length; panc; diag
 439750; AL359053; Hs.57654; Homo sapiens mRNA full length; panc, fibro, breast; diag
 439755; AW748482; Hs.77873; B7 homolog 3; sarc; mAb
 439759; AL359055; Hs.67709; Homo sapiens mRNA full length; colon, stom, panc, leuk, lung; diag
 439778; AL109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 439780; AL109688; ; gb:Homo sapiens mRNA full leng; blad, esoph; diag
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length; ovar, uter, cerv, breast, pros; diag
 439864; AL720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag
 439867; AA847510; Hs.161292; ESTs; panc; diag

- 439920; H05430; Hs.288433; neurotrophin; panc; mAb+diag
 439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv; diag
 439963; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad, s.m.
 440042; A1073387; Hs.133898; ESTs; ovar; CTL+s.m.
 440086; NM_005402; Hs.6906; v-rat simian leukemia viral on; angio; diag
 440099; AL080058; Hs.6909; DKFZP564G202 protein; panc; diag
 440119; AA865455; Hs.125331; ESTs, Moderately similar to un; test; diag
 440138; AB033023; Hs.318127; hypothetical protein FLJ10201; lung; CTL+s.m.
 440151; AA868167; ; gb:ak38e07.s1 Soares_testis_NH; sarc; diag
 440207; A1371978; Hs.128326; ESTs; test; diag
 440209; H05049; Hs.247837; neuraxin 3; fibro; diag
 440210; AW674562; Hs.122128; ESTs; glio; diag
 440225; BE295782; Hs.159; tumor necrosis factor receptor; glio; mAb
 440238; AW451970; Hs.155644; paired box gene 2; ovar; diag
 440260; A1972867; Hs.7130; copine IV; pros; diag
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 f1; lung, fibro; diag
 440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag
 440311; A1733079; Hs.125407; ESTs, Moderately similar to AL; renal; diag
 440325; NM_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb
 440333; A1378424; Hs.288761; hypothetical protein FLJ21749; pros; CTL+s.m.
 440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 f1; breast; diag
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_H; fibro; diag
 440457; BE387593; Hs.21321; Homo sapiens clone FLB9213 PRO; mela; diag
 440484; BE328156; Hs.150356; ESTs; panc; diag
 440529; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 f1; pros; diag
 440659; AF134160; Hs.7327; claudin 1; lung; mAb
 440704; M69241; Hs.162; insulin-like growth factor bin; lung, glio, ovar; diag
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN; test; diag
 440801; AA906366; Hs.370038; ESTs; pros; diag
 440819; A1809444; Hs.202108; ESTs; pros; diag
 440901; AA909358; Hs.128612; ESTs; ovar; pros; diag
 440943; AW082298; Hs.146161; hypothetical protein MGC2408; lung; diag
 440983; M20681; Hs.7594; solute carrier family 2 (facit; test; mAb
 441020; W79283; Hs.35962; ESTs; lung, panc; diag
 441031; A1110684; Hs.7845; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 f1; panc, ovar, stom, uter, lung; diag
 441134; W29092; Hs.346950; cellular retinoic acid-binding; sarc; diag
 441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag
 441321; H17182; Hs.7771; B-cell associated protein; test; diag
 441345; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 441350; AB020690; Hs.7782; paraneoplastic antigen MA2; panc; mAb+CTL
 441377; BE218239; Hs.202656; ESTs; uter, endo, lung; diag
 441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.
 441392; AW451831; Hs.222119; ESTs, Weakly similar to S30433; renal; diag
 441457; AW996651; Hs.43838; ESTs; angio; diag
 441495; AW294603; Hs.127039; ESTs; blad; diag
 441525; AW241867; Hs.127728; ESTs; lung; diag
 441553; AA281219; Hs.121296; ESTs; lung, test, ovar; CTL+s.m.
 441633; AW958544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag
 441790; AW294909; Hs.132208; ESTs; lung; diag
 441801; AW242799; Hs.86366; ESTs; blad; diag
 441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb
 441859; AW194364; Hs.380444; interleukin-4 induced gene-1 p; ovar, mela, fibro; mAb
 441878; A1801869; Hs.127982; ESTs; test; diag
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482; fibro, angio; CTL+s.m.
 442082; R41823; Hs.7413; calsynenin-2; breast, pros, ovar; diag
 442104; L20971; Hs.188; phosphodiesterase 4B, cAMP-spe; angio; CTL+s.m.
 442108; AW452649; Hs.343259; ESTs; lung; diag
 442242; AV647908; Hs.90424; Homo sapiens cDNA: FLJ23285 f1; BPH; diag
 442323; AW016669; Hs.25190; ESTs; breast; diag
 442333; A1650877; Hs.129302; ESTs; test; diag
 442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mela; CTL+s.m.
 442438; AA995998; Hs.370007; gb:ros26b03.s1 NCI_CGAP_Kid5 Ho; uter, ovar, renal; diag
 442441; A1820682; Hs.129598; ESTs; breast; diag
 442503; AF147078; Hs.375031; p53-responsive gene 5; mela; diag
 442506; BE566411; Hs.41726; ESTs; angio; diag
 442573; H93366; Hs.7667; branched chain aminotransferas; ovar, panc, angio, test; s.m.
 442577; AA292998; Hs.163900; ESTs; blad, panc, colon, stom, ovar; diag
 442580; A1733682; Hs.130239; ESTs; breast; diag
 442609; AL020996; Hs.8518; selenoprotein N; mela; diag
 442613; A1004002; Hs.130522; Kv channel-interacting protein; glio; diag
 442622; NM_000435; Hs.8546; Notch (Drosophila) homolog 3; ovar; mAb
 442711; AF151073; Hs.8645; hypothetical protein; angio, mela, sarc; diag
 442739; NM_007274; Hs.8679; cytosolic acyl coenzyme A thio; mela; s.m.
 442757; A1739528; Hs.28345; ESTs; mela; diag
 442818; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 442821; BE391929; Hs.8752; transmembrane protein 4; ovar; diag
 442832; AW206560; Hs.253569; ESTs; pros, fibro; diag
 442896; R37725; Hs.283093; ESTs; panc; diag
 442994; A1026718; Hs.16954; ESTs; blad, fibro; diag
 443054; A1745185; Hs.84520; yes-associated protein 65 kDa; blad; diag
 443162; T49951; Hs.9029; DKFZP434G032 protein; blad, lung; CTL+s.m.
 443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

- 5 443184; AI638728; Hs.135159; ESTs; sarc; diag
 443211; AJ128388; Hs.143655; ESTs; blad, ovar, lung, headnk, stom, colon; diag
 443216; W80487; Hs.324521; hypothetical protein OC50; test; diag
 443257; AI334040; Hs.11614; HSPC055 protein; fibro; CTL+s.m.
 443400; R28424; Hs.250648; ESTs; lung; diag
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; test; CTL+s.m.
 443537; D13305; Hs.203; cholecystokinin B receptor; test; mAb
 443548; AI085377; Hs.143610; ESTs; lung, headnk; diag
 10 443709; AI082692; Hs.134662; ESTs; fibro; diag
 443715; AI583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.
 443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.
 443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag
 443883; AA114212; Hs.9930; serine (or cysteine) proteinase; sarc; s.m.
 15 443885; H91806; Hs.15284; ESTs; melar; diag
 443892; AI889572; Hs.246875; ESTs; lung; diag
 443950; NM_001425; Hs.9999; epithelial membrane protein 3; melar; mAb
 443968; AA287702; Hs.10031; KIAA0955 protein; angio; diag
 443983; H04482; Hs.163724; ESTs; melar; mAb
 20 443991; NM_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb
 444009; AJ380792; Hs.135104; ESTs; angio; diag
 444151; AW972917; Hs.128743; alpha-methylacyl-CoA racemase; pros; mAb
 444159; AF116846; Hs.10431; daad ringer (Drosophila)-like ; test; CTL+s.m.
 444163; AI126098; ; FGENESH predicted RNaseH domat; blad; s.m.
 25 444301; AK000138; Hs.10760; asporin (LRR class 1); panc; diag
 444325; AW152618; Hs.16757; ESTs; esoph; diag
 444330; AI597655; Hs.49265; ESTs; angio; diag
 444342; NM_014398; Hs.10887; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag
 444378; R41339; Hs.47860; neurotrophic tyrosine kinase, ; lung, glio; mAb+s.m.
 30 444409; AJ792140; Hs.49265; ESTs; angio; diag
 444444; AI149332; Hs.14855; ESTs; blad; diag
 444471; AB020684; Hs.11217; KIAA0877 protein; glio, lung, colon ; mAb
 444476; AF020038; Hs.11223; isocitrate dehydrogenase 1 (NA); blad; s.m.
 444484; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 35 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb
 444649; AW207523; Hs.371001; ESTs; blad; diag
 444670; H58373; Hs.332938; hypothetical protein MGC5370; sarc; diag
 444754; T83911; Hs.11881; transmembrane 4 superfamily ma; panc, omuc, stom, lung, colon; mAb+s.m.
 444809; BE207568; Hs.208219; oculostatin; melar; mAb
 444823; BE262989; Hs.12045; putative protein; test; diag
 444863; AW384082; Hs.104879; serine (or cysteine) proteinase; melar; s.m.
 40 444895; AJ674383; Hs.22891; solute carrier family 7 (catio); ovar; mAb+s.m.
 444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag
 445019; AI205540; Hs.281295; ESTs; headnk, lung, colon; diag
 445070; NM_000677; Hs.258; adenosine A3 receptor; glio, renal; mAb
 45 445076; AI206888; Hs.154131; ESTs; test; diag
 445084; H38914; Hs.250848; hypothetical protein FLJ14761; sarc; mAb
 445093; AJ207197; Hs.156905; ESTs; test; diag
 445109; AF039916; Hs.12330; ectonucleoside triphosphate d; pros; s.m.
 50 445119; AF035121; Hs.12337; kinase insert domain receptor ; angio; mAb
 445160; AJ299144; Hs.101937; sine oculis homeobox (Drosophila); sarc; CTL+s.m.
 445182; AW189787; Hs.361778; ESTs; blad; diag
 445247; AW274290; Hs.153997; ESTs; melar; diag
 445279; R41900; Hs.22245; ESTs; angio; diag
 55 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; test; diag
 445413; AA151342; Hs.12677; CGI-147 protein; pros, colon, uter, ovar, lung, panc ; diag
 445418; AW139377; Hs.127179; cryptic gene; panc; diag
 445424; AB028945; Hs.12696; cortactin SH3 domain-binding p; pros ; diag
 445443; AV653838; Hs.295131; ESTs; lung; diag
 60 445654; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.
 445684; AK001696; Hs.13109; Ran binding protein 11; angio; diag
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.
 445784; AI253155; Hs.146065; ESTs; melar; CTL+s.m.
 445885; AJ734009; Hs.127699; KIAA1603 protein; pros, fibro; diag
 65 445900; AF070526; Hs.125036; Homo sapiens clone 24787 mRNA ; renal, leuk; mAb
 445911; AJ985987; Hs.145645; ESTs, Moderately similar to AL; blad; diag
 445982; BE410233; Hs.13501; pescadillo (zebrafish) homolog; melar; diag
 446057; AJ420227; Hs.366053; Trp-p8 transient receptor pote; pros; mAb
 446082; AJ274139; Hs.156452; ESTs; blad; diag
 70 446098; AW072215; Hs.208470; ESTs; angio; diag
 446100; AW967109; Hs.13804; hypothetical protein dJ462023.; pros; diag
 446102; AW168067; Hs.317694; ESTs; lung; diag
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.
 75 446291; BE397753; Hs.14623; interferon, gamma-inducible pr; melar; diag
 446292; AF081497; Hs.279682; Rh type C glycoprotein; lung, cerv; mAb
 446293; AJ420213; Hs.149722; LIM domain transcription facto; ovar, test; diag
 446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase ; pros; s.m.
 446332; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 80 446342; BE238665; Hs.14846; solute carrier family 7 (catio); uter, colon, pros, melar; mAb
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4_H; fibro; diag
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); lung, test; diag
 446608; N75217; Hs.175622; ESTs; uter, fibro; diag
 446626; AW292180; Hs.156142; ESTs; pros; diag

- 5 446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.
446644; NM_003272; Hs.21065; transmembrane 7 superfamily me; mela; mAb
446673; NM_015361; Hs.15871; LPAP for lysophosphatidic acid; blad; diag
446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.
446733; AA863360; Hs.26040; ESTs, Weakly similar to fatty; breast; s.m.
446755; AW451473; Hs.16134; serine/threonine kinase 10; mela; CTL+s.m.
446791; A1632278; Hs.195922; ESTs; test; diag
10 446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag
446856; A1814373; Hs.164175; ESTs; lung; diag
446868; AV660737; Hs.348297; ESTs; panc; diag
446872; X97056; Hs.16362; pyrimidinergic receptor P2Y, G; lung; mAb
446932; AA961459; Hs.125644; ESTs; fibro; diag
446967; A1699629; Hs.156781; ESTs; fibro; diag
446979; A1654443; Hs.197683; ESTs; test; diag
15 446984; AB020722; Hs.16714; Rho guanine exchange factor (G; angio; CTL+s.m.
446989; AK001898; Hs.16740; hypothetical protein FLJ11036; lung, headnk; diag
446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag
446999; AA151520; Hs.351416; hypothetical protein MGC4485; headnk; diag
20 447004; AW296968; Hs.157539; FGENSEH predicted secreted pro; glio; diag
447078; AW885727; Hs.9914; ESTs; lung; diag
447126; AW150632; Hs.170307; Rat guanine nucleotide exchang; angio; diag
447164; AF026941; Hs.17518; virlin; similar to Inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag
447178; AW594641; Hs.192417; ESTs; mela; diag
25 447188; H65423; Hs.17631; hypothetical protein DKFZp434E; test; diag
447210; AF035269; Hs.17752; phosphatidylserine-specific ph; pros, mela; s.m.
447289; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL
447334; AA515032; Hs.91109; ESTs; blad; diag
447343; AA256641; Hs.236894; ESTs, Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.
30 447350; A1375572; Hs.172634; v-erb-a avian erythroblastic t; breast, ovar, uter; diag
447377; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung, mela; CTL+s.m.
447395; A1418412; Hs.184793; Homo sapiens cDNA: FLJ21880 fi; panc; diag
447437; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
447499; AW262580; Hs.147674; protocadherin beta 16; pros, glio, ovar; mAb+s.m.
35 447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.
447534; AW953935; Hs.288655; ESTs; lung, test; diag
447578; AA912347; Hs.136585; ESTs, Weakly similar to JC5314; ovar; s.m.
447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
447604; AW089933; Hs.301342; hypothetical protein MGC4342; mela; diag
40 447636; Y10043; Hs.19114; high-mobility group (nonhistone); lung; CTL+s.m.
447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag
447749; T53260; Hs.8297; ESTs; rena; diag
447761; AF061573; Hs.19492; protocadherin 8; EWS, glio; mAb
447768; X88400; Hs.19520; FXD domain-containing ion tra; rena; mAb
45 447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA; rena; diag
447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022; renal, ovar, uter; diag
447881; BE620886; Hs.355279; GCN1 (general control of amino; rena; diag
447937; AL109716; Hs.20034; Homo sapiens mRNA full length; mela; mAb
447993; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
50 448030; N30714; Hs.325960; membrane-spanning 4-domains, s; panc, leuk, renal, stom lung; mAb
448045; AJ297436; Hs.20166; prostate stem cell antigen; blad, panc, pros; mAb
448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.
448133; AA723157; Hs.73769; folate receptor 1 (adult); ovar, fibro; mAb
448140; AF146761; Hs.20450; BCM-like membrane protein prec; fibro, mela, leuk; mAb
55 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase); test; CTL+s.m.
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag
448204; AW475124; Hs.170561; ESTs; sarc; diag
448231; A1701916; Hs.202509; ESTs; angio; diag
448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb
60 448262; AW880830; Hs.186273; ESTs; blad; diag
448275; BE514434; Hs.20830; kinesin-like 2; ovar, esoph, mela; diag
448278; W07369; Hs.11782; ESTs; lung; diag
448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 fis; pros; diag
448321; NM_005883; Hs.20912; adenomatous polyposis coli like; glio; CTL+s.m.
65 448357; N20169; Hs.108923; RAB38, member RAS oncogene fam; lung, mela; diag
448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag
448437; AW470125; Hs.220529; gbxxw60c04.x1 NCI_CGAP_Pan1 Hc; panc, colon; diag
448499; BE613280; Hs.77550; p53-regulated DDA3; glio; diag
448569; BE382657; Hs.21486; signal transducer and activator; panc, headnk, fibro, cerv, mela, rena; CTL+s.m.
70 448588; A1970276; Hs.156905; KIAA1676; test; CTL+s.m.
448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glio; mAb
448664; A1879317; Hs.334691; splicing factor 3a, subunit 1; mela; CTL+s.m.
448674; W31178; Hs.154140; ovary-specific acidic protein; angio; diag
448692; AW013907; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
75 448706; AW291095; Hs.21814; Interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb
448719; AA033627; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
448775; AB025237; Hs.388; nudix (nucleoside diphosphate); test; diag
448811; A1590371; Hs.199460; ESTs; esoph, panc; mAb
448939; BE267795; Hs.22595; hypothetical protein FLJ10637; test; CTL+s.m.
80 448956; AW372914; Hs.86149; phosphoinositol 3-phosphate-bi; mela; CTL+s.m.
448981; A1968719; Hs.195387; ESTs; test; diag
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb
448993; A1471630; Hs.355952; KIAA0144 gene product; lung, blad; diag
448999; AF179274; Hs.22791; transmembrane protein with EGF; pros, glio; mAb

- 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class; lung, headnk; s.m.
 449019; AI949095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; blad, colon, ovar; s.m.
 449040; NM_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.
 449078; AK001256; Hs.22975; KIAA1576 protein; mel; diag
 449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb
 449109; AW270992; Hs.120949; ESTs, Weakly similar to ALU7_H; sarc; diag
 449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL
 449207; AL044222; Hs.23255; nucleoporin 155kD; lung; diag
 449228; AJ403107; Hs.146590; protein related with psoriasis; lung; diag
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; lung, cerv, headnk, blad, ovar, colon; mAb
 449317; AW293413; Hs.132906; 19A24 protein; mel; mAb
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN; headnk, lung, angio; CTL+s.m.
 449322; AI638616; Hs.196566; ESTs; test; diag
 449338; H73444; Hs.394; adrenomedullin; renal; diag
 449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 f5; angio; mAb
 449437; AJ702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1; test; diag
 449448; D60730; Hs.57471; ESTs; blad, lung, headnk, breast; diag
 449467; AW205006; Hs.197042; ESTs; lung; diag
 449494; AW237014; Hs.315369; aquaporin 4; fibro; diag
 449569; AI656634; Hs.195389; ESTs; test; diag
 449592; AI655494; Hs.195718; ESTs; panc; diag
 449618; AJ076459; Hs.15978; KIAA1272 protein; angio; diag
 449625; NM_014253; Hs.349094; odz (odd Oz/ten-m, Drosophila); pros; diag
 449650; AF055575; Hs.23838; calcium channel, voltage-depen; pros; mAb
 449680; AJ033821; Hs.12160; ESTs; renal; diag
 449961; AW265634; Hs.133100; ESTs; glio, esoph, lung, blad; diag
 449976; H06350; Hs.135068; Human DNA sequences from clone; lung; diag
 450096; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 450149; AW969781; Hs.132863; Zic family member 2 (odd-paire; sarc; CTL+s.m.
 450152; AI138635; Hs.22968; intron of VEGFR; renal; diag
 450377; AB033091; Hs.355925; KIAA1265 protein; ovar, colon; diag
 450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 f5; pros; diag
 450400; AI694722; Hs.279744; ESTs; panc; diag
 450431; AW136797; Hs.266041; ESTs; test; diag
 450451; AW591528; Hs.202072; ESTs; uter, endo; diag
 450506; NM_004460; Hs.418; fibroblast activation protein.; panc, esoph; diag
 450534; AI570189; Hs.25132; KIAA0470 gene product; angio; CTL+s.m.
 450581; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag
 450635; AW403954; Hs.25237; mesenchymal stem cell protein; blad; mAb
 450642; R39773; Hs.7130; copine IV; pros; diag
 450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.
 450663; H43540; Hs.25292; ribonuclease H1, large subunit; mel; s.m.
 450676; AI147155; Hs.279727; ESTs; sarc; diag
 450684; AA872605; Hs.25333; Interleukin 1 receptor, type I; blad, lung, headnk; mAb
 450690; AA296696; Hs.333418; FXD domain-containing ion tra; mel; diag
 450693; AW450481; Hs.203965; ESTs; pros, uter; diag
 450718; AI086837; Hs.21349; ESTs, Weakly similar to RB88_H; test; diag
 450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 450785; AA852713; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 450832; AW970602; Hs.105421; ESTs; lung; diag
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glio; diag
 451035; AU076785; Hs.430; plastin 1 (I isoform); panc; diag
 451050; AW937420; Hs.351869; ESTs; mel; diag
 451099; R52795; Hs.25954; Interleukin 13 receptor, alpha; glio, fibro, mel; mAb
 451106; BE382701; Hs.25960; N-MYC oncogene; test, ovar; CTL+s.m.
 451110; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.
 451181; AI786330; Hs.207461; ESTs; panc; diag
 451253; H48299; Hs.26126; claudin 10; lung, ovar, panc; mAb
 451291; R39288; Hs.6702; ESTs; lung; diag
 451295; AI557212; Hs.17132; ESTs, Moderately similar to I5; panc; diag
 451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1); lung; s.m.
 451346; NM_006338; Hs.26312; glioma amplified on chromosome; ovar; mAb
 451386; AB029006; Hs.26334; spastic paraplegia 4 (autosoma; lung; diag
 451398; AI793124; Hs.144479; ESTs; breast, ovar; diag
 451411; AA017492; Hs.135855; EST; pros; diag
 451497; H83294; Hs.284122; Wnt Inhibitory factor-1; uter, fibro, pros, colon, sarc; diag
 451541; BE279383; Hs.26557; plakophilin 3; lung, blad, ovar; diag
 451592; AI805416; Hs.213897; ESTs; lung, headnk; diag
 451635; AA018899; Hs.127179; cryptic gene; panc; diag
 451663; AI872360; Hs.209293; ESTs; pros; diag
 451720; AW970985; Hs.290853; ESTs; pros; diag
 451743; AW074266; Hs.336428; ESTs; lung; diag
 451820; AW058357; Hs.199248; ESTs; panc; mAb
 451844; T61430; g; gbyc06a03.s1 Stratagene lung; blad; diag
 451982; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp5; pros, blad; mAb
 451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/Hs) b; test; CTL+s.m.
 452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.
 452208; AA024792; Hs.31895; hypothetical protein MGC4093; renal; diag
 452240; AI591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag
 452243; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 452244; N33530; Hs.176674; ESTs; mel; diag

- 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S; test; CTL+s.m.
 452295; BE379936; Hs.28866; programmed cell death 10; lung; diag
 452298; AI039243; Hs.278585; ESTs; angio; diag
 5 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro, colon; s.m.
 452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag
 452340; NM_002202; Hs.505; ISL1 transcription factor, LIM; panc, pros; CTL+s.m.
 452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb
 452355; N54926; Hs.29202; G protein-coupled receptor 34; glio, fibro, panc; mAb
 10 452367; U71207; Hs.29278; eyes absent (Drosophila) homolog; lung, pros, ovar, uter; CTL+s.m.
 452416; AA026115; Hs.114777; ESTs; fibro; diag
 452461; N78223; Hs.108108; transcription factor; blad, lung, headnk, ovar, glio, stom, colon, cerv; CTL+s.m.
 452571; W31518; Hs.34665; ESTs; stom, lung, panc, colon, fibro; diag
 452594; AU076405; Hs.29981; solute carrier family 26 (sulf; ovar; mAb
 15 452613; AA461599; Hs.23459; ESTs; lung; diag
 452678; Z42387; Hs.63883; transmembrane, prostate androg; pros, colon, panc, pros; mAb
 452705; H49805; Hs.246005; ESTs; panc; diag
 452717; AW160399; Hs.30376; hypothetical protein; pros; diag
 452721; AJ269529; Hs.301871; solute carrier family 37 (glyc; pros; mAb
 20 452732; BE300078; Hs.80449; Homo sapiens, clone IMAGE:3535; blad; diag
 452744; AJ267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; mel; diag
 452792; AB037765; Hs.30652; KIAA1344 protein; pros, uter, breast; diag
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL
 452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag
 25 452833; BE559581; Hs.30736; KIAA0124 protein; lung, mel; CTL+s.m.
 452865; AJ924046; Hs.119567; ESTs, Weakly similar to A47582; lung; diag
 452899; M96739; Hs.30956; nescent helix loop helix 1; sarc; CTL+s.m.
 452924; AW580939; Hs.97199; complement component C1q recep; angio; diag
 452933; AW391423; Hs.28855; Homo sapiens cDNA: FLJ22425 f; angio; CTL+s.m.
 30 452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 452955; AW390282; Hs.31130; transmembrane 7 superfamily me; pros; mAb+s.m.
 453006; AI362575; Hs.303171; ESTs; pros; diag
 453028; AB006532; Hs.31442; RecQ protein-like 4; blad, lung, test; CTL+s.m.
 453085; AW954243; Hs.351573; KIAA0251 protein; angio; diag
 35 453096; AW294631; Hs.351270; ESTs; pros; diag
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog; lung, headnk, colon; mAb
 453107; NM_016113; Hs.279746; vanilloid receptor-like prot; mel; mAb
 453134; AA032211; Hs.118493; ESTs; blad; diag
 453142; AA033648; Hs.7473; Homo sapiens gap junction prot; fibro; mAb
 40 453160; AI263307; Hs.356901; H2B histone family, member L; lung, panc, pros; diag
 453210; AL133161; Hs.32360; hypothetical protein FLJ10867; lung; CTL+s.m.
 453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.
 453256; AI565587; Hs.32556; KIAA0379 protein; mel; diag
 453310; X70697; Hs.553; solute carrier family 6 (neuro; fibro; mAb
 45 453321; AI984381; Hs.232521; ESTs; blad; diag
 453323; AF034102; Hs.32951; solute carrier family 29 (nuct; ovar; CTL+s.m.
 453331; AI240665; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.
 453344; BE349075; Hs.44571; ESTs; mel; diag
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.
 50 453365; AA035211; Hs.17404; SOX7 SRY (sex determining reg; angio, blad; CTL+s.m.
 453370; AJ470523; Hs.139335; ATP-binding cassette, sub-fam; pros; mAb
 453389; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; renal, ovar, blad; mAb+s.m.
 453392; U23752; Hs.32964; SRY (sex determining region Y); ovar, lung, glio, sarc; CTL+s.m.
 453459; BE047032; Hs.257789; ESTs; ovar, cerv, blad, uter, panc, angio, lung; diag
 55 453464; AI884911; Hs.32989; receptor (calcitonin) activity; pros; mAb
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; lung, esoph, test; diag
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); headnk; mAb
 453642; AI370936; Hs.34074; dipeptidylpeptidase VI; glio; mAb
 453779; N35187; Hs.43388; 28kd interferon responsive pro; mel; diag
 60 453789; AA628517; Hs.118502; ESTs; angio; diag
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1; glio, lung, uter, headnk, cerv, panc, pros, sarc; mAb
 453883; AJ638516; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag
 453884; AA355925; Hs.36232; KIAA0186 gene product; lung, ovar, test, esoph; diag
 453912; AL121031; Hs.356843; SWI/SNF related, matrix associ; mel; diag
 65 453922; AF053308; Hs.36708; budding uninhibited by benzimid; colon, stom, lung, test; CTL+s.m.
 453935; AI633770; Hs.42572; ESTs; panc; diag
 453941; U39817; Hs.36820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.
 453964; AI961488; Hs.249196; ESTs; lung; diag
 453966; BE148734; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 70 453985; N44545; Hs.251865; ESTs; test; diag
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family; lung, headnk; s.m.
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag
 454066; X00356; Hs.37058; calcitonin/calcitonin-related; lung; diag
 454071; AI041793; Hs.42502; ESTs; breast; diag
 75 454077; AC005952; Hs.37062; Insulin-like 3 (Leydig cell); test; diag
 454098; W27953; Hs.217493; Plakophilin; lung; diag
 454117; BE410100; Hs.40368; adaptor-related protein complex; mel; CTL+s.m.
 454360; L78207; Hs.54470; ATP-binding cassette, sub-fam; glio; mAb
 454429; BE273437; Hs.301406; hypothetical protein PP3501; mel; mAb
 80 454439; AW819152; Hs.154320; DKFZP566O1846 protein; lung; diag
 454478; AW805749; Hs.372783; superoxide dismutase 2, mito; mel; s.m.
 455601; AI368680; Hs.816; SRY (sex determining region Y); lung, cerv, esoph; s.m.
 456034; AW450978; ; gb:U-I-BI3-gta-e-12-Q-ULs1 N; blad, fibro; diag
 456052; AI866286; Hs.71962; ESTs, Weakly similar to B36298; fibro, ovar, uter; diag

- 456177; NM_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag
456266; L29073; Hs.198726; cold shock domain protein A; panc; CTL+s.m.
456321; NM_001327; Hs.87225; cancer/testis antigen; lung; CTL
456553; AA721325; Hs.189058; ESTs, Highly similar to Simla; panc; diag
456723; Z43902; Hs.4748; adenylate cyclase activating p; glio; mAb+s.m.
456736; AW248217; Hs.1619; achaete-scute complex (Drosophila); lung; diag
456759; BE259150; Hs.127792; delta (Drosophila)-like 3; glio; lung; mAb
456847; AI360456; Hs.86088; ESTs; test; diag
456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.
456977; AK000252; Hs.169758; hypothetical protein FLJ20245; angio; diag
457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.
457211; AW972565; Hs.32399; ESTs, Weakly similar to S51797; meta; pros; CTL+s.m.
457292; A921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb
457313; AF047002; Hs.241520; transcriptional coactivator; test; CTL+s.m.
457411; AW085961; Hs.130093; iroquois-class homeobox protein; breast, fibro; diag
457465; AW301344; Hs.122908; DNA replication factor; test, meta; diag
457498; A732230; Hs.191737; ESTs; pros; diag
457561; AA331517; Hs.286055; chimerin (chimaerin) 2; glio; mAb
457590; AI612809; Hs.5378; hypothetical protein MGC10724; ovar; diag
457869; AU077186; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
458092; W67353; Hs.350558; KIAA0251 protein; lung; diag
458124; AW005548; Hs.124590; ESTs; fibro; diag
458435; AI418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag
458471; AV648609; Hs.194240; ESTs; renal, panc, hepC; diag
458933; AI638429; Hs.24763; RAN binding protein 1; lung, test; diag
459373; BE408266; Hs.301406; hypothetical protein PP3501; meta; mAb
459578; AW612538; Hs.304491; EST; meta; diag
459702; AI204995; Hs.103033.x1 Stratagene schiz; blad, fibro; diag
459705; BE082764; Hs.270252; ESTs, Weakly similar to androg; fibro; mAb+s.m.

TABLE 3B

35	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
	Pkey	CAT Number	Accession	
40	103739	49403_2	AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075779 AA075221 AA076395 AA650486 AA083500	
	108282	108971_1	AA065143 AA065142	
	113230	2327174_1	AI820546 AI821336 T61430	
	118417	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594	
45			AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951	
			N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703386 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611	
			AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833	
			AA207155 BI004758 AA206262 AI365204 H77608 AW590511	
50	121335	1369289_1	AA404418 AI217248	
	126872	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945	
	322521	14637_1	AF147347 T55503 T55426	
	322975	1784158_1	C16391 C16413	
55	323332	245301_1	AI829520 AI791832 AI791823 AA229315 AA228414 AA229211	
	323817	887879_1	AA410943 BF366582 AA334202 AA332882 BF371899 AW948953	
	324261	1026976_1	AL044891 AI908240 AA393080 AW748403 BE069341 BF330573	
	406685	0_0	M18728	
60	409051	107834_1	AA075419 AA082953 AA080912 AA062835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083821 AA062836 AA113892	
			AA075318 AA076594 AA078900 AA134801 AA063293 AA083403 AW974305	
	409123	108378_1	AA070050 AA070823 AA063403	
	409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722	
65			BI007625 BI027864 BI009100 BI006275 BI008270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762	
			BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445	
	411880	1139083_1	BE088101 T05990 AW872477	
	413804	1556651_1	BE168256 BE168190 T64682	
70	414221	685588_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945	
	417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572	
	427260	11272_60	AA401424 AA400100 AA653848	
	427298	115241_1	AA833717 BF061897 AW628327 AA641788 AA400495	
75	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165	
			AA548736 AA768578 AI539081 AW025957 AA736837 N79576 AW594357 AA480892	
	429163	1238297_1	AW974271 AA592975 AA447312 AA884766	
	432189	112710_1	AA527941 AA635266 AI810608 AI620190	
80	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354	
	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104	
			AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279	
			BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849	

		AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175		
		BF854337		
5	434598	14701_1 AF147374 T59538 T59589 T59598 T59542		
	434609	14739_1 AF147390 R76593 R76594		
	438966	1242593_1 AW979074 AA834841 AA828650		
	438993	2580163_1 AI926361 AA834879 AA828995		
	439092	919640_1 AW978407 AA830149 M85983 AW503637 BF352096		
	439780	49082_1 AL109688 R23665 R26578		
10	440151	1879911_1 AA868167 F21558 F31418 F35624		
	444163	682245_1 BG403189 AI148521 AI184748 AI126098 R05933 BI057330		
	451844	2327174_1 AI820546 AI821338 T61430		
	456034	685586_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945		
	459702	539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354		
15	TABLE 3C			
	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA		
20	Strand:	sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	NI_position:	Indicates DNA strand from which exons were predicted.		
		Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NI_position
25	325372	5856920	Minus	1117061-1117304
	325544	6682452	Plus	171228-171286
	327036	6531965	Plus	319951-320040
	327075	6531965	Plus	4041318-4041431
30	327414	5867750	Plus	102461-102586
	328700	5868264	Plus	764089-764203
	330211	6013592	Plus	59158-59215
	332798	Dunham, I. et al.	Minus	232147-231974
	333769	Dunham, I. et al.	Plus	7696625-7696707
	333904	Dunham, I. et al.	Minus	8217374-8217261
35	334223	Dunham, I. et al.	Minus	12734365-12734269
	334447	Dunham, I. et al.	Plus	14308764-14308824
	335115	Dunham, I. et al.	Minus	21388250-21388146
	335809	Dunham, I. et al.	Plus	26310772-26310909
40	335824	Dunham, I. et al.	Plus	26376860-26376942
	335825	Dunham, I. et al.	Plus	26378175-26378268
	335936	Dunham, I. et al.	Minus	27360474-27360400
	336034	Dunham, I. et al.	Plus	29014404-29014590
	336152	Dunham, I. et al.	Minus	30156053-30155870
45	336636	Dunham, I. et al.	Plus	988418-989185
	338008	Dunham, I. et al.	Plus	7697068-7697236
	338033	Dunham, I. et al.	Plus	8092128-8092271
	338158	Dunham, I. et al.	Minus	11794465-11794343
	338255	Dunham, I. et al.	Minus	16242294-16242231
50	400494	9714719	Plus	169845-170272
	400517	9796586	Minus	49996-50346
	400651	8117978	Minus	81488-81646
	400665	8118496	Plus	16879-17023
	400773	8131629	Minus	44116-44238,48208-48321
55	400844	9188605	Plus	24746-24872,25035-25204
	400846	9188605	Plus	39310-39474
	400881	2842777	Minus	91446-91603,92123-92265
	401093	8516137	Minus	22335-23166
	401234	9929642	Plus	120173-120337
60	401424	8176894	Plus	24223-24428
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
	401704	3097841	Plus	24712-25374
	401732	1200312	Plus	19346-19525,19625-19708,19897-19973,2006
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
65	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	401785	7249190	Minus	165776-165989,166189-166314,166408-16656
	401797	6730720	Plus	6973-7118
70	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	402145	8018280	Plus	113086-114800
	402199	8576116	Minus	84187-84744
	402230	9966312	Minus	29782-29932
	402239	7690131	Plus	38175-38304,42133-42266
75	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	402265	3287673	Plus	21059-21168
	402305	7328724	Plus	40832-41362
	402420	9796339	Plus	129750-129919
	402424	9796344	Minus	64925-65073
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
80	402474	7647175	Minus	53528-53628,55755-55920,57530-57757
	402550	7652009	Minus	80413-80673
	402604	9909420	Plus	20393-20767
	402605	9909420	Minus	47680-47973

	402606	9909429	Minus	81747-82094
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402777	9588235	Plus	126786-126948
5	402860	9588237	Minus	76423-76560
	402888	9930892	Minus	54727-54901
	402992	7767907	Minus	42137-42515
	402994	2996643	Minus	4727-4969
	403046	3540153	Minus	55707-55859,56369-56511
10	403047	3540153	Minus	59793-59968
	403071	8954241	Plus	136688-137096
	403088	8954241	Plus	169894-170193,170504-170806
	403171	9838164	Minus	74502-74703
	403328	8469086	Minus	120428-120703
15	403329	8516120	Plus	96450-96598
	403381	9438267	Minus	26009-26178
	403409	9438598	Plus	6860-7054,12573-12771
	403433	9719611	Minus	72225-72437
	403478	9958258	Plus	116458-116564
20	403715	7239669	Plus	85128-85292
	403740	7630882	Plus	86504-87227
	403776	7770611	Minus	1414-1513,1624-1758
	403903	7710671	Minus	101165-102597
	404029	7671252	Plus	108716-111112
25	404049	3688074	Minus	75765-78155
	404210	5006246	Plus	169926-170121
	404240	5002624	Minus	116132-116407,116653-116922
	404253	9367202	Minus	55675-56055
	404288	2326514	Plus	51086-51301
30	404298	9944263	Minus	73591-73723
	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404866	9366919	Minus	11743-11929
	404877	1519284	Plus	1095-2107
35	404927	7342002	Plus	68590-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	405001	6015406	Minus	104646-104819
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
40	405238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144464,144690-144836,151750-15188
	405451	7622517	Minus	145949-146227
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405546	1054740	Plus	124010-124183
45	405547	1054740	Plus	124361-124520,124914-125050
	405646	4914350	Plus	741-969
	405704	4204244	Plus	138842-139051
	405770	2735037	Plus	61057-62075
	405849	7651817	Minus	17705-18287
50	405832	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406173	7230224	Plus	12925-13213
	406348	9255985	Minus	71764-71944
55	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406487	9795551	Plus	182212-182958
	406506	7711374	Minus	6843-8077
60	406547	7711513	Minus	172780-174358

Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 60th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

Key: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: Unigene number
 Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: Unigene gene title
 R1: Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Key	ExAccn	UniGeneID	Pred.Protdomains	UniGeneTitle	R1
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5	419551	AW582255	Hs.81011	TM=M;SS=M	anterior gradient 2 (Xenopus laevis)	9.7
	426174	AA547959	Hs.115838		Homo sapiens similar to Echinoidin	7.0
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	6.8
	428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	stratiferin	6.4
	417931	W95642	Hs.82961	trefoil;TM=N;SS=M	trefoil factor 3 (intestinal)	6.3
	447956	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, Weakly similar to Homolog of Target Exon	6.1
10	406387					6.0
	421814	L12350	Hs.108823	EGF,isp_1,vwc,TSPN,isp_3;	thrombospondin 2	5.8
	406857	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	5.8
	426104	A0204418	Hs.190080		ESTs	5.8
	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	5.8
	422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
15	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	5.6
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	5.5
	419329	AY007220	Hs.288998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
	418344	AA216387			gbcnc16b02.s1 NCL_CGAP_Pr1 Homo sap	5.2
20	407116	AA130986	Hs.271627		ESTs	5.1
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midline (neurite growth-promoting f	5.1
	419452	U33635	Hs.90572	lg,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
	421552	AF026692	Hs.105700	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
	409453	AB885516	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
	409632	W74001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
25	417515	L24203	Hs.82237	zf-B_box,zf-UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
	411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KIAA1077 protein	5.0
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	5.0
	422087	X58968	Hs.111301	fn2,homopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
	421143	AB024536	Hs.102171	lg,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	4.9
30	408491	A088063	Hs.7882		ESTs	4.9
	417944	AU077196	Hs.82985	vwc,Collagen,COLFI;TM=N;S	collagen, type V, alpha 2	4.9
	409062	AL157488	Hs.50150		Homo sapiens mRNA; cDNA DKFZp564B18	4.9
	422281	M36803	Hs.346935	homopexin;TM=N;SS=M	homopexin	4.9
35	425308	M97639	Hs.155585	lg,xringle,pkinase,Fz;TM=	receptor tyrosine kinase-like orpha	4.8
	408349	BE546947	Hs.44276	homeobox;TM=M;SS=N	homeo box C10	4.8
	449019	AB49095	Hs.67776		ESTs, Weakly similar to T22341 hypo	4.8
	435561	AA351978	Hs.4943	MAGE,Cys_kno,EGF,laminin	hepatocellular carcinoma associated	4.8
	410687	U24389	Hs.65436	Lysyl oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
40	429455	AA72111	Hs.278694	lactin_c	CD209 antigen	4.8
	414407	AA147026	Hs.76704		ESTs	4.8
	419390	AT071182	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGC11138	4.7
	453902	BE502341	Hs.3402		ESTs	4.7
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
45	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
	449717	AB040935	Hs.23954	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
	451529	AB17901	Hs.208641	actin,none	ESTs	4.6
	435370	AB84074	Hs.225838	EGF,fn3,fibrinogen_C,toxi	ESTs	4.6
	411761	AT33848	Hs.71935	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
	424223	AJ243706	Hs.143323	PHD,ARID,jmjC,jmjN,zf-C5H	putative DNA/chromatin binding mol	4.6
50	426935	NM_000088	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	4.5
	408796	AA688292	Hs.170345	hormone_rec,zf-C4	ESTs	4.5
	407230	AA157857	Hs.182265	filament,bZIP;TM=N;SS=M	keratin 19	4.4
	422830	AC007954	Hs.121371		hypothetical protein DKFZp434P0111	4.4
55	447528	AB12027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	4.4
	430168	AW958343	Hs.145582	erhand,erhand	DKFZP4341735 protein	4.4
	423225	AA852604	Hs.125359	lg,Ribosomal,S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
	414822	AA156542	Hs.72127	homeobox,HLH	ESTs	4.4
	452683	AB08575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
60	444784	D12485	Hs.11951	Somatomedin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
	453857	AL080235	Hs.35861	TM=Y;SS=M	Ras-Induced senescence 1 (RIS1)	4.4
	413859	AW892356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	4.3
	440369	AW176150	Hs.132449		downstream of breast cancer antigen	4.3
	418140	BE613836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
65	441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	4.3
	424464	R68537	Hs.17962	homeobox,none	ESTs	4.3
	423582	BE000831	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fis, clo	4.3
	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
	433320	D60647	Hs.250879	rm	ESTs, Highly similar to CTXN RAT CO	4.2
	429165	AW008885	Hs.118258		prostate cancer associated protein	4.2
70	416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
	448913	AA184422	Hs.22584	rm,zf-RanBP,pkinase,GST_-	myosin VI	4.2
	430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
	400496			TM=Y;SS=N	ENSP00000224716:GTP-binding protei	4.2
75	442599	AF078037	Hs.324051	SH3,ank;TM=M;SS=N	RelA-associated inhibitor	4.2
	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	4.2
	431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to E38022 hypo	4.2
	426485	NM_006207	Hs.170040	lg;TM=N;SS=M	platelet-derived growth factor rece	4.2
	435858	AF254260	Hs.283009	bZIP;TM=M;SS=N	turfurin 1	4.2
80	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsrm,z-al	ephrin-A3	4.2
	451982	F13038	Hs.27373	NA,NA	Homo sapiens mRNA; cDNA DKFZp564O17	4.2
	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
	431890	X17033	Hs.271986	vwa,Integrin_A,FG-GAP;TM=	Integrin, alpha 2 (CD49B, alpha 2 s	4.1
	434449	AW953484	Hs.3849	erhand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	4.1

5	423057	AW961597	Hs.130816	HLH;TM=M;SS=N	ESTs, Moderately similar to I38022	4.1
	452063	R53185	Hs.32366	ras,none	ESTs, Weakly similar to TWST_HUMAN	4.1
	450680	AF131784	Hs.25318	Peptidase_C1;TM=N;SS=M	Homo sapiens clone 25194 mRNA sequ	4.1
	418283	S79895	Hs.83942		cathepsin K (pseudosclerosis)	4.1
	416361	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
	426255	BE262530	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
	408113	T82427	Hs.194101	7tm_3,none	Homo sapiens cDNA: FLJ20869 fis, cl	4.1
	407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted ligand homologous	4.1
10	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
	429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	4.0
	448826	AI580252	Hs.255565		ESTs, Weakly similar to putative p1	4.0
	419648	T73661	Hs.91877	TM=N;SS=M	thyroid hormone responsive SPOT14 (4.0
15	421485	AA243499	Hs.104800	TM=Y;SS=M	hypothetical protein FLJ10134	4.0
	440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fis, cl	4.0
	417363	AW129357	Hs.329700		ESTs	4.0
	451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
	421823	N40850	Hs.28625		ESTs	4.0
20	452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	4.0
	444286	AI625304	Hs.201008	Armadillo_sag;TM=M;SS=N	ESTs	4.0
	451541	BE279383	Hs.26557	Collagen,TSPN;TM=M;SS=M	plakophilin 3	4.0
	451304	M92642	Hs.26208	TM=M;SS=N	collagen, type XVI, alpha 1	4.0
25	429556	AW139399	Hs.314807		ESTs	4.0
	441094	U33819	Hs.7647	zf-C2H2,LIM,PHD,TFIIIS;TM=	MYC-associated zinc finger protein	4.0
	407788	BE514982	Hs.38991	efhand,S_100,S_100,efhand	S100 calcium-binding protein A2	4.0
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
	437762	T78028	Hs.154679	C2,none	synaptotagmin I	3.9
30	433399	N46406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	3.9
	404578	AF183810	Hs.26102	zf-C2H2,rubredoxin;TM=M;S	trichorhinophalangeal syndrome I gene	3.9
	443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	3.9
	445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
35	453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	3.9
	424125	M31669	Hs.1735	TGF-beta,TGFb_propeptide;	inhibin, beta B (activin AB beta po	3.9
	437377	AF359573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
	422562	AI962060	Hs.118397	Zn_carbOpept,F5_F8_type_C	AE-binding protein 1	3.9
	422320	AI745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly similar to AAB47496 NG	3.9
40	433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fis, clo	3.9
	411894	M57609	Hs.72916	zf-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Gre	3.9
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
	418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
	418753	BE217818	Hs.87016		hypothetical protein FLJ22938	3.8
45	452679	Z42387	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.8
	421030	AW161357	Hs.101174	tubulin-binding;TM=N;SS=M	microtubule-associated protein tau	3.8
	431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fis, cl	3.8
	426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
	447151	AI022813	Hs.92679	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
	448717	R67419	Hs.21851	HLH,homeobox,none	Homo sapiens cDNA FLJ12900 fis, clo	3.8
50	425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calyculin-2	3.8
	423940	NM_012429	Hs.277728	CRAL_TRIO;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
	426742	AA383828	Hs.181131		ESTs	3.8
	435818	AA700553	Hs.368614	arf,ras,RacR,none	ESTs	3.8
55	420005	AW271108	Hs.133294		ESTs	3.8
	410867	X63556	Hs.760	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
	402531	AB037745	Hs.104696	TM=M;SS=M	KIAA1324 protein	3.8
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
	424806	AA382523	Hs.105689	TM=Y;SS=N	MSTP031 protein	3.8
	443933	AI091631	Hs.203845	ion_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
60	432652	AA813887	Hs.188173		Homo sapiens cDNA FLJ12187 fis, clo	3.8
	424036	AA770688	Hs.348495	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member L	3.7
	453828	AW970960	Hs.293821	Pep_M12B_propep,Reprotysi	ESTs	3.7
	407112	AA070801	Hs.51615	hormone_rec,zf-C4	ESTs, Weakly similar to ALU7_HUMAN	3.7
	445669	AI570830	Hs.174870		ESTs	3.7
65	446091	AW022192	Hs.200197	homeobox,none	ESTs	3.7
	424651	AI493205	Hs.120785		ESTs	3.7
	409178	BE393948	Hs.50915	trypsin;TM=M;SS=Y	kallikrein 5	3.7
	417059	AL037672	Hs.81071	TM=N;SS=Y	extracellular matrix protein 1	3.7
70	431194	D43704	Hs.250712	Ca_channel_LB,RepB_protein	calcium channel, voltage-dependent,	3.7
	430397	AI924533	Hs.105807	HCO3_cotransp;TM=Y;SS=N	bicarbonate transporter related pro	3.7
	418969	W33191	Hs.28907	SH3;TM=M;SS=N	hypothetical protein FLJ20258	3.7
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	3.7
	424012	AW368377	Hs.137569	SAM,PS3;TM=M;SS=N	tumor protein 63 kDa with strong ho	3.7
	418840	AI821614	Hs.185831		ESTs	3.7
75	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	3.7
	433430	AI863735	Hs.359982	thyroglobulin_1,GFGB,zf-	ESTs	3.7
	422491	AA338548	Hs.117546	TM=M;SS=Y	neurostatin	3.7
	435114	AA775483	Hs.288936	ODC_AZ,Ribosomal_L9_N;TM=	mitochondrial ribosomal protein L9	3.7
	416899	BE262645	Hs.80420	ILR;TM=M;SS=M	small inducible cytokine subfamily	3.7
80	422110	AI376736	Hs.121555	kazal,none	secreted protein, acidic, cysteine-	3.7
	448560	BE613183	Hs.23213	zf-RamBP,MDM2,Ndr	ESTs	3.6
	414945	BE076358	Hs.77667	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
	422119	AI277829	Hs.111882	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
	447335	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20940	3.6

5	450663	H43540	Hs.25292	RNase_HII;TM=N;SS=M	ribonuclease HI, large subunit	3.6
	417387	AW021102	Hs.21509	zf-C2H2,none	ESTs	3.6
	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	light junction protein 3 (zona ooc	3.6
	439755	AW748482	Hs.77873	lg;TM=Y;SS=M	B7 homolog 3	3.6
	439873	BE159253	Hs.300638		ESTs	3.6
	439039	AI556707	Hs.48713	pktnase,none	ESTs	3.6
	419235	AW470411	Hs.288433		neurotrophin	3.6
10	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependant kinase inhibitor 2	3.6
	404394	AF332975	Hs.307004	EGF,fn1,vwc,vwd,MAM,Kerat	Zonadhesin	3.6
	452222	AW806287	Hs.21432	Sema,TIG,PSI,GDI	SEX gene	3.6
	422961	Y13620	Hs.122607	TM=M;SS=N	B-cell CLL/lymphoma 9	3.6
	420988	AW006352	Hs.159643		ESTs, Weakly similar to T32554 hypo	3.6
	439680	AW245741	Hs.58461	zf-C2H2,TFIIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 krue	3.6
15	426815	D59505	Hs.351344	lg,SET,PHD,zf-CXXC,Adap_c	ESTs, Weakly similar to K1CL_HUMAN	3.6
	437446	AA788948	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA	3.6
	421690	AW162657	Hs.106857	efhand;TM=M;SS=N	catbindin 2, (29kD, catenin)	3.5
	453939	AA418160	Hs.86043		Homo sapiens cDNA FLJ13558 fis, clo	3.5
	426158	NM_001982	Hs.199067	Furin-like,pktnase,Recep_	v-erb-b2 avian erythroblastic leuke	3.5
20	439246	AI498072	Hs.351474	ank,pktnase,UPF0073;TM=N;	membrane-associated tyrosine- and t	3.5
	410653	BE383768	Hs.65238	zf-C3HC4,AlP3;TM=M;SS=N	85 kDa retinoblastoma protein bindi	3.5
	412703	AW984744			gb:RC1-HN0015-040400-011-d03 HN0015	3.5
	427871	AW992405	Hs.352406	TM=M;SS=N	Homo sapiens, clone IMAGE:3507281,	3.5
	444273	AI903474	Hs.230	LRR,LRRT;TM=M;SS=M	fibromodulin	3.5
25	434936	AI285970	Hs.183817	UCH-2	ESTs	3.5
	457869	AU077186	Hs.108885	vwa,Collagen;TM=M;SS=M	Homo sapiens, alpha-1 (VI) collagen	3.5
	422575	AK000546	Hs.118552	PTR2;TM=Y;SS=M	hypothetical protein FLJ20539	3.5
	428343	AL043021	Hs.12705	WD40;TM=N;SS=M	ESTs	3.5
	426716	NM_006379	Hs.171921	lg,Sema,PSI;TM=N;SS=M	sema domain, immunoglobulin domain	3.5
30	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	3.5
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	3.5
	407926	AW956382	Hs.59771	TYA;TM=N;SS=M	ESTs	3.5
	447041	AL135480	Hs.250705		Homo sapiens cDNA FLJ11685 fis, clo	3.5
35	419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	Homo sapiens cDNA FLJ12797 fis, clo	3.5
	446945	AI193115	Hs.166511	TM=M;SS=N	tumor protein D52-like 1	3.5
	416322	BE019494	Hs.79217	P5CR,NAD_Gly3P_dh,Octopin	pyrroline-5-carboxylate reductase 1	3.5
	447347	AA570056	Hs.122730	NA;NA	ESTs, Moderately similar to KIAA121	3.5
	448984	AW151955	Hs.22753	TM=M;SS=N	hypothetical protein FLJ22318	3.5
40	421778	AA428000	Hs.283072	NA;NA	actin related protein 2/3 complex,	3.5
	423363	BE544348	Hs.127562	homeobox;TM=M;SS=N	homeo box C11	3.5
	432545	X52486	Hs.3041	cyclin,none	uracil-DNA glycosylase 2	3.5
	408495	W68796	Hs.237731		ESTs	3.5
	406851	AA609784	Hs.352392	lg,MHC_II_beta;TM=M;SS=Y	major histocompatibility complex, c	3.5
45	418736	T18979	Hs.87908	helicase_C,AT_hook,SNF2_N	Snf2-related CBP activator protein	3.4
	410197	NM_005518	Hs.59889	HMG_CoA_synth;TM=N;SS=N	3-hydroxy-3-methylglutaryl-Coenzyme	3.4
	453597	BE281130	Hs.33713	KH-domain,Ribosomal_S3_C,	myo-inositol 1-phosphate synthase A	3.4
	417259	AW903838	Hs.81800	EGF,lg,lectin_c,sushi,Xil	chondroitin sulfate proteoglycan 2	3.4
	453985	N44545	Hs.251865	PH,none	ESTs	3.4
	412634	U55984	Hs.356531		heat shock 90kD protein 1, alpha	3.4
50	407204	R41933	Hs.140237	histone,histone	ESTs, Weakly similar to ALU1_HUMAN	3.4
	444371	BE540274	Hs.239	Fork_head;TM=M;SS=N	forkhead box M1	3.4
	447334	AA515032	Hs.91109		ESTs	3.4
	426530	U24578	Hs.278625	A2M,NTR,ANATO,A2M_N,preny	complement component 4A	3.4
55	419749	X73608	Hs.93029	kazal,thyroglobulin_1;TM=	sparc/osteonectin, cwcr and kazal-4	3.4
	423595	R82826	Hs.220702	homeobox,none	ESTs	3.4
	406673	M34996	Hs.198253	lg,MHC_II_alpha;TM=M;SS=M	major histocompatibility complex, c	3.4
	434241	AF119913		TM=N;SS=M	Homo sapiens PRO3077 mRNA, complete	3.4
	412490	AW803564	Hs.288850		Homo sapiens cDNA: FLJ22528 fis, cl	3.4
60	452277	AL049013	Hs.28783	ank;TM=M;SS=N	KIAA1223 protein	3.4
	431457	NM_012211	Hs.256297	FG-GAP,vwa;TM=Y;SS=M	Integrin, alpha 11	3.4
	421777	BE562088	Hs.108196	TM=M;SS=N	HSPC037 protein	3.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	3.4
	414085	AA114016	Hs.75746	aldedh;TM=N;SS=M	aldehyde dehydrogenase 1 family, me	3.4
	440300	N39760	Hs.8859	TM=M;SS=N	Homo sapiens, Similar to RIKEN cDNA	3.4
65	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	3.4
	433339	AF019226	Hs.8036	ras,arf;TM=M;SS=N	glioblastoma overexpressed	3.4
	419301	AA236166	Hs.132957	TM=Y;SS=M	tenomodulin protein	3.4
	414792	BE314949	Hs.87128	TM=Y;SS=M	hypothetical protein FLJ23309	3.4
	451428	AW083384	Hs.11067		ESTs, Highly similar to T46395 hypo	3.4
70	432210	AI567421	Hs.273330	EGF,kazal,Jamninin_EGF,Jam	Homo sapiens, clone IMAGE:3544662,	3.4
	452242	R50956	Hs.159993		glycosyltransferase	3.4
	450678	AI147155	Hs.279727		ESTs	3.4
	413014	AW250533	Hs.75139	TM=M;SS=N	partner of RAC1 (arap2in 2)	3.4
	427919	AA173942	Hs.326416	CTF_NFI,none	Homo sapiens mRNA; cDNA DKFpZp564H19	3.4
75	424005	AB033041	Hs.137507	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2	3.4
	422072	AB018255	Hs.111138	RhoGAP;TM=M;SS=N	KIAA0712 gene product	3.4
	440995	T57773	Hs.10263		ESTs	3.4
80	426150	NM_003858	Hs.167218	homeobox;TM=N;SS=M	BarH-like homeobox 2	3.3
	416877	BE388266	Hs.85658	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436	3.3
	452191	AU078408	Hs.28309	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase	3.3
	450273	AW296454	Hs.24743	rmr,none	hypothetical protein FLJ20171	3.3
	456177	NM_012391	Hs.79414	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr	3.3
	423062	NM_003555	Hs.5637	chromo;TM=Y;SS=M	ESTs	3.3
	421848	X15880	Hs.108885	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1	3.3

5	433577	AW007080	Hs.284192		ESTs	3.3
	409636	AA305729	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	3.3
	404730	AA486704	Hs.33287	CTF_NFI:none	Nuclear factor I/B	3.3
	422940	BE077458		Sec7_P4ANF_receptor,fig	gb:RC1-BT0606-090500-015-b04 BT0606	3.3
	410001	AB041036	Hs.57771	trypsin;TM=M;SS=M	kbikrein 11	3.3
	427461	AA531527	Hs.332040	TM=Y;SS=M	hypothetical protein MGC13010	3.3
	453468	W00712	Hs.32990	TM=M;SS=N	DKFZP566F084 protein	3.3
	443807	W52930	Hs.9822	HAT;TM=N;SS=M	HCNP protein; XPA-binding protein 2	3.3
10	456034	AW450979			gb:UH-H813-ata-a-12-0-ULs1 NCL_OG	3.3
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
	412755	BE144306	Hs.179891		ESTs, Weakly similar to P4HA_HUMAN	3.3
	429690	AW956329	Hs.23721	sugar_tr;Ribosomal_S25	ESTs	3.3
	423472	AF041260	Hs.129057	TM=M;SS=N	breast carcinoma amplified sequence	3.3
15	424118	BE269041	Hs.140452	penilpin;TM=N;SS=M	cargo selection protein (mannose 6	3.3
	437275	AW976035	Hs.292396	Frtzzled,Fz	ESTs, Weakly similar to A47582 B-ae	3.3
	437464	AA323296	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	3.3
	434931	AW968941	Hs.166254		hypothetical protein DKFZp568I133	3.3
20	451691	AI809278	Hs.208152	C2	ESTs	3.3
	430433	AA478883	Hs.273766	VWV:none	ESTs	3.3
	429343	AK000785	Hs.199480	VHS,ENTH,UIM;TM=N;SS=M	Homo sapiens, Similar to epsin 3, c	3.3
	450835	BE262773	Hs.25584	ArfGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
	414591	AI888490	Hs.248107		ESTs, Weakly similar to ALU8_HUMAN	3.3
25	452579	AA131657	Hs.23830	CN_hydrolase	ESTs	3.3
	409960	BE261944	Hs.355264		hexokinase 1	3.3
	406850	AI824300	Hs.172928	wvc, Collagen, COLFI;TM=M;S	collagen, type I, alpha 1	3.3
	453874	AW591783	Hs.36131		collagen, type XIV, alpha 1 (unduli	3.2
	425964	AW889928	Hs.9071	homeobox:none	progesterone membrane binding prote	3.2
30	428412	AA428240	Hs.126083		ESTs	3.2
	430316	NM_000875	Hs.239176	fn3,Furin-like,pkinase,Re	insulin-like growth factor 1 recept	3.2
	440087	W28969	Hs.7718	KOW,Ribosomal_S4e,S4_rnm;	hypothetical protein FLJ22678	3.2
	449933	AW157098	Hs.324104	DUF176,efhand;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
	441128	AA570256	Hs.348504	TM=Y;SS=M	ESTs, Weakly similar to T23273 hypo	3.2
35	434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	G-protein gamma-12 subunit	3.2
	422737	M26939	Hs.119571	Collagen,COLFI;TM=N;SS=M	collagen, type III, alpha 1 (Ehlers	3.2
	408202	AA227710	Hs.43658	OLF;TM=M;SS=N	DKFZP586L151 protein	3.2
	424971	AA479005	Hs.154038	PH;TM=M;SS=N	tumor suppressing subtransferable c	3.2
	407869	AI827976	Hs.24391	efhand;TM=M;SS=N	hypothetical protein FLJ13612	3.2
40	444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	7-dehydrocholesterol reductase	3.2
	426991	AK001536	Hs.214410		Homo sapiens cDNA FLJ10674 fis, clo	3.2
	414081	AW969976	Hs.365706	glx;TM=N;SS=Y	matrix Gla protein	3.2
	408795	AW749126	Hs.170345	hormone_rec,zf-C4	hypothetical protein FLJ13710	3.2
	452345	AA293279	Hs.29173	DSPC;TM=M;SS=N	hypothetical protein FLJ20515	3.2
45	437879	BE262082	Hs.5894	TM=N;SS=N	hypothetical protein FLJ10305	3.2
	407872	AB039723	Hs.40735	Fz,Frtzzled,7m_2,DUF81;T	fritzzled (Drosophila) homolog 3	3.2
	427289	AI097346	Hs.323878	aminotran_5,SDF:none	phosphoserine aminotransferase	3.2
	432375	BE536069	Hs.2962	efhand,S_100;TM=N;SS=M	S100 calcium-binding protein P	3.2
	429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	procollagen C-endopeptidase enhance	3.2
50	412774	AA120865	Hs.380149	hormone_rec,zf-C4	ESTs	3.2
	445942	T80334	Hs.13479	TM=M;SS=N	hypothetical protein FLJ20847	3.2
	439456	AI752409	Hs.109314	zf-C2H2;TM=N;SS=M	hypothetical protein FLJ20980	3.2
	414774	X02419	Hs.77274	kringle,trypsin,plant_lhi	plasminogen activator, urokinase	3.2
	433336	AF017886	Hs.31386	Fz,NTR;TM=N;SS=M	secreted fritzzled-related protein 2	3.2
55	439905	AW799755	Hs.110953	HLH;TM=M;SS=N	retinoic acid induced 1	3.2
	420251	AW374968	Hs.378829		Human DNA sequence from clone RP5-1	3.2
	413004	T35901	Hs.75117	TM=M;SS=N	Interleukin enhancer binding factor	3.2
	418688	Z38830	Hs.87268	annexin;TM=M;SS=N	annexin A8	3.2
	410279	BE271977	Hs.61809	ras;TM=M;SS=N	hypothetical protein FLJ14117	3.2
60	424391	BE550112	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.2
	440409	AW294316	Hs.125608	thione	ESTs	3.2
	452689	F33868	Hs.284176	transferrin,KH-domain,rm	transferrin	3.2
	418154	BE165866	Hs.352403	hormone_rec,zf-C4:none	nuclear receptor subfamily 1, group	3.2
	434384	AA631910	Hs.370133		ESTs	3.2
65	413436	AF238083	Hs.68061	DAGKc;TM=M;SS=N	sphingosine kinase 1	3.2
	431683	NM_016569	Hs.267182	T-box;TM=M;SS=N	TBX3-iso protein	3.2
	432874	W94322	Hs.278651	SH3;TM=M;SS=Y	melanoma inhibitory activity	3.2
	436252	AI539519	Hs.142827		Homo sapiens cDNA FLJ11562 fis, clo	3.2
	421044	AF061871	Hs.101302	fn3,vwa, Collagen, TSPN;TM=	Human DNA sequence from clone RP1-2	3.2
70	419102	AA234098	Hs.42424		ESTs, Weakly similar to 2004399A ch	3.2
	419359	AL043202	Hs.90073	CAS_CSE1;TM=M;SS=N	chromosome segregation 1 (yeast hom	3.2
	441859	AW194364	Hs.9877	Amino_oxidase,FAD_binding	Interleukin-4 induced gene-1 protai	3.1
	426418	M80464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	collagen, type IV, alpha 5 (Alport	3.1
	413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	3.1
	407874	AI766311	Hs.289047	COQ7	Homo sapiens cDNA FLJ14059 fis, clo	3.1
75	448019	AW947164	Hs.195641		ESTs, Moderately similar to I38022	3.1
	427024	AA397572	Hs.348902		chromosome 11 open reading frame 14	3.1
	410281	AF076612	Hs.166186	vwc,W2,MA3,MIF4G	Homo sapiens clone 23928 mRNA seque	3.1
	447205	BE617015	Hs.11006	LEA,penilpin;TM=M;SS=N	ESTs, Moderately similar to T17372	3.1
80	434433	AW629759			gb:hh70e05.y1 NCL_CGAP_GU1 Homo sap	3.1
	439737	AI751438	Hs.41271	C1q, Collagen, none	Homo sapiens mRNA full length inser	3.1
	450157	AW961576	Hs.60178	PH,Band_41,RhoGEF:none	ESTs	3.1
	445989	H97754	Hs.11108		ESTs	3.1
	442213	N38110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	3.1

402496				Target Exon	3.1
438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	3.1
439335	AA742697	Hs.62492	TM=N;SS=M	NM_052853:Homo sapiens secretoglobi	3.1
412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	3.1
416950	AL049798	Hs.80552		dermatopontin	3.1
456157	AW979153	Hs.335881	transmembrane4,none	ESTs	3.1
452753	AA028049	Hs.277728	CRAL_TRIO,none	SEC14 (S. cerevisiae)-like 2	3.1
414420	AA043424	Hs.76095	TM=M;SS=N	immediate early response 3	3.1
446229	A1744964	Hs.14449	TM=M;SS=N	KIAA1609 protein	3.1
453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	3.1
411441	AL042355	Hs.70202	WD40;TM=M;SS=N	WD repeat domain 10	3.1
422921	BE062045	Hs.351625	AAA,hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23260 fis, cl	3.1
444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	3.1
436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	3.1
427890	AA435761	Hs.373623	RFX_DNA_binding,none	ESTs	3.1
444838	AV651680	Hs.208558	integrin_A,FG-GAP,none	ESTs	3.1
427876	A1494291	Hs.369171		ESTs	3.1
413040	AA193338	Hs.12321	Na_Ca_Ex;TM=Y;SS=M	sodium calcium exchanger	3.1
427515	T79526	Hs.178516	EMP24_GP25L;TM=Y;SS=M	integral type I protein	3.1
451092	A1207256	Hs.13766	filament;TM=N;SS=N	Homo sapiens mRNA for FLJ00074 prot	3.1
442222	A1061301	Hs.164773	trypsin,kringle,UPAR_LY6	ESTs	3.1
452613	AA461599	Hs.23459		ESTs	3.1
447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	3.1
412890	T85247	Hs.351875	COX6C;TM=M;SS=M	cytochrome c oxidase subunit VIc	3.1
418313	BE244231	Hs.84038	TM=Y;SS=N	CGI-06 protein	3.1
440006	AK000517	Hs.6844	AAA,NB-ARC,PAAD_DAPIN;NA;	NALP2 protein; PYRIN-Containing APA	3.1
434042	A1589941	Hs.8264		Homo sapiens, Similar to tumor diff	3.1
420576	AA297634	Hs.54925		KIAA1858 protein	3.1
432269	NM_002447	Hs.2942	kinase,Sema,PSI,TIG,A4_E	macrophage stimulating 1 receptor (3.1
424927	AW973666	Hs.163850		hypothetical protein C321D2.4	3.1
440100	BE382685	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.1
452408	AA306477	Hs.29379	TM=M;SS=N	hypothetical protein FLJ10687	3.1
441362	BE614410	Hs.23044	TM=N;SS=N	RAD51 (S. cerevisiae) homolog (E co	3.1
418444	AF902899	Hs.85155	zf-CCCH;TM=M;SS=N	butyrate response factor 1 (EGF-res	3.1
423464	NM_016240	Hs.128856	Collagen;TM=Y;SS=N	CSR1 protein	3.1
424604	AW865388	Hs.151076	TM=M;SS=N	KIAA1243 protein	3.1
420059	AF161486	Hs.94769	ras,none	RAB23, member RAS oncogene family	3.1
453271	AA903424	Hs.6786	LIM;TM=M;SS=N	ESTs	3.1
411274	NM_002776	Hs.69423	trypsin;TM=M;SS=N	kallikrein 10	3.1
434095	AA011117	Hs.3745	EGF,F5_F8_type_C;TM=N;SS=	milk fat globule-EGF factor 8 prote	3.1
403439			ank;TM=M;SS=N	NM_031419*:Homo sapiens molecule po	3.1
413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	3.1
411756	BE294350	Hs.71891	kinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	3.1
409007	AL122107	Hs.49599		Homo sapiens mRNA; cDNA DKFZp434G08	3.1
452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	3.1
414359	M62194	Hs.75929	cadherin,Cadherin_C_term;	cadherin 11, type 2, OB-cadherin (o	3.1
433212	BE218049	Hs.121820		ESTs	3.1
449123	D50920	Hs.23106	TM=M;SS=N	KIAA0130 gene product	3.1
431176	A1026984	Hs.293662	MCPsignal,laminin_B,lamin	ESTs	3.0
419245	A1732742	Hs.87440		ESTs	3.0
434493	AA635305	Hs.375591		ESTs	3.0
449177	BE616694	Hs.288042		hypothetical protein FLJ14299	3.0
430449	AA352723	Hs.241471	WH1;TM=M;SS=N	RN86	3.0
452887	A1702223	Hs.107253	K-box;TM=N;SS=M	hypothetical protein DKFZp761F241	3.0
451678	AA374181	Hs.26799		DKFZP564D0764 protein	3.0
445457	AF168793	Hs.12743	Carn_acyltransf;TM=M;SS=N	camitine O-octanoyltransferase	3.0
407597	AA043925	Hs.339352	fn3,lg;TM=Y;SS=M	Homo sapiens brother of CDO (BOC) m	3.0
431629	ALU077025	Hs.265827	TM=M;SS=Y	Interferon, alpha-inducible protein	3.0
432302	AA345857	Hs.274307	TIG;TM=M;SS=N	KIAA1442 protein	3.0
442549	A1751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	3.0
437959	A1472068	Hs.375604	elF5_elF2B,W2;TM=M;SS=N	KIAA1856 protein	3.0
447400	AK000322	Hs.18457	zf-C3HC4;TM=Y;SS=M	hypothetical protein FLJ20315	3.0
411734	AW374954	Hs.71779		Homo sapiens DNA from chromosome 19	3.0
443547	AW271273	Hs.356487	fn3,none	hypothetical protein FLJ12666	3.0
417000	BE277819	Hs.306019	TM=Y;SS=M	ESTs, Weakly similar to ALU7_HUMAN	3.0
416987	D86957	Hs.80712	GTP_CDC;TM=N;SS=M	KIAA0202 protein	3.0
424494	U78575	Hs.149255	PIP5K;TM=N;SS=M	phosphatidylinositol-4-phosphata 5-	3.0
414496	W73853	Hs.355424	kinase,F5_F8_type_C,adh_L	ESTs	3.0
413336	A1569936	Hs.296178	Ooctudin;TM=M;SS=N	hypothetical protein FLJ22637	3.0
434314	BE392921	Hs.3797	ras,art;TM=M;SS=N	RAB26, member RAS oncogene family	3.0
401038			TM=M;SS=N	C11000425:glj4507721:refjNP_003310.	3.0
418245	AA088767	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.0
407688	W25317	Hs.37616		Human D9 splice variant B mRNA, com	3.0
456906	AF117646	Hs.156637	zf-C3HC4,Cbl_N,Cbl_N2,Cbl	Cas-Br-M (murine) ectropic retrovir	3.0
424744	AW175781	Hs.152720	TM=M;SS=N	M-phase phosphoprotein 6	3.0
452195	AA994712	Hs.116878		ESTs	3.0
415988	BE407713	Hs.78943	Pept_C1-like;TM=N;SS=M	bleomycin hydrolase	3.0
418399	AF131781	Hs.84753	TM=N;SS=N	hypothetical protein FLJ12442	3.0
420568	F09247	Hs.247735	cadherin,Ipocadin;TM=M;S	protocadherin alpha 10	3.0
404661			TM=M;SS=N	C9000306:zgj12737280:refjXP_006682	3.0
414152	NM_003248	Hs.75774	EGF,TSPN,bsp_3;TM=M;SS=M	thrombospondin 4	3.0
421307	BE539976	Hs.103305	chromo	Homo sapiens mRNA; cDNA DKFZp434B04	3.0
444868	BE560471	Hs.12101	TM=N;SS=M	hypothetical protein	3.0

5	450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
	452664	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
	422105	AJ929700	Hs.111680	TM=M;SS=N	endosulfine alpha	3.0
	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
	434067	H18913	Hs.124023		Homo sapiens cDNA FLJ14218 fis, cto	3.0
	412676	NM_000165	Hs.74471	connexin,Connexin43;TM=Y;	gap junction protein, alpha 1, 43kD	3.0
	426801	AA485846	Hs.271795		ESTs, Weakly similar to I38022 hypo	3.0
	421983	AJ252640	Hs.110364	pro_isomerase,none	peptidylprolyl isomerase C (cycloph	3.0
10	429299	AI620463	Hs.347408	TM=Y;SS=N	hypothetical protein MGC13102	3.0
	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	3.0
	438746	AI885815	Hs.184727	transferrin,Guanylate_kin	Human melanoma-associated antigen p	3.0

TABLE 4B

15 Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

20	Pkey	CAT Number	Accession
	418344	245371_1	AA216387 T63548 AA228676
	412703	1243670_1	AW984759 AW984744
	434241	63414_1	AF119913 AJ207698 R57074
25	422940	58443_1	BC012771 BG397153 BF366196 AA337277 AA319285 AW843252
	456034	686586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	434433	111338_1	AA633408 AW749955 AW629759 AI651005

TABLE 4C

30 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

35	Pkey	Ref	Strand	NL_position
	406387	9256180	Plus	116229-116371,117512-117651
	400496	9743564	Plus	41515-41695
40	402496	9797769	Minus	8615-9103
	403439	9719679	Plus	91463-91632
	401038	7232177	Minus	4277-4469
	404661	9797073	Plus	33374-33675,33769-34008

45 TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

50 Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: Ratio of 90th percentile tumor to 50th percentile of normal body tissue

55	Pkey	ExAccn	UniGeneID	Pred.Prod.Domains	UniGeneTitle	R1
60	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
	421481	AW391972	Hs.104698	TM=M;SS=M	KIAA1324 protein	16.3
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXRD domain-containing ion transpor	13.7
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	mdkline (neurite growth-promoting 1	13.7
	414521	D28124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
	438091	AW373062	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	13.4
65	413815	AL046341	Hs.75562	pkinase,F5_F8_type_C;TM=Y	discoilin domain receptor family, m	13.2
	439180	AI393742	Hs.199087	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	13.2
	431441	U81961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.5
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
	452239	AW378378	Hs.356289		protein tyrosine phosphatase, recep	12.1
70	441384	AA447849	Hs.288660	7tm_3,none	retinoic acid induced 3	11.9
	419223	X60111	Hs.1244	transmembrane4;TM=Y;SS=M	CD9 antigen (p24)	11.7
	413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	11.5
	410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	11.2
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	erns1 sequence (mammary tumor and sq	10.1
75	419452	U33635	Hs.90572	lg,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
	444784	D12485	Hs.11951	Somatostatin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	9.9
	436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
	412926	A1879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-r	9.5
80	425280	U31519	Hs.1872	PEPCK;TM=M;SS=N	phosphoenolpyruvate carboxykinase 1	9.5
	432638	AA340864	Hs.278562	PMP22_Claudin;TM=Y;SS=M	claudin 7	9.4
	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	9.4
	424208	NM_003734	Hs.198241	Cu_amine_oxid,Cu_amine_ox	amine oxidase, copper containing 3	9.4
	444797	AB018333	Hs.12002	SH3,SAM;TM=M;SS=N	KIAA0790 protein	9.0

5	402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphatase type 2B	9.0
	443932	AW888222	Hs.8973	SH2;WW,PID:none	tensin	8.9
	421143	AB024536	Hs.102171	Ig_LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	8.8
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	8.7
	410668	BE379794	Hs.159651	daah,TNFR_c6;TM=Y;SS=M	hypothetical protein	8.7
	433662	W07162	Hs.150826	ras,ABC_tran,arf;TM=M;SS=M	RAB25 RAB25, member RAS oncogene fa	8.6
	421853	AL117472	Hs.108924	SH3,Sorb;TM=M;SS=N	SH3-domain protein 5 (ponsin)	8.6
	425335	BE394327	Hs.296267	efhand,kazal,arf,ras,7tm_	folistatin-like 1	8.5
10	400290	H18838	Hs.31608	Cys_knot	hypothetical protein FLJ20041	8.5
	438089	W06391	Hs.351546	hormone_rec,zf-C4:none	nuclear receptor subfamily 1, group	8.4
	426158	NM_001982	Hs.199067	Furin-like,pkinase,Recep_	v-erb-b2 avian erythroblastic leuke	8.3
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	8.2
	439941	AJ392640	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	8.2
15	439318	AW837046	Hs.6527	7tm_2,CytC_asm,GPS;TM=Y;S	G protein-coupled receptor 56	8.1
	447213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	8.1
	412649	NM_002206	Hs.74369	integrin_A,FG-GAP;TM=M;SS	integrin, alpha 7	8.1
	448913	AA194422	Hs.22564	rm,zf-RanBP,pkinase,GST_	myosin VI	8.1
	420168	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	transmembrane 4 superfamily member	8.0
20	407102	AA007629	Hs.348601	transport_prot,SWIB,ASC	glycerol-3-phosphate dehydrogenase	7.9
	452516	AA058630	Hs.29759	TM=N;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
	413076	U10564	Hs.75188	pkinase;TM=M;SS=N	wee1 (S. pombe) homolog	7.9
	443604	C03577	Hs.9615	efhand;TM=M;SS=N	myosin regulatory light chain 2, sm	7.7
	429002	AW248439	Hs.2340	Armadiillo_seg;TM=M;SS=N	junction plakoglobin	7.6
25	423562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	7.6
	436359	AA376409	Hs.10862	adenylatekinase:none	Homo sapiens cDNA: FLJ23313 fis, cl	7.5
	417733	AL048678	Hs.82503	NA;NA	H.sapiens mRNA for 3'UTR of unknown	7.5
	451541	BE279383	Hs.26557	Armadiillo_seg;TM=M;SS=N	plakophilin 3	7.4
	443951	F13272	Hs.356835	PMP22_Claudin:none	fertilin, light polypeptide	7.4
30	409960	BE261944	Hs.355264		hexokinase 1	7.3
	423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	ephrin-A1	7.3
	405121	X04385	Hs.110802	Cys_knot,TGF-beta,vwa,vwc	von Willebrand factor (VWF), mRNA	7.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	7.1
	417771	AA804698	Hs.82547		retinoic acid receptor responder (t	7.0
35	424118	BE269041	Hs.140452	peritipln;TM=N;SS=M	cargo selection protein (mannose 6	7.0
	402705	X67951	Hs.180909	AhpC-TSA;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
	417115	AW952792	Hs.334612	Sm,pkinase;TM=N;SS=N	small nuclear ribonucleoprotein pol	7.0
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	6.9
40	447216	R76812	Hs.169248	cytochrome_c;NA;NA	p76NTR-associated cell death execut	6.9
	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	6.9
	414657	AA424074	Hs.76780	TM=M;SS=N	protein phosphatase 1, regulatory (6.9
	447528	AI612027	Hs.76277	BD_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	6.9
	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	6.9
45	428013	AF151020	Hs.181444	TM=Y;SS=M	hypothetical protein	6.9
	444143	AW747996	Hs.160999	Bcl-2:none	ESTs, Moderately similar to A56194	6.8
	414443	AU077268	Hs.76144	Ig,pkinase;TM=Y;SS=N	platelet-derived growth factor rece	6.7
	418751	BE389014	Hs.372548	SH2:none	phosphoinositide-3-kinase, regulato	6.7
	448479	H96115	Hs.21293	UDPGP;TM=M;SS=N	UDP-N-acetylglucosamine pyrophospho	6.6
50	410552	X66945	Hs.748	Ig,pkinase,SH2,SH3,C2,PH,	fibroblast growth factor receptor 1	6.6
	414883	AA926950	Hs.348669	CKS;TM=N;SS=N	CDC28 protein kinase 1	6.6
	417426	NM_002291	Hs.82124	laminin_EGF,laminin_Nterm	laminin, beta 1	6.6
	428179	AI127772	Hs.279696	pkinase,PX,pkinase_C;TM=N	serum/glucocorticoid regulated kina	6.6
	443195	BE148235	Hs.193063	Aa_trans:none	Homo sapiens cDNA FLJ14201 fis, clo	6.5
55	424512	X53002	Hs.149846	Integrin_B,EGF;TM=Y;SS=M	Integrin, beta 5	6.5
	421733	AL119671	Hs.1420	Ig,pkinase;TM=Y;SS=M	fibroblast growth factor receptor 3	6.5
	428950	BE311879	Hs.194673	DED;TM=M;SS=N	phosphoprotein enriched in astrocyt	6.5
	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	6.5
	416078	AL034349	Hs.79005		protein tyrosine phosphatase, recep	6.5
60	408912	AB011084	Hs.48924	Armadiillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	6.4
	428373	AI751656	Hs.183986	Ig;TM=Y;SS=M	poliovirus receptor-related 2 (herp	6.4
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	6.4
	406621	X57809	Hs.181125	Ig,HSP70,Ppx-GppA;TM=M;SS	immunoglobulin lambda locus	6.4
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	6.4
65	428169	AJ928984	Hs.182793	photoRC,UPF0118;TM=Y;SS=N	golgi phosphoprotein 2	6.4
	443337	Y07604	Hs.9235	NDK;TM=N;SS=N	non-metastatic cells 4, protein exp	6.4
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	6.4
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	6.4
	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	6.3
70	417208	S67773	Hs.81665	Ig,pkinase;TM=Y;SS=M	v-kit Hardy-Zuckerman 4 feline sarc	6.3
	438278	BE409248	Hs.57988	TFIIS,RNA_POL_M_15KD,UPF0	hypothetical protein FLJ22357 simil	6.3
	429455	AA721111	Hs.278694	lectin_c	CD209 antigen	6.3
	431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	vav 3 oncogene	6.3
	445033	AV652402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	6.3
	411756	BE294350	Hs.71891	pkinase,F5_F8_type_C;TM=Y	discolidin domain receptor family, m	6.3
75	453902	BE502341	Hs.3402		ESTs	6.3
	418005	AI188220	Hs.83164	Collagen,TSPN;TM=M;SS=M	collagen, type XV, alpha 1	6.2
	449924	W30581	Hs.146233	SH3:none	Homo sapiens cDNA: FLJ22130 fis, cl	6.2
	426520	BE545684	Hs.343566	aa_permeases,pyridoxal_de	KIAA0251 protein	6.2
	453064	R40334	Hs.89463		potassium large conductance calcium	6.2
80	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	6.2
	452683	AI089575	Hs.374574	homeobox:none	progesterone membrane binding prote	6.2
	402575	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat. type 2B	6.2
	444672	Z95636	Hs.11669	laminin_EGF,laminin_G,EGF	laminin, alpha 5	6.2
	450440	AB024334	Hs.25001	14-3-3;TM=M;SS=N	tyrosine 3-monooxygenase/tryptophan	6.2

	432314	AA533447	Hs.285173	Xlink:none	ESTs	6.1
	438564	AA381553	Hs.198253	Ig,MHC_IL_alpha:none	major histocompatibility complex, c	6.1
	444252	R21135	Hs.54985		ESTs	6.1
5	425184	BE278288	Hs.155048	Ig;TM=Y;SS=M	Lutheran blood group (Aubergier b an	6.1
	431890	X17033	Hs.271986	vwa,Integrin_A,FG-GAP;TM=	Integrin, alpha 2 (CD49B, alpha 2 s	6.1
	449475	AJ348027	Hs.129826	transmembrane4;TM=Y;SS=M	hypothetical protein PP1057	6.1
	449538	AJ559444	Hs.104679	TM=M;SS=M	ESTs	6.0
	414496	W73853	Hs.355424	pkinase,F5_F8_type_C,adh_	ESTs	6.0
10	414217	AI309298	Hs.279898	NA;NA	Homo sapiens cDNA: FLJ23165 fs, cl	6.0
	445333	BE537641	Hs.44278	ras,arf;TK;TM=N;SS=M	hypothetical protein FLJ12538 simil	5.9
	431183	NM_006855	Hs.250696	ER_lumen_recept;TM=M;SS=M	KDEL (Lys-Asp-Glu-Leu) endoplasmic	5.9
	409645	AI142265	Hs.55498	polyprenyl_synt;TM=M;SS=N	geranylgeranyl diphosphate synthase	5.9
	412276	BE262621	Hs.73798	MIF,sugar_tr:none	macrophage migration inhibitory fac	5.9
15	416137	BE279513	Hs.278607	pkinase,UBA,ThiF;TM=M;SS=	ubiquitin activating enzyme E1-like	5.9
	412969	AJ373162	Hs.75103	14-3-3;TM=N;SS=M	tyrosine 3-monooxygenase/tryptophan	5.9
	414504	AW069181	Hs.116175	pkinase,SAM;TM=M;SS=N	sterile-alpha motif and leucine zip	5.9
	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,laminl	cadherin, EGF LAG seven-pass G-type	5.9
	436415	BE265254	Hs.343258	Peptidase_M24,Furin-like,	proliferation-associated 2G4, 38kD	5.9
20	413900	AW049747	Hs.75612	TPR,PDZ,VW,Guanylate_kin;	stress-induced-phosphoprotein 1 (Hs	5.9
	441455	AJ271671	Hs.7854	Zip;TM=Y;SS=M	zinc/iron regulated transporter-like	5.9
	444006	BE395085	Hs.334762	Idl_recept_a,PKD,MHC_J;TM	type I transmembrane protein Fn14	5.8
	408269	AW888219	Hs.44077	CH;TM=M;SS=N	parvin, alpha	5.8
	411372	AI147861	Hs.213289	Glyco_transf_11,EGF,Idl_r	low density lipoprotein receptor (f	5.8
25	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	tight junction protein 3 (zona ocl	5.8
	456534	X91195	Hs.100623	LIM,PDZ,pkinase;TM=N;SS=M	phospholipase C, beta 3, neighbor p	5.7
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.7
	468112	AL042279	Hs.16206	pkinase	uncharacterized hypothalamus protei	5.7
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	5.7
30	405484	XM_093451		TM=N;SS=M	C3002124:gil12737280ref XP_006682	5.7
	425367	BE271188	Hs.155975	TM=M;SS=Y	protein tyrosine phosphatase, recep	5.7
	444607	AW045635	Hs.293687	PI-PLC-X,PH,PI-PLC-Y	ESTs	5.7
	421456	AW579842	Hs.104557	zf-C2H2,DUF18,ethand,C2,P	hypothetical protein FLJ10697	5.6
	412810	M21574	Hs.74615	Ig,pkinase,DUF11;TM=M;SS=	platelet-derived growth factor rece	5.6
35	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	5.6
	453880	AJ803166	Hs.135121	HSP70:none	ESTs, Weakly similar to I38022 hypo	5.6
	439578	AW263124	Hs.350547	WD40;TM=M;SS=N	nuclear receptor co-repressor/HDAC3	5.6
	450954	AJ504740	Hs.25691	TM=Y;SS=M	receptor (calcitonin) activity modi	5.6
	414555	N98569	Hs.76422	phoslip;TM=M;SS=Y	phospholipase A2, group IIA (platel	5.6
40	409963	AA133590	Hs.377830	MBOAT:none	calcium/calmodulin-dependent protei	5.6
	450463	AW952018	Hs.201398	C1q,Collagen;TM=M;SS=Y	G protein coupled receptor interact	5.6
	425177	AF127577	Hs.155017	TM=N;SS=M	nuclear receptor interacting protei	5.5
	445496	AB007860	Hs.12802	SH3,ank,PH,ArfGap;TM=M;SS	development and differentiation enh	5.5
	426981	BE313077	Hs.93135	nm	ESTs, Weakly similar to ALU2_HUMAN	5.5
	424441	X14850	Hs.147097	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member X	5.5
45	415662	AW972481	Hs.170610	pkinase:none	ESTs, Highly similar to G01887 MEK	5.5
	422105	AJ929700	Hs.111680	TM=M;SS=N	endosulfine alpha	5.5
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	5.5
	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	5.5
50	425205	NM_005854	Hs.155106	TM=Y;SS=N	receptor (calcitonin) activity modi	5.5
	444633	AF111713	Hs.12284	Ig;TM=Y;SS=M	junctional adhesion molecule 1	5.5
	431565	AF161470	Hs.260622	TM=Y;SS=N	butyrate-induced transcript 1	5.5
	429655	U48959	Hs.211582	pkinase,fn3,Ig:none	myosin, light polypeptide kinase	5.5
	431886	L77864	Hs.271980	pkinase;TM=M;SS=N	mitogen-activated protein kinase 6	5.5
55	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	5.4
	451863	AL120634	Hs.331803	cpn60_TCP1,E1-E2_ATPase,C	ATPase, Ca transporting, plasma mem	5.4
	422293	X94453	Hs.114366	aldedh,acknase;TM=M;SS=N	pyruvate-5-carboxylate synthetase	5.4
	432179	X75208	Hs.2913	EPH_bdf,fn3,pkinase,SAM,T	EphB3	5.4
	408048	NM_007203	Hs.42322	Parakemnin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.4
60	448153	Y10805	Hs.20521	NusG;TM=N;SS=M	HMT1 (hnRNP methyltransferase, S. c	5.4
	421251	Z28913	Hs.102948	LIM,PDZ;TM=N;SS=M	enigma (LIM domain protein)	5.4
	439039	AI656707	Hs.48713	pkinase:none	ESTs	5.4
	409882	AJ243191	Hs.56874	HSP20;TM=N;SS=M	heat shock 27kD protein family, mem	5.4
65	451295	AI557212	Hs.17132	pkinase,DAG_PE-bind,pkina	ESTs, Moderately similar to I54374	5.4
	442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	5.4
	445930	AF055009	Hs.13458	DAGKc,DAGKa,ank,WD40,bZIP	Homo sapiens clone 24747 mRNA seque	5.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	5.4
	426432	AF001601	Hs.169857	Arylesterase;TM=M;SS=N	paraoxonase 2	5.4
	415753	U52819	Hs.78781	PDGF;TM=M;SS=M	vascular endothelial growth factor	5.4
70	450778	U81375	Hs.25450	Nucleoside_tran;TM=Y;SS=M	solute carrier family 29 (nucleosid	5.4
	414739	U83867	Hs.77196	ethand,SH3,spectrin;TM=N;	spectrin, alpha, non-erythrocytic 1	5.3
	421233	AA209534	Hs.284243	transmembrane4;TM=Y;SS=M	tetraspan NET-6 protein	6.3
	414774	X02419	Hs.77274	kringle,bypsin,plant_lhl	plasminogen activator, urokinase	5.3
	414368	W70171	Hs.75939	PRK,CoaE;TM=N;SS=N	uridine monophosphate kinase	5.3
75	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsm,z-al	ephrin-A3	5.3
	423619	T48691	Hs.249159	7tm_1,7tm_2;TM=Y;SS=M	adrenergic, alpha-2A-, receptor	5.3
	440188	AK001812	Hs.7036	ROK;TM=M;SS=N	N-Acetylglucosamine kinase	5.3
	414135	NM_004419	Hs.2128	Rhodanese,DSPc,Y_phosphat	dual specificity phosphatase 5	5.3
80	444838	AV651680	Hs.208558	Integrin_A,FG-GAP:none	ESTs	5.3
	447918	AI129320	Hs.115175	pkinase,SAM:none	ESTs, Highly similar to JC5818 gamm	5.3
	405517	AF000974	Hs.119498	LIM;TM=M;SS=N	thyroid hormone receptor interactor 6	5.3
	413588	AA971014	Hs.75432	IMPDH_C,CBS,IMPDH_N;TM=M;	IMP (inosine monophosphate) dehydro	5.2
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	5.2
	416157	NM_003243	Hs.342874	zona_peflucida;TM=Y;SS=M	transforming growth factor, beta re	5.2

5	407744	AB020629	Hs.38095	ABC_tran,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2
	446108	AL036596	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.2
	422034	AC006486	Hs.333069	Ets;TM=M;SS=N	Ets2 repressor factor	5.2
	417098	AB017355	Hs.173859	Frizzled,Fz,7tm_2,toxin_2	frizzled (Drosophila) homolog 7	5.2
	430526	AF181862	Hs.242407	7tm_3;TM=Y;SS=M	G protein-coupled receptor, family	5.2
	414176	BE140538	Hs.75794	7tm_1,CRCB;TM=Y;SS=N	EDG-2 (endothelial differentiation	5.2
	416710	AI268325	Hs.54890	Peptidase_M49,EGF,Jg,Neur	hypothetical protein FLJ23590	5.2
	417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2
10	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	5.2
	421837	AF135158	Hs.108802	AAA,cdc48_N,cdc48_2,NB-AR	N-ethylmaleimide-sensitive factor	5.2
	429379	NM_014840	Hs.200598	pkinase,RJO1;TM=M;SS=N	KIAA0537 gene product	5.2
	429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2
	437275	AW976035	Hs.292396	Frtzzled,Fz	ESTs, Weakly similar to A47582 B-ca	5.1
15	421071	AI311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGHUIE coil	5.1
	448581	NM_002709	Hs.21537		protein phosphatase 1, catalytic su	5.1
	452568	AA805634	Hs.300870	PI3_P14_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1
	452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1
20	437175	AW968078	Hs.87773	pkinase,pkinase_C,none	protein kinase, cAMP-dependent, cat	5.1
	437056	AI147061		spectrin,SH3,PH,CH	gb:ok33a11.s1 Soares_NSF_F8_9W_OT_P	5.1
	450998	BE387614	Hs.25797	rm;TM=M;SS=N	splicing factor 3b, subunit 4, 49kd	5.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	5.1
	448528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1
	452345	AA283279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	5.1
25	443412	W84893	Hs.9305		angiotensin receptor-like 1	5.1
	412853	M34175	Hs.74626	Adaptin_N,Alpha_adaptinC2	adaptor-related protein complex 2,	5.1
	439866	AA280717	Hs.6727	rm,NTF2;TM=M;SS=N	Ras-GTPase activating protein SH3 d	5.1
	439975	AW328081	Hs.6817	Ham1p_lik;TM=M;SS=N	inosine triphosphatase (nucleoside	5.1
	435523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1
30	433423	BE407127	Hs.8997	HSP70,Jg,Ppx-GppA;TM=M;SS	heat shock 70kD protein 1A	5.1
	412641	M16660	Hs.74335	HSP90,HATPase_c;TM=M;SS=N	heat shock 90kD protein 1, beta	5.1
	431236	AV656840	Hs.285115	tn3;TM=Y;SS=M	Interleukin 13 receptor, alpha 1	5.1
	436552	AJ245820	Hs.5314		type I transmembrane receptor (seiz	5.0
	422765	AW409701	Hs.1578	BIR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0
35	427502	AB11865	Hs.71133	TM=M;SS=N	Homo sapiens, clone IMAGE:3161564,	5.0
	414166	AW888941	Hs.75789	DEAD,helicase_C,rm,Ndr,C	N-myc downstream regulated	5.0
	424954	NM_000546	Hs.1846	P53,WD40,IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni synd	5.0
	422089	AA523172	Hs.103135	REJ,PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFR4_HUMAN	5.0
	426636	BE242634	Hs.2055	ThIF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0
40	410793	AW581906	Hs.66392	SH3,afhand,C2,PH,RhoGEF,M	Intersectin 1 (SH3 domain protein)	5.0

TABLE 5B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
437056	428504_3	AW976398 AI147061 AA765223 AA743380 AI803927

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
405484	5922025	Plus	199214-199579,199672-199920,200262-20049

TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists 777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90th percentile amongst 95 colon cancers. The "average" normal adult tissue level was set to the 90th percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

	Phy	ExAcn	UnigeneID	Unigene Title	R1
5	447033	AI357412	Hs.157601	ESTs	31.35
	409041	AB033025	Hs.50081	KIAA1199 protein	29.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	26.41
	422330	D30783	Hs.115263	epiregulin	24.38
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
10	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
	422958	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.60
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	21.15
	415989	AI267700	Hs.317584	ESTs	20.95
15	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.35
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
	421470	R27496	Hs.1378	annexin A3	18.05
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
20	450531	AW301032	Hs.203800	ESTs	16.60
	432867	AW016936	Hs.233364	ESTs	16.35
	443211	AI128388	Hs.143655	ESTs	15.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
	406964	M21305		gb:Human alpha satellite and satellite 3	15.00
25	410355	S58544	Hs.153057	sperm associated antigen 1	14.70
	441377	BE218239	Hs.202656	ESTs	14.45
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.35
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	14.35
	440304	BE159984	Hs.125395	ESTs	14.25
30	426427	M86699	Hs.159840	TTK protein kinase	13.60
	451561	N52812	Hs.177403	ESTs	12.80
	434032	AW009951	Hs.206892	ESTs	12.75
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	12.55
35	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.40
	446232	AI281848	Hs.194691	retinoic acid induced 3	12.25
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
	450149	AW969781	Hs.132853	Zic family member 2 (odd-paired Drosophi	11.85
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	11.80
40	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
	452461	N78223	Hs.108106	transcription factor	11.42
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
	400534				11.00
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	10.75
45	453688	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
	426890	AA393167	Hs.41294	ESTs	10.60
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.50
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
50	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.40
	425761	AW664214	Hs.196729	ESTs	10.25
	404567				10.15
	428536	AI143139	Hs.2288	visinin-like 1	10.10
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
55	459504	BE514127		gb:G01315874F1 NIH_MGC_8 Homo sapiens cD	9.95
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	9.85
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
60	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	8.73
	420900	AL045833	Hs.44269	ESTs	9.68
	438639	AI278360	Hs.31409	ESTs	9.65
	439521	AI808955	Hs.58248	ESTs	9.55
	445676	AI247763	Hs.16928	ESTs	9.50
65	408489	AI082437	Hs.26690	ESTs	9.50
	418738	AW388833	Hs.6682	solute carrier family 7, (cationic amino	9.37
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
	423349	AF010258	Hs.127428	homeo box A9	8.96
	400195	NA		NA	8.90
70	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	8.90
	418895	AA894638	Hs.14600	ESTs	8.85
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.75
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
75	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	8.64
	445436	AI224105	Hs.151408	ESTs	8.60
	403778				8.50
	433447	U29195	Hs.3281	neuronal pentraxin II	8.50
	407168	R45175	Hs.117183	ESTs	8.31
80	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	8.30
	422505	AL120862	Hs.124165	ESTs	8.25
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	409687	T51125	Hs.8493	ESTs	8.05

	416681	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443814	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
5	443450	N66045	Hs.133529	ESTs	7.75
	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	7.70
	438604	AA811896	Hs.44604	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
	400250	NA		NA	7.53
10	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404996				7.50
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
15	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
	448816	AB033052	Hs.22151	KIAA1226 protein	7.25
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	7.20
	433859	AW896758	Hs.273789	ESTs	7.20
20	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	7.20
	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.83121	KIAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.a	7.15
	421373	AA808229	Hs.167771	ESTs	7.10
25	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	6.95
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.95
	413573	AI733859	Hs.149089	ESTs	6.95
30	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CGI-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.85
	422711	D06641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518 (f	6.82
35	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.80
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.75
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	6.71
	401644				6.70
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	6.69
	406747	AI925153	Hs.217493	annexin A2	6.65
45	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	AA889120	Hs.110637	homeo box A10	6.53
50	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	6.50
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	6.50
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	6.60
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
55	410908	AA121686	Hs.10592	ESTs	6.47
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.45
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
60	438202	AW169287	Hs.22588	ESTs	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.39
	436539	AI005457	Hs.275048	ESTs	6.35
65	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
70	429529	AA454190	Hs.24283	ESTs, Moderately similar to reduced expr	6.30
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.25
	407748	AK001962	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
75	416857	AA188775	Hs.292453	ESTs	6.20
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.15
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associat	6.15
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.15
80	433393	AF038564	Hs.98074	litchy (mouse homolog) E3 ubiquitin prote	6.11
	424745	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172405	cell division cycle 27	6.08
	407771	AL138272	Hs.62713	ESTs	6.08

	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
5	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
	412246	AI160873	Hs.69233	zinc finger protein	5.96
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	418421	AA134006	Hs.79306	eukaryotic translation initiation factor	5.95
10	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	408908	BE296227	Hs.250822	serine/threonine kinase 15	5.86
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
15	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	5.85
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.85
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23405 hypotheti	5.85
	409187	AF154830	Hs.60966	carbamoyl-phosphate synthetase 1, mitoch	5.85
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.82
	429945	NM_008729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	459309	AA040620	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58367	glypican 4	5.79
	423806	AA331247	Hs.86617	ESTs	5.77
25	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.75
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.75
	411086	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.75
	442957	AI949952	Hs.49397	ESTs	5.75
30	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystatin SN	5.69
35	433687	AA743891		gb:ny57g01.s1 NCL CGAP_Pr18 Homo sapiens	5.68
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.60
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
	417235	AA810278	Hs.24250	ESTs	5.60
40	451177	AI969716	Hs.13034	ESTs	5.60
	415227	AW821113	Hs.72402	ESTs	5.58
	438217	T53925	Hs.107	fibrinogen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.55
45	426235	AI631964	Hs.34447	ESTs	5.55
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sapi	5.53
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked mol	5.52
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
	419502	AU076704	Hs.80765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
55	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	5.45
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
	428046	AW812795	Hs.156381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ12092	5.41
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	5.35
	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	415139	AW975942	Hs.48524	ESTs	5.30
65	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakbines	5.29
	424086	AI351010	Hs.102267	lysyl oxidase	5.27
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycnamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
70	436016	AA806465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.25
	449347	AV649748	Hs.295901	KIAA0493 protein	5.25
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453921	AI824009	Hs.44577	ESTs	5.25
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.25
	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypotheti	5.25
75	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	5.24
	433384	AI021992	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.20
	441795	N58115	Hs.21137	ADO24 protein	5.20
80	449416	AI651016	Hs.246311	ESTs	5.20
	418379	AA218940	Hs.137616	fdgellin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17

	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	5.17
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.15
5	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.15
	447713	AA20733	Hs.207083	ESTs	5.15
	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.15
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
10	441139	AW449009	Hs.126647	ESTs	5.13
	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
	435202	AI871313	Hs.170204	KIAA0551 protein	5.10
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
15	422805	AA436989	Hs.121017	H2A histone family, member A	5.07
	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	5.06
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
20	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.05
	441875	AI914329	Hs.5461	ESTs	5.00
	448802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.00
	401480	NA	NA	NA	5.00
25	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.95
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
	414718	H95348	Hs.107987	ESTs	4.91
	419139	AI123517	Hs.269940	ESTs	4.90
	430769	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	4.90
30	425420	BE536911	Hs.234545	hypothetical protein NUF2R	4.90
	408758	NM_003686	Hs.47504	exonuclease 1	4.90
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	4.90
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	4.90
	433927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
35	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.88
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	4.87
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (f	4.87
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	4.86
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
40	418396	AI765805	Hs.26691	ESTs	4.85
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.84
	408430	ST9876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW449612	Hs.152475	ESTs	4.71
45	411901	AA166730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
	404025	NA	NA	NA	4.70
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	4.68
	436662	AI582393	Hs.126695	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	4.68
50	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	4.65
	410658	AW105231	Hs.192035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
55	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.65
	436397	AA715013	Hs.169835	ESTs	4.60
	439225	AA192669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125166	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
60	412723	AA848459	Hs.335951	hypothetical protein AF301222	4.59
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.59
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
65	433326	AI379486	Hs.159430	ESTs	4.55
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	4.55
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324643	Hs.246106	ESTs	4.55
	416467	H57585	Hs.37467	ESTs	4.55
70	408867	AA437199	Hs.656	cell division cycle 25C	4.54
	419423	D28488	Hs.90315	KIAA0007 protein	4.54
	414132	AI801235	Hs.48480	ESTs	4.53
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acyl	4.50
75	451009	AA013140	Hs.115707	ESTs	4.50
	431084	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
	432725	AL137496	Hs.9001	ESTs	4.50
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
	410486	AW235094	Hs.69233	zinc finger protein	4.50
80	428532	AF157326	Hs.184786	TBP-interacting protein	4.50
	429782	NM_005754	Hs.220689	Res-GTPase-activating protein SH3-domain	4.50
	408380	AF123050	Hs.44532	diubiquitin	4.49
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S5	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	4.46
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypotheti	4.45
	410142	AA081924	Hs.124918	KIAA1795 protein	4.45
	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
5	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA		NA	4.45
	430967	H16791	Hs.31445	ESTs	4.41
	438078	AI016377	Hs.131693	ESTs	4.41
10	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	4.40
	429774	AI522215	Hs.50883	KIAA1804 protein	4.40
	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
15	421211	AA284966	Hs.266308	mosaic serine protease	4.40
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	4.40
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	4.37
	448305	AA626207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410568	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
20	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
	448243	AW369771	Hs.62620	Integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.35
	446152	AI292036	Hs.150028	ESTs	4.34
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	4.32
25	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.30
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	439619	AW975998	Hs.68595	ESTs, Weakly similar to I38022 hypotheti	4.30
30	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	4.28
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibitor	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
35	409723	AW885757	Hs.257862	ESTs	4.25
	417956	AA210704	Hs.190465	ESTs	4.25
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	4.25
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	4.24
40	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
	424583	AF017445	Hs.150926	fucose-1-phosphate guanylyltransferase	4.20
	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like	4.20
	448912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	AI005668	Hs.134779	EST	4.20
45	411893	R82845	Hs.273789	ESTs	4.20
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	AI793163		gb:cn52g03.y5 NCI_CGAP_Co8 Homo sapiens	4.20
	404516	NA		NA	4.20
50	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	419229	AI827237	Hs.282884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
	453911	AW503857	Hs.4007	Sarcolemma-associated protein	4.16
55	433159	AB035898	Hs.150587	kinesin-like protein 2	4.15
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	4.15
	422093	AF151852	Hs.111449	CGI-94 protein	4.15
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
60	446999	AA151520	Hs.334822	hypothetical protein MGC4485	4.15
	414538	AW612228	Hs.107987	ESTs	4.14
	453931	AL121278	Hs.25144	ESTs	4.12
	427718	AI798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	orosomucoid 1	4.10
65	440209	H05049	Hs.22269	neurexin 3	4.10
	435148	AI918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	4.10
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	4.10
70	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.10
	457059	BE561665	Hs.177677	exosome component Rps40	4.10
	407162	N63855	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	4.09
75	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
	448666	NM_014953	Hs.323348	KIAA1008 protein	4.07
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
80	434082	AI373481	Hs.131715	hypothetical protein PRO1777	4.05
	443646	AI085198	Hs.164228	ESTs	4.05
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.05
	418524	AA300576	Hs.85769	actin 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of the	4.05

	447207	AA442233	Hs.17731	hypothetical protein FLJ12692	4.05
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-essoc	4.04
	424176	AL137273	Hs.142307	hypothetical protein	4.04
5	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.04
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	406666	V00495	Hs.184411	albumin	4.02
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
10	449448	D60730	Hs.57471	ESTs	4.00
	421037	AI684808	Hs.197653	ESTs	4.00
	448310	AI480316		gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	4.00
	408155	AB014528	Hs.43133	KIAA0628 gene product	4.00
	413841	M34276	Hs.75576	plasminogen	3.98
15	400110	NA		NA	3.98
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.97
	443715	AI583187	Hs.9700	cyclin E1	3.97
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.97
	450164	AI239923	Hs.30098	ESTs	3.97
20	451592	AI805416	Hs.213897	ESTs	3.95
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome delta	3.95
	426199	AA371865	Hs.97090	ESTs	3.95
	414148	BE084049		gb:PM0-BT0651-270400-003-02 BT0651 Homo	3.95
	417005	AW673606	Hs.80758	aspartyl-HRNA synthetase	3.94
25	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	3.93
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.93
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.92
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.91
	416185	AW975861	Hs.47367	KIAA1785 protein	3.91
30	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.90
	432596	AJ224741	Hs.278461	matrilin 3	3.90
	451229	AW957707	Hs.48473	ESTs	3.90
	413583	AL120806	Hs.5888	ESTs	3.90
	432702	AW973953	Hs.293744	ESTs	3.90
35	437207	T27503	Hs.15929	hypothetical protein FLJ12910	3.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.90
	423697	BE088697	Hs.131834	Homo sapiens mRNA; cDNA DKFZp43480328 (f	3.90
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	3.90
	432289	AI860145	Hs.55118	ESTs	3.89
40	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.88
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281896	Homo sapiens cDNA FLJ11660 fis, clone HE	3.88
	410094	BE147897	Hs.58593	general transcription factor IIF, polype	3.88
	441826	AW503603	Hs.129915	phosphotriesterase related	3.87
45	444059	R69743	Hs.116774	integrin, alpha 1	3.86
	426262	AI792141	Hs.196270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	3.85
50	448315	AW290912	Hs.20797	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	3.85
	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016670	Hs.233275	ESTs	3.84
	453116	AI276680	Hs.146086	ESTs	3.83
55	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	3.82
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.82
	435040	AI932350	Hs.152825	ESTs	3.81
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.81
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
60	437631	AA764749	Hs.267245	hypothetical protein FLJ14803	3.80
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
	438295	AI394151	Hs.37932	ESTs	3.80
65	453628	AW243307	Hs.83937	hypothetical protein	3.80
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	3.80
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.76
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	3.75
	406728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
70	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.75
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	3.74
	418413	R95735	Hs.117753	ESTs, Weakly similar to A48666 cell prol	3.73
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
75	406687	M12523	Hs.184411	albumin	3.72
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
	417246	AI760098	Hs.21411	ESTs	3.72
	410664	NM_006033	Hs.65370	lipase, endothelial	3.71
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	3.70
80	442881	AI023175	Hs.167022	ESTs	3.70
	432356	AA831032	Hs.111670	ESTs, Highly similar to JC2257 proyl of	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405460	NA		NA	3.70
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
5	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.69
	444471	AB020684	Hs.11217	KIAA0877 protein	3.69
	419559	Y07828	Hs.91096	ring finger protein	3.69
	437641	AA811452	Hs.291911	ESTs	3.68
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.67
10	417791	AW965339	Hs.111471	ESTs	3.66
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.66
	432023	AW273128	Hs.330144	EST	3.66
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
15	420595	AA278865	Hs.88523	ESTs	3.65
	404477	NA	NA	NA	3.65
	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.65
	452220	BE158006	Hs.212296	ESTs	3.65
20	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.65
	457465	AW301344	Hs.122908	DNA replication factor	3.64
	436149	AI754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
25	424641	AB001106	Hs.151413	glia maturation factor, beta	3.63
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic)	3.62
	411975	AI916058	Hs.144583	ESTs	3.61
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	429528	H09604	Hs.13268	ESTs	3.61
30	449722	BE280074	Hs.23960	cyclin B1	3.60
	428389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	3.60
	419945	AW290975	Hs.118923	ESTs	3.60
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	3.60
	420585	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (f	3.60
35	407809	AW082279	Hs.244106	ESTs	3.60
	457708	AA805443	Hs.179909	hypothetical protein FLJ22995	3.60
	427943	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028892	Hs.193143	KIAA1069 protein	3.60
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
40	418688	T85017	Hs.1192	KIAA0074 protein	3.59
	436961	AW375974	Hs.156704	ESTs	3.58
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.58
	415245	N59650	Hs.27252	ESTs	3.57
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
45	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
	401165	NA	NA	NA	3.55
	415382	AI743539	Hs.72465	ESTs, Weakly similar to non-lens beta ga	3.55
	433968	AL157518	Hs.90421	PRO2463 protein	3.55
	421628	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
50	443325	BE398006	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	3.55
55	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.54
	434208	AW136973	Hs.288518	ESTs, Weakly similar to S69890 myogen I	3.54
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.53
	433675	AW977653	Hs.76319	ribonucleotide reductase M2 polypeptide	3.52
60	423441	R68649	Hs.278359	absent in melanoma 1 like	3.51
	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.51
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	3.50
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW389351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.48
65	449915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukem	3.47
	427975	AI536065	Hs.122460	ESTs	3.46
	400297	AI127078	Hs.334473	hypothetical protein DKFZp564O1278	3.45
	404253				3.45
	435567	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 fis, clone NT	3.45
70	432158	W33165	Hs.22983	UDP-glucose:glycoprotein glucosyltransfe	3.45
	417315	AI080042	Hs.336901	ribosomal protein S24	3.45
	419140	AI982847	Hs.215725	ESTs	3.44
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	3.43
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
75	411571	AA122393	Hs.70811	hypothetical protein FLJ20518	3.42
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	3.41
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA406293	Hs.41167	ESTs	3.41
	430264	AA470519		gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	3.40
80	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	3.40
	453531	AA417940	Hs.271400	ESTs, Weakly similar to JCS795 CDEP prot	3.40
	444826	AI674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

	418939	AW630803	Hs.89497	lamin B1	3.40
	418134	AA397769	Hs.86617	ESTs	3.40
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39
5	427927	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.39
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39
	410406	AI959703	Hs.1466	glycerol kinase	3.38
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothe	3.38
10	446432	AI377320	Hs.150058	ESTs	3.36
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.35
	425322	U83630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35
	421039	NM_003478	Hs.101299	cutlin 5	3.35
	407819	R42185	Hs.274803	ESTs	3.35
15	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35
	433361	AW469373	Hs.300141	ribosomal protein L39	3.35
	435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	3.35
20	454018	AW016892	Hs.100855	ESTs	3.35
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35
	453941	U39817	Hs.36820	Bloom syndrome	3.34
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.33
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33
25	438008	AA775026	Hs.203802	ESTs	3.33
	421246	AW582982	Hs.102897	CGI-47 protein	3.33
	451707	AW051061	Hs.60973	ESTs	3.33
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	3.31
	443613	AI079356		gb:acc39b09.s1 Soares_NbHMPu_S1 Homo sapl	3.31
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ111381 fis, clone HE	3.31
	438746	AI885815	Hs.184727	ESTs	3.30
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	3.30
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD, Ze	3.30
	458855	AW381299	Hs.107000	hypothetical protein FLJ11294	3.30
35	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
	424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	3.30
	417720	AA205825	Hs.208067	ESTs	3.29
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	3.29
	452862	AW378065	Hs.8687	ESTs	3.28
40	414343	AL036166	Hs.323378	coated vesicle membrana protein	3.28
	437222	AL117588	Hs.12778	ESTs	3.28
	422665	AJ011812	Hs.119018	transcription factor NRF	3.28
	414708	AW340125	Hs.76989	KIAA0097 gene product	3.28
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27
45	447829	AI433029	Hs.164104	ESTs	3.27
	427576	BE242811	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.27
	456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26
	407305	AA715284		gb:mv35f03.r1 NC_CGAP_Br5 Homo sapiens	3.26
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.26
50	424581	M62062	Hs.150917	catenin (cadherin-associated protein), a	3.25
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothe	3.25
	453320	AW450240	Hs.257274	ESTs	3.25
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.25
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25
55	410659	AI080175	Hs.68826	ESTs	3.25
	446202	AI279706	Hs.149474	ESTs	3.25
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	3.25
	439262	AA832333	Hs.333045	ESTs	3.25
	401823	NA		NA	3.25
60	441264	AA927170	Hs.23290	ESTs	3.25
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.24
	408321	AW405882	Hs.44205	corbistatin	3.24
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi	3.24
	404519				3.24
65	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.23
	422660	AW297582	Hs.103267	hypothetical protein FLJ22548 similar to	3.23
	427961	AW293165	Hs.143134	ESTs	3.22
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.21
70	458652	AW375810	Hs.117102	hypothetical protein FLJ13046 similar to	3.21
	426472	BE246138	Hs.30853	ESTs	3.21
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.21
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.21
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.20
75	443162	T49951	Hs.9029	DKFZP434G032 protein	3.20
	431678	AW072372	Hs.267446	hypothetical protein FLJ11184	3.20
	430439	AL133561	Hs.241426	DKFZP434B061 protein	3.20
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.20
	437905	AW363121	Hs.175596	ESTs, Weakly similar to T26935 hypothe	3.20
80	434160	BE551198	Hs.114275	ESTs	3.20
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.20
	412866	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19
	414386	X00442	Hs.75990	haptoglobin	3.19
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	3.18

	429597	NM_003818	Hs.2442	a disintegrin and metalloproteinase domain	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypothe	3.17
5	429616	AI982722	Hs.120845	ESTs	3.17
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.16
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.16
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.16
	423629	AW021173	Hs.18512	Homo sapiens cDNA: FLJ21909 fis, clone H	3.15
	443830	AI142095	Hs.143273	ESTs	3.15
10	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	NA5214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.15
	427687	AW003867	Hs.1570	histamine receptor H1	3.15
15	455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp5648176 (fr	3.15
	441720	AI346487	Hs.28739	ESTs	3.15
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	3.15
	445921	AW015211	Hs.146181	ESTs	3.15
	429957	AW204530	Hs.99500	ESTs	3.15
20	403137				3.14
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	3.14
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
25	408806	AW847814	Hs.299005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.14
	439277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.13
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406688	T62745	Hs.184411	albumin	3.13
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
30	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
	433769	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.13
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	3.11
	441790	AW294909	Hs.132208	ESTs	3.11
35	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.10
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.10
	402963				3.10
40	428967	AW978441	Hs.296100	ESTs	3.10
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (kr-znf1) m	3.10
	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
45	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420617	AK001852	Hs.99423	ATP-dependent RNA helicase	3.10
	421841	AA908197	Hs.108850	MAK-related kinase	3.10
	429534	AW978987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
50	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.10
	433037	NM_014158	Hs.279938	HSPC067 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.09
	457726	AI217477	Hs.194591	ESTs	3.09
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	3.08
55	433013	AI697890	Hs.127337	axin 2 (conductin, axil)	3.08
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.08
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL1_HUMAN SORT1	3.07
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.07
60	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.07
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.07
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	3.06
	436554	AI985810	Hs.301173	ESTs	3.06
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
65	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
	445413	AA151342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pannexin 1	3.06
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AJ077195	Hs.164038	glucosamine (N-acetyl)-6-sulfatase (Senf	3.05
	406333				3.05
70	428454	U55936	Hs.184378	synaptosomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RCO-MT0013-280300-031-e03 MT0013 Homo	3.05
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypothe	3.05
75	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
80	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

5	419186	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04
	446881	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.03
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.02
	452834	AI638627	Hs.105685	KIAA1688 protein	3.02
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.02
	416568	H64844	Hs.138558	ESTs	3.02
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
10	412719	AW016510	Hs.129911	ESTs	3.01
	439586	AA922936	Hs.110039	ESTs	3.01
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	3.01
	429703	T93154	Hs.28705	ESTs	3.00
	400296	AA305627	Hs.139338	ATP-binding cassette, sub-family C (CFTR	3.00
15	415261	T40928	Hs.8346	ESTs	3.00
	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	3.00
	429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
	407182	AA312551	Hs.230157	ESTs	3.00
20	424202	BE350295	Hs.15032	RAN binding protein 17	3.00
	444585	AW170015	Hs.6594	ESTs	3.00
	420552	AK000492	Hs.98806	hypothetical protein	3.00
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
	441928	AI370188	Hs.211454	ESTs	3.00
25	430888	BE155293	Hs.76064	ribosomal protein L27a	3.00
	417806	AI867277	Hs.183733	ESTs	3.00
	447175	AI365208	Hs.293606	ESTs	3.00
	417177	NM_004458	Hs.81452	fatty acid-Coenzyme A ligase, long-chain	3.00
	435447	AI872932		gb:wm72e03.x1 NCI_CGAP_U12 Homo sapiens	3.00
30	405394				3.00
	454975	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.00
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	3.00
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.00

35

TABLE 6B

40

Pkey:Unique Eos probeset identifier number

CAT number:Gene cluster number

Accession:Genbank accession numbers

45

Pkey

CAT number

Accession

411765125700_1H43346 AA248302 AA095182

4118641262055_1AW948147 BE092318 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160

412359129085_1AW837985 AW837938 AA101955 AW837913 AW837935

4135161374595_1BE145907 BE145786 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856

414148142133_1BE084049 AW292907 AA135584

424492240008_1AI133482 AI207619 AA341626

430264315008_1AA470519 BE303010 BE302954 BE384120

431064327472_1AI903735 AA491283 AI694953 AW976903 AA761382

433687373061_1AA743991 AA604852 AW272737

43441438585_1AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231

50

AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139

AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730

AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957

N86951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659

BE081531 H59570

55

AI872932 AA682306 BE220163 W88695 T81307 H91447

AW674352 AA715374 Z25205

AI079356 W23287

AI347274 AW844024

AI480316 AW847535

60

AI793163 AW875182 AW875178 AW875176

BE065985 BE065944 BE066008 BE066083 BE066093

AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905

AW848214

BE145808 BE145807 BE181883

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4558381374605_1

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TABLE 6C

75

Pkey:Unique number corresponding to an Eos probeset

Ref:Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.

Strand:Indicates DNA strand from which exons were predicted.

NI_position:Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	400534	6981826	Minus	278637-279292
	401165	9438376	Minus	168244-168423
	401480	7321503	Plus	166120-166347,166451-166557,169551-169832
	401644	8576138	Plus	82655-83959
	401823	2262095	Minus	42575-42697,43189-43287,45830-45974
10	402167	8571795	Plus	109122-110357
	402963	5418653	Minus	12950-15959
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403776	7770611	Minus	1414-1513,1624-1756
	404025	7341444	Plus	131740-131905
15	404232	8218045	Minus	71800-71956
	404253	9367202	Minus	55675-56055
	404477	8080699	Plus	113390-113577
	404516	8151967	Plus	114153-114322
	404519	8152000	Plus	12817-13000
20	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405394	6624123	Minus	31900-32373
	405460	7684569	Minus	52223-52389
	405769	3046270	Minus	76844-77193
25	406117	9142932	Plus	54304-54584
	406333	9213235	Plus	64689-64798
	406360	9256107	Minus	7513-7673
	406414	9256407	Plus	49593-49850

30 TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon. These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

35	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
45	441031	AI110584	Hs.7645	fibrinogen, B beta polypeptide	57.52
	406667	M12523	Hs.184411	albumin	49.94
	409041	AB033025	Hs.50081	KIAA1199 protein	49.18
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	42.22
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	34.64
50	429201	X03178	Hs.198246	group-specific component (vitamin D bind	33.38
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	33.10
	447033	AI357412	Hs.157601	ESTs	31.24
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	26.84
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	25.40
55	413841	M34276	Hs.75576	plasminogen	24.68
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	23.18
	452862	AW378065	Hs.8687	ESTs	21.34
	415989	AI267700	Hs.317584	ESTs	20.92
60	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.22
	421470	R27496	Hs.1378	annexin A3	17.92
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.08
65	421462	AF016495	Hs.104624	aquaporin 9	17.02
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.70
	432340	AA534222		gbn 21d02.s1 NCL_CGAP_AA1 Homo sapiens	16.64
	433447	U29195	Hs.3281	neuronal pentraxin II	16.59
70	414386	X00442	Hs.75990	haptoglobin	16.19
	425260	L47726	Hs.1870	phenylalanine hydroxylase	16.08
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
	439518	W76326		gbzd60d04.r1 Soares_fetal_heart_NbHH19W	15.80
	443211	AI128388	Hs.143655	ESTs	15.78
75	439608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	15.42
	412719	AW016610	Hs.129911	ESTs	15.24
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	15.18
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03

	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	orosomucoid 1	14.35
	441243	AJ767056	Hs.193002	ESTs	14.30
5	413318	AU076607	Hs.75285	Inter-alpha (globulin) inhibitor, H2 pol	14.30
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
	433213	AW665130	Hs.137190	ESTs	13.80
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AA811244	Hs.164168	ESTs	13.40
10	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	13.00
	449199	AJ990122	Hs.196988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AJ133452	Hs.75431	fibrinogen, gamma polypeptide	12.83
	451561	N52812	Hs.177403	ESTs	12.72
15	420734	AW972872	Hs.293736	ESTs	12.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily	12.50
	441377	BE218239	Hs.202656	ESTs	12.45
	435981	H74319	Hs.188620	ESTs	12.38
20	417296	L36195	Hs.81884	sulfotransferase family, cytosolic, 2A,	12.38
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypothe	12.34
	430290	AJ734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
25	450628	AW382884	Hs.204715	ESTs	12.24
	446232	AJ281848	Hs.194691	retinoic acid induced 3	12.16
	428223	AA424313	Hs.98402	ESTs	12.08
	432582	AJ623817	Hs.168457	ESTs	12.08
	407884	BE075316	Hs.95011	synrophin, beta 1 (dystrophin-associate	12.02
30	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
	407202	N58172	Hs.109370	ESTs	11.84
	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	11.68
	447532	AK000814	Hs.18791	hypothetical protein FLJ20607	11.67
35	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.62
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	11.34
40	452903	AJ953425	Hs.246911	ESTs, Weakly similar to I38022 hypothe	11.32
	433011	H07960	Hs.306044	CGI-05 protein	11.30
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	11.22
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
45	407168	R45175	Hs.117183	ESTs	10.91
	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	10.68
50	440526	AJ832243	Hs.211471	ESTs	10.63
	427544	AJ767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	10.62
	447974	R76886		gb:64b03.s1 Soares placenta Nb2HP Homo	10.52
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	10.52
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
55	457065	AJ476318	Hs.192480	ESTs	10.40
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.28
60	404567				10.14
	428536	AJ143139	Hs.2288	vishin-like 1	10.06
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	10.05
	437267	AW511443	Hs.258110	ESTs	10.00
	420583	H77859	Hs.65450	reticulin 4	10.00
65	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	9.97
	449655	AJ021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.90
	434609	R76593		gb:60c11.1 Soares placenta Nb2HP Homo	9.90
70	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14245 fis, clone OV	9.84
	448106	AJ800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
75	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	9.44
	440404	AJ015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	9.36
	401742	NA		NA	9.30
80	416393	N54037	Hs.262869	plasminogen-like	9.28
	413339	AJ818080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

	434008	AA740878	Hs.112982	ESTs	9.20
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.16
	419968	X04430	Hs.93913	Interleukin 6 (interferon, beta 2)	9.16
5	413597	AW302885	Hs.117183	ESTs	9.15
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
	409327	L41182	Hs.53563	collagen, type IX, alpha 3	9.14
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	8.98
10	450164	AI239923	Hs.30098	ESTs	8.95
	432867	AW016936	Hs.233364	ESTs	8.93
	437396	BE140396	Hs.21621	hypothetical protein DKFp762O076	8.92
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
	452712	AW838616		gb:RCS-LT0054-140200-013-D01 LT0054 Homo	8.90
15	419131	AA406293	Hs.41167	ESTs	8.86
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.82
	418895	AA894638	Hs.14600	ESTs	8.82
	422665	AJ011812	Hs.119018	transcription factor NRF	8.82
	409757	NM_001898	Hs.123114	cystatin SN	8.78
20	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
	412446	AJ768015	Hs.92127	ESTs	8.71
	433285	AW975944	Hs.237396	ESTs	8.68
	414538	AW612228	Hs.107987	ESTs	8.64
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
25	430835	AI240006	Hs.192326	ESTs	8.60
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
	445537	AJ245871	Hs.12844	EGF-like-domain, multiple 6	8.52
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	8.50
30	444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
	439398	AA284267	Hs.221504	ESTs	8.44
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
	403776				8.42
	418973	AA233056	Hs.191518	ESTs	8.42
35	445436	AI224105	Hs.151408	ESTs	8.38
	417958	AA767382	Hs.193417	ESTs	8.34
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	8.34
	425761	AW664214	Hs.196729	ESTs	8.33
	449419	R34910	Hs.119172	ESTs	8.29
40	407007	U22961		gb:Human mRNA clone with similarity to L	8.28
	420900	AL045633	Hs.44269	ESTs	8.25
	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	8.23
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.18
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
45	432363	AA534489		gb:nl76g11.s1 NCL_CGAP_Co3 Homo sapiens	8.16
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	8.12
	446155	AI563695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	418379	AA218940	Hs.137516	fidgetin-like 1	8.07
	424580	AA158727	Hs.150555	protein predicted by clone 23733	8.06
50	453116	AI276680	Hs.146086	ESTs	8.04
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.04
	409687	T51125	Hs.8493	ESTs	8.00
	407780	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	8.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
55	418036	Z37976	Hs.83337	latent transforming growth factor beta b	7.99
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	7.96
	421633	AF121860	Hs.106260	sorting nexin 10	7.92
	432542	AW083920	Hs.16096	claudin 2	7.86
	414869	AA157291	Hs.21479	ubiquitin 1	7.84
60	419502	AJ076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
	406666	V00495	Hs.184411	albumin	7.78
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	7.77
	406360	NA		NA	7.76
65	406687	M31128	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
	431510	AA580082	Hs.112264	ESTs	7.76
	414312	AA155694	Hs.191060	ESTs	7.71
	443450	N66045	Hs.133529	ESTs	7.70
	449870	AJ672487	Hs.15423	hypothetical protein HDCMC04P	7.64
70	425681	AB018297	Hs.159183	KIAA0754 protein	7.63
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
	443285	AJ301918	Hs.334264	ESTs	7.60
	420807	AA280827	Hs.57846	ESTs	7.60
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	7.60
75	410718	AI920783	Hs.191435	ESTs	7.60
	430848	AW021726		gb:dl27e02.y1 Morton Fetal Cochlea Homo	7.60
	434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
	445808	AV555234	Hs.298083	ESTs, Moderately similar to PC4259 ferri	7.56
	438604	AA811896	Hs.44604	ESTs	7.54
80	458997	AW837420	Hs.69662	ESTs	7.54
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
	409187	AF154830	Hs.50986	carbamoyl-phosphate synthetase 1, mitoch	7.52
	445640	AW959626	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sapi	7.49
	404996				7.48

	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433859	AW896758	Hs.273789	ESTs	7.44
	423952	AW877787	Hs.136102	KIAA0853 protein	7.44
5	431193	AW749505	Hs.296770	KIAA1719 protein	7.43
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	7.40
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
	449347	AV649748	Hs.295901	KIAA0493 protein	7.34
10	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.34
	447499	AW262580	Hs.147674	protocadherin beta 16	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
15	445019	AI205540	Hs.281285	ESTs	7.28
	419474	AW968619	Hs.155849	ESTs	7.24
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H43346		gb:yp09a04.r1 Soares breast 3NbHBst Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
20	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	7.18
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
25	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.14
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	AI377320	Hs.150058	ESTs	7.10
30	439295	AW206091	Hs.253536	ESTs	7.08
	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431765		gb:zw80c03.a1 Soares_testis_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
35	432435	BE218866	Hs.282070	ESTs	7.05
	427933	AW974643	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
40	446322	N23033	Hs.155814	ESTs	6.98
	442577	AA292998	Hs.163900	ESTs	6.96
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
45	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothe	6.90
	453204	R10799	Hs.191990	ESTs	6.90
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427878	C05766	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
50	424402	M63108	Hs.1769	lutelizing hormone/choriogonadotropin r	6.86
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419629	AB020695	Hs.91662	KIAA0888 protein	6.80
55	451686	AA059246	Hs.110293	ESTs	6.80
	430829	AW451999	Hs.194024	ESTs	6.78
	446501	AI302616	Hs.150819	ESTs	6.78
	442973	BE587665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.76
60	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.72
	425478	AB007953	Hs.268840	ESTs	6.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418555	AA172115	Hs.87159	hypothetical protein FLJ12577	6.67
65	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.62
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.62
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.56
70	414575	H11257	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	6.54
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	6.54
	410116	AW630671	Hs.58638	squamous cell carcinoma antigen recogniz	6.54
	449894	AK001578	Hs.24129	CULL7 protein	6.53
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	6.53
	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
75	441801	AW242799	Hs.86366	ESTs	6.52
	435542	AA687376	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.46
80	436217	TS3925	Hs.107	fibrinogen-like 1	6.46
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.46
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB009284	Hs.61152	exostosins (multiple)-like 2	6.43
	417057	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma fib	6.36
5	451389	N73222	Hs.279009	matrix Gla protein	6.36
	427899	AA829288	Hs.332053	serum amyloid A1	6.35
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
10	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
	433908	AW298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99640	ESTs	6.32
	434032	AW009951	Hs.206892	ESTs	6.31
	444656	AI277824	Hs.145199	ESTs	6.30
15	433607	AA602004	Hs.23260	ESTs	6.26
	440659	AF134160	Hs.7327	claudin 1	6.25
	435663	AI023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
20	447500	AI381900	Hs.159212	ESTs	6.24
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	AC003034	Hs.125261	Homo sapiens Chromosome 16 BAC clone CIT	6.20
	438138	R98299	Hs.177502	ESTs	6.20
25	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
	416857	AA188775	Hs.292453	ESTs	6.20
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.18
	429598	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
30	438940	AF075045	Hs.271609	ESTs	6.18
	400195	NA		NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDG7 (cell division cycle 7, S. cerevisi	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
35	427513	AJ476318	Hs.192480	ESTs	6.10
	448934	AI598134	Hs.225592	ESTs, Highly similar to T51146 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	6.08
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
40	409048	H59990	Hs.37699	ESTs	6.08
	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33868	Hs.284176	transferrin	6.06
	453804	AA300204	Hs.35276	KIAA0852 protein	6.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	6.05
45	408243	Y00787	Hs.624	Interleukin 8	6.04
	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AI928513	Hs.59203	ESTs	6.04
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.04
50	407746	AK001952	Hs.38114	hypothetical protein FLJ11100	6.02
	442116	AI884570	Hs.128813	ESTs	6.00
	423568	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
55	434739	AA804487	Hs.144130	ESTs	5.98
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.96
	420218	AW958037	Hs.286	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.94
	445546	AW468821	Hs.156054	ESTs	5.94
60	439096	AA830185	Hs.269680	ESTs	5.94
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.94
	417246	AJ760098	Hs.21411	ESTs	5.94
	433190	M26901	Hs.3210	renin	5.92
65	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	5.92
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AJ791138	Hs.116768	ESTs	5.92
	406668	T62745	Hs.184411	albumin	5.92
70	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
	408867	AA437199	Hs.656	cell division cycle 25C	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.88
	450380	AI883675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
75	454653	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo	5.87
	457876	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.86
	437222	AL117588	Hs.12778	ESTs	5.86
	455530	AV555701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	5.85
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.84
80	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434D0615 (f	5.84
	441645	AJ222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.84
	401352				5.84
	419088	AI538323	Hs.52620	integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.82
	419220	AA811938	Hs.291759	ESTs	5.82
5	439303	W00605	Hs.102784	ESTs	5.80
	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	5.80
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	439527	AW298119	Hs.202535	ESTs	5.78
10	435380	AA679001	Hs.192221	ESTs	5.78
	424086	AI351010	Hs.102267	lysyl oxidase	5.76
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	5.76
	428460	AA428865	Hs.98563	ESTs	5.74
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	5.74
	413982	BE503035	Hs.279193	ESTs	5.74
15	453240	AI969564	Hs.166254	hypothetical protein DKFZp566i133	5.74
	410505	AW762139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.72
20	448968	AW372914	Hs.88149	phosphoinositol 3-phosphate-binding prot	5.71
	433384	AI021892	Hs.124244	ESTs	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
25	448666	NM_014953	Hs.323346	KIAA1008 protein	5.68
	412246	AI160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
30	422805	AA436989	Hs.121017	H2A histone family, member A	5.62
	442252	AI733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	435040	AI932350	Hs.152825	ESTs	5.59
	438777	AA825487	Hs.142179	ESTs	5.58
35	433849	BE465884	Hs.280728	ESTs	5.58
	438639	AI278360	Hs.31409	ESTs	5.58
	411274	NM_002776	Hs.69423	kaillikrein 10	5.55
	435008	AF150262	Hs.162898	ESTs	5.55
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
40	452881	AW135220	Hs.241921	ESTs	5.54
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
45	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
	417543	AA203620	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90315	KIAA0007 protein	5.51
	434674	AA831879	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
50	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
	404227	NA		NA	5.49
	412766	BE544475	Hs.54347	ESTs	5.49
	441708	AA69911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW195262		gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	5.48
55	437440	AA846804	Hs.123694	ESTs	5.48
	410486	AW235094	Hs.69233	zinc finger protein	5.46
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437378	AI198823	Hs.160473	ESTs	5.44
	436907	AA737171	Hs.131809	ESTs	5.44
60	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	N58115	Hs.21137	AD024 protein	5.42
	452449	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.40
65	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	5.40
	441217	AI922183	Hs.213248	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.40
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	5.40
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	5.40
70	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	5.39
	446142	AI754693	Hs.145968	ESTs	5.38
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	5.38
	433929	AI375499	Hs.27379	ESTs	5.36
	421155	H87879	Hs.102267	lysyl oxidase	5.34
75	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.34
	453931	AL121278	Hs.25144	ESTs	5.34
	409091	AW970386	Hs.269423	ESTs	5.33
	416057	AI927382	Hs.29857	ESTs	5.33
	438647	AA813118	Hs.163230	ESTs	5.32
80	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.30
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ2166 fis, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

	401714	NA	NA	5.28
	449508	AK001566	Hs.23618 hypothetical protein FLJ10704	5.28
	413151	H47969	Hs.141971 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
5	414853	U31116	Hs.77501 sarcoglycan, beta (43kD dystrophin-assoc	5.28
	417372	T99755	Hs.334728 ESTs	5.28
	443613	AI079356	gb0039b09.s1 Soares_NhlMPu_S1 Homo sapi	5.28
	412610	X90908	Hs.74126 fatty acid binding protein 6, ileal (gas	5.27
	408943	NM_007070	Hs.49105 FKBP-associated protein	5.26
10	415139	AW975942	Hs.48524 ESTs	5.26
	447982	H22953	Hs.137551 ESTs	5.26
	430789	AA632577	Hs.310235 ESTs, Weakly similar to I78885 serine/th	5.24
	453921	AI824009	Hs.44577 ESTs	5.24
	409582	R27430	Hs.271565 ESTs	5.24
15	420911	U77413	Hs.100293 O-linked N-acetylglucosamine (GlcNAc) tr	5.23
	422956	BE545072	Hs.122579 hypothetical protein FLJ10461	5.23
	418661	NM_001949	Hs.1189 E2F transcription factor 3	5.22
	446271	D82484	Hs.330994 ESTs	5.22
	435905	AW997484	Hs.5003 KIAA0458 protein	5.21
20	434551	BE387162	Hs.280858 ESTs, Highly similar to A35661 DNA excis	5.21
	415245	N59650	Hs.27252 ESTs	5.20
	436016	AA806465	Hs.121536 Human DNA sequence from clone RP11-472E5	5.20
	431242	AA987742	Hs.251278 KIAA1201 protein	5.20
	439818	AL360137	Hs.19934 Homo sapiens mRNA full length insert cDN	5.20
25	424281	AA766243	gb00a13b11.s1 NCLCGAP_GC81 Homo sapiens	5.20
	449138	AW294215	Hs.195631 ESTs	5.20
	449416	AI651016	Hs.246311 ESTs	5.20
	430092	AI821399	Hs.16514 ESTs	5.20
	436574	AW293527	Hs.126465 ESTs	5.18
30	433377	AI752713	Hs.43845 ESTs	5.18
	440987	AA911705	Hs.130229 ESTs	5.18
	426116	AA868729	Hs.144694 ESTs	5.18
	441928	AI370188	Hs.211454 ESTs	5.17
35	432657	AA831815	Hs.270940 ESTs, Weakly similar to I78885 serine/th	5.17
	438011	BE466173	Hs.145696 splicing factor (CC1.3)	5.16
	437257	AI283085	Hs.290931 ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
	423926	X03833	Hs.1722 Interleukin 1, alpha	5.16
	433393	AF038564	Hs.98074 Itchy (mouse homolog) E3 ubiquitin prote	5.15
	415757	AA830854	Hs.187810 ESTs	5.14
40	420170	U43374	Hs.95631 Human normal keratinocyte mRNA	5.14
	420493	AI635113	Hs.270366 ESTs, Weakly similar to I78885 serine/th	5.12
	425739	T19016	Hs.159410 molybdopterin synthase sulfurylase	5.12
	440652	AI216751	Hs.143977 ESTs	5.12
	419706	C04649	Hs.77899 tropomyosin 1 (alpha)	5.12
45	427728	AJ245600	Hs.180545 Homo sapiens mRNA for hypothetical prote	5.12
	416113	AA173525	Hs.118758 ESTs, Weakly similar to RLF [H.sapiens]	5.12
	446223	BE300091	Hs.119699 hypothetical protein FLJ12969	5.11
	407624	AW157431	Hs.248941 ESTs	5.11
	447197	R36075	gb0yh88b01.s1 Soares placenta Nb2HP Homo	5.11
50	452465	AA610211	Hs.34244 ESTs	5.10
	442833	AA328153	Hs.88201 ESTs, Weakly similar to A Chain A, Cryst	5.10
	448952	AI609595	Hs.208038 ESTs	5.10
	408170	AW204516	Hs.31835 ESTs	5.08
	424238	AA337401	Hs.137635 ESTs	5.07
55	421072	AI215069	Hs.89113 ESTs	5.06
	424717	H03764	Hs.152213 wingless-type MMTV integration site fam1	5.06
	423654	AI674253	Hs.35828 ESTs	5.06
	436862	AI821940	Hs.264622 ESTs, Moderately similar to ALU8_HUMAN A	5.06
	436554	AI985810	Hs.301173 ESTs	5.05
60	433264	D85782	Hs.3229 cysteine dioxygenase, type I	5.04
	452387	AI680772	Hs.306094 trinucleotide repeat containing 12	5.04
	412666	AL080116	Hs.74420 origin recognition complex, subunit 3 (y	5.03
	430287	AW182459	Hs.125759 ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
	413293	AL047483	Hs.302498 GTP-binding protein homologous to Saccha	5.00
65	418217	AI910647	Hs.13442 ESTs	5.00
	401480	NA	NA	5.00
	456179	H75490	Hs.271930 ESTs	5.00

TABLE 7B

70	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

75	Pkey	CAT number	Accession
	408432	1058667_1	AW195262 R27868 AW811262
	408690	107490_1	AW884542 AA056567 AW882724
	411765	125700_1	H43346 AA248302 AA095182
80	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	424281	237742_1	AA766243 AA338252 AA338213

5	424492	240008_1	AI133482 AI207619 AA341626
	428679	294049_1	AA431765 AA432015
	430848	324621_1	AW021726 AA487752 AA488085
	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432639	351744_1	AW973785 H60163 AA557608
	434609	38950_1	R76593 AF147390 R76594
	439518	47334_1	W76326 AF086341 W72300
10	443613	575391_1	AI079356 WZ3287
	447197	711623_1	R36075 AI366546 R38187
	447974	745643_1	R76886 AI453674 R77049
	452712	928309_1	AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784
	454653	1228081_1	AW812227 AW812294 AW812092
15	458311	543550_1	AF069478 AF069479 AF069480

TABLE 7C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	NL_position
	400534	6981826	Minus	278637-279292
	401352	9931258	Minus	26064-26208
30	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401714	6715702	Plus	96484-96681
	401742	2911728	Plus	64003-64147
	403432	9719611	Minus	68204-68392
	403776	7770611	Minus	1414-1513,1624-1756
	404227	7838233	Minus	93110-93259
35	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	406360	9256107	Minus	7513-7673

40 Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

45	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
50	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
55	421896	AW583807	Hs.1460	glucagon	0.0233
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.0307
	457407	AA505035	Hs.195651	ESTs	0.0418
	423690	AA328648	Hs.23804	ESTs, Weakly similar to PNU099 son3 prot	0.0664
	426651	AI076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0567
60	425920	AL049977	Hs.162209	claudin 8	0.0601
	431436	AA505035	Hs.195651	ESTs	0.0607
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
	442009	AI733281	Hs.128320	ESTs	0.0634
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	0.0707
	429050	X81333	Hs.194777	meprin A, beta	0.0714
65	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
	429657	D13626	Hs.2465	KIAA0001 gene product, putative G-prote	0.0769
	443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypothet	0.0838
70	415314	N88802	Hs.5422	glycoprotein M6B	0.0853
	451181	AI796330	Hs.207461	ESTs	0.0873
	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.0888
	426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.0900
	429350	AI754634	Hs.131987	ESTs	0.0927
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

5	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	0.0951
	441066	AW205427	Hs.190726	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0957
	431252	NM_005478	Hs.251380	insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
	433546	AJ075877	Hs.125461	hypothetical protein FLJ11539	0.1007
	415154	D63175		gb:HUM501809B Clontech human placenta po	0.1032
	409921	AW600239		gb:EST00009 pGEM-T library Homo sapiens	0.1067
	432440	X63597	Hs.2996	sucrase-isomaltase	0.1107
10	430468	NM_004673	Hs.241519	angiotensin-like 1	0.1114
	427167	AJ239607	Hs.99196	hypothetical protein MGC11324	0.1147
	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.1167
	423605	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 fis, clone H	0.1211
15	412639	AW961284	Hs.296235	ESTs	0.1239
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.1240
	403548				0.1248
	421913	AJ934365	Hs.109439	osteoglycin (osteoinductive factor, mtrm	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
20	448835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
25	454790	AW820852		gb:RC2-ST0301-120200-011-412 ST0301 Homo	0.1328
	451742	T77609	Hs.117970	ankyrin 2, neuronal	0.1335
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm30f03.x1 NCL CGAP_Thy4 Homo sapiens	0.1393
	416585	X54162	Hs.79386	telomodin 1 (smooth muscle)	0.1395
30	435869	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
	404767				0.1460
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	0.1462
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	0.1463
35	452768	AW069459	Hs.61539	ESTs	0.1466
	418692	AK000268	Hs.87383	hypothetical protein	0.1471
	414831	M31158	Hs.77439	protein kinase, cAMP-dependant, regulator	0.1471
	407551	Y10516		gb:H.sapiens mRNA for CD58 T3 protein.	0.1488
	402076				0.1487
40	453500	AJ478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
	442080	AW444761	Hs.44565	ESTs	0.1500
	431706	AJ816086	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AJ824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	418390	AF133820	Hs.84665	tin immunoglobulin domain protein (myo	0.1529
45	435056	AW023337	Hs.5422	glycoprotein M6B	0.1532
	426034	AJ276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	0.1538
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
	425220	AW975317	Hs.162987	ESTs	0.1558
50	445200	AA084460	Hs.12409	somatostatin	0.1558
	443238	T78886	Hs.284450	ESTs	0.1563
	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW167727	Hs.11873	ESTs	0.1605
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.1615
55	437734	AA693951	Hs.180284	ESTs	0.1637
	414290	AI568801	Hs.71721	ESTs	0.1638
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411839	AB36585	Hs.146246	ESTs	0.1660
	442496	R55073	Hs.124130	ESTs	0.1676
60	450693	AW450461	Hs.203965	ESTs	0.1698
	420736	AI263022	Hs.82204	ESTs	0.1718
	405385				0.1745
	404638				0.1751
	427333	AF067797	Hs.176658	aquaporin 8	0.1757
65	404246				0.1763
	433785	BE044593	Hs.112704	ESTs	0.1767
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.1769
	406980	S69265		(NONE)	0.1781
	421666	AL035250	Hs.1408	endothelin 3	0.1784
70	452854	AA437061	Hs.14060	prokinectin 1 precursor	0.1795
	400514				0.1805
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	0.1808
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	0.1812
75	412474	AJ791451	Hs.58785	gb:nl50c09.y5 NCL CGAP_Ov2 Homo sapiens	0.1812
	436008	AJ078428	Hs.58785	ESTs	0.1820
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.268107	multimerin	0.1832
	419746	AW867943	Hs.127216	hypothetical protein FLJ13465	0.1835
80	410877	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.1838
	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
	413714	AJ560944	Hs.71428	ESTs	0.1845

	427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
	405282				0.1848
	400163				0.1855
5	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
	407891	AA486620	Hs.41135	endomucin-2	0.1895
	437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
	431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fis, clone CO	0.1904
10	436659	AI217900	Hs.144464	ESTs	0.1905
	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	0.1926
	453698	AA037615	Hs.42746	ESTs	0.1928
	423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
	428412	AA428240	Hs.126083	ESTs	0.1942
15	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.1944
	434583	AW298724	Hs.202639	ESTs	0.1957
	421865	AA609911	Hs.109012	MAX dimerization protein	0.1957
	452786	R61362	Hs.105642	ESTs, Weakly similar to T09052 hypotheti	0.1969
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1981
20	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
	437740	AA810265	Hs.122915	ESTs	0.2016
	405610				0.2017
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
	416961	BE391476	Hs.80617	ribosomal protein S16	0.2041
25	401465				0.2045
	437425	AW183714	Hs.20981	hypothetical protein DKFZp547M236	0.2049
	416231	H30333	Hs.165062	ESTs	0.2049
	401753				0.2050
	433430	AI863735	Hs.186755	ESTs	0.2051
30	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.2059
	403957				0.2063
	435900	AI243036	Hs.16094	ESTs	0.2070
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
35	445500	AW451938	Hs.257512	ESTs	0.2075
	419956	AL137939	Hs.40096	ESTs	0.2090
	416026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
	423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
	401381				0.2120
40	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014 8 simil	0.2122
	433476	AA594394	Hs.152616	ESTs	0.2125
	423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
	442826	AI018777	Hs.131241	ESTs	0.2132
	427060	AW378993	Hs.90286	ESTs	0.2137
45	437354	AA749215	Hs.291886	ESTs	0.2137
	447734	AI421412	Hs.163659	ESTs	0.2144
	424585	AA464840	Hs.131987	ESTs	0.2146
	458016	AW188099	Hs.131813	ESTs	0.2151
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	0.2151
50	401521				0.2157
	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (0.2165
	401024				0.2171
	414802	AI793107	Hs.27018	Ris	0.2179
	441083	BE562611		gb:501336446F1 NIH_MGC_44 Homo sapiens c	0.2185
55	417355	D13168	Hs.82002	endothelin receptor type B	0.2186
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
	442930	AW881975	Hs.213923	ESTs	0.2193
	431089	BE041395	Hs.283876	ESTs, Weakly similar to unknown protein	0.2209
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypotheti	0.2212
60	405654				0.2217
	415471	F09747	Hs.268707	ESTs	0.2222
	449243	AW295031	Hs.198671	ESTs	0.2229
	436088	AA704687	Hs.191294	ESTs	0.2232
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	0.2242
65	427552	NM_005771	Hs.179608	retinol dehydrogenase homolog	0.2243
	416439	AA180363	Hs.118769	ESTs	0.2244
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	0.2254
	459395	Z30300	Hs.281935	ESTs	0.2257
	439039	AI656707	Hs.48713	ESTs	0.2268
70	433575	AA600175	Hs.39720	ESTs	0.2268
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.2273
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
	441899	AI372588	Hs.8022	TU3A protein	0.2283
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 6	0.2290
75	434839	AI743069	Hs.134736	ESTs	0.2294
	435731	AA699581	Hs.186811	ESTs	0.2299
	400865				0.2304
	446294	AI284935		gb:qk55g09.x1 NCL_CGAP_Co8 Homo sapiens	0.2305
	414193	BE260069		gb:601150364F1 NIH_MGC_19 Homo sapiens c	0.2309
80	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	0.2315
	453098	Z25935	Hs.86379	ESTs	0.2315
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	0.2319
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	0.2320
	443482	AW188093	Hs.250385	ESTs	0.2328

5	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	AB002367	Hs.21355	doubtless and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95295	ESTs	0.2347
	409331	M36634	Hs.53973	vasoactive intestinal peptide	0.2351
10	431094	AW972276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99387	ESTs	0.2358
	404958				0.2361
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	0.2364
	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
15	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129806	ESTs	0.2412
	447482	AB033059	Hs.18705	KIAA1233 protein	0.2415
	418332	R34976	Hs.78293	ESTs	0.2416
20	454145	AA046872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279939	mitochondrial carrier homolog 1	0.2424
	404070				0.2427
	421232	AA989220	Hs.292100	ESTs	0.2427
	414539	BE379046	Hs.171959	gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
25	412622	AW664708	Hs.171959	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416694	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
	426724	AA383623	Hs.293616	ESTs	0.2444
	405073				0.2445
30	401236	H24185	Hs.92918	hypothetical protein	0.2445
	414203	BE262170	Hs.78629	ATPase, Na ⁺ /K ⁺ transporting, beta 1 poly	0.2451
	401776				0.2452
	404696				0.2462
	426666	AW500131	Hs.171763	CD22 antigen	0.2471
35	427078	AI576082	Hs.111902	ESTs	0.2474
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2478
	440383	AA884208	Hs.30484	ESTs	0.2481
	419118	AA234223	Hs.139204	ESTs	0.2494
	443515	AV657547	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2495
40	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	0.2499
	404605				0.2500
	446066	AI343931	Hs.149383	ESTs	0.2505
	408345	R93851	Hs.63063	ESTs	0.2506
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	0.2508
45	416950	AL049798	Hs.80552	dermatopontin	0.2510
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2513
	449833	R82262	Hs.106106	protein kinase (cAMP-dependent, catalytic)	0.2515
	459275	AI080913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	0.2519
	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2523
50	422743	BE304678	Hs.119598	ribosomal protein L3	0.2526
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telen	0.2532
	450880	AK002183	Hs.285885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2536
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
	451979	F06972	Hs.27372	BMX non-receptor tyrosine kinase	0.2549
55	440274	R24595	Hs.7122	scrapie responsive protein 1	0.2553
	430097	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
	453992	AW014995	Hs.281080	ESTs	0.2569
60	453888	AW450670	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE299427	Hs.21446	KIAA1716 protein	0.2579
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	0.2580
	422591	L07648	Hs.118630	MAX-interacting protein 1	0.2582
65	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
	420321	D78761	Hs.96657	hypothetical protein	0.2595
	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
70	437032	AW887372	Hs.302063	immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW628433	Hs.271296	ESTs, Weakly similar to I54374 gene NF2	0.2605
	424885	AI333771	Hs.82204	ESTs	0.2608
	425381	D84371	Hs.1698	paraoxonase 1	0.2611
75	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022620	Hs.52170	ESTs	0.2624
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
80	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	0.2660
	402182				0.2660
	402610				0.2661
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

5	408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667
	444209	AI753134	Hs.146494	ESTs	0.2668
	415022	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677
	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681
	422909	AA533356		gbmj67110.s1 NCL_CGAP_Pr10 Homo sapiens	0.2681
	412047	AA934589	Hs.49696	ESTs	0.2693
	426356	BE536836	Hs.98682	hypothetical protein FKSG32	0.2703
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709
10	402425				0.2710
	450545	AW135582	Hs.201767	ESTs	0.2710
	417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.2725
	419850	F06844		gb:HSC1ME091 normalized infant brain cDN	0.2727
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730
15	441493	AW070446	Hs.127037	ESTs	0.2733
	413541	BE147036		gb:QV4-HT0222-091199-024-e10 HT0222 Homo	0.2733
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.2734
	455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	0.2740
20	444195	AB002351	Hs.10587	KIAA0353 protein	0.2743
	415160	T82802		gbryd38a04.r1 Soares fetal liver spleen	0.2747
	421823	N40850	Hs.28625	ESTs	0.2755
	434464	BE063921	Hs.295971	ESTs	0.2755
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [0.2756
25	430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762
	432018	AA524447	Hs.152377	ESTs	0.2763
	422954	AW998605		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768
	418397	H53035	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	0.2775
	442420	AI024834	Hs.131729	ESTs	0.2775
30	410950	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778
	427114	AI219896	Hs.97592	ESTs	0.2778
	448466	AI522109	Hs.171066	ESTs	0.2778
	434445	AI349306	Hs.11782	ESTs	0.2784
	457115	AA420712		gb:nc63c07.s1 NCL_CGAP_Pr1 Homo sapiens	0.2785
35	459511	AI142379		gb:gg64c01.r1 Soares testis_NHT Homo sap	0.2786
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase (alanine	0.2794
	433633	AI880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799
	440236	AW996722	Hs.125297	ESTs	0.2799
	405691				0.2804
40	405334				0.2804
	403047				0.2809
	412506	AW957159		gb:EST369229 MAGE resequences, MAGD Homo	0.2809
	441042	AA077738		gb:7B48A07 Chromosome 7 Fetal Brain cDNA	0.2815
45	434660	AA764768	Hs.121158	hypothetical protein DKFZp434J0113	0.2816
	444453	AW379394	Hs.145126	ESTs	0.2817
	457736	AK000390	Hs.4205	hypothetical protein FLJ20124	0.2820
	454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	0.2822
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827
50	435021	AA922192	Hs.54709	ESTs	0.2828
	413344	U46024	Hs.75302	myotubular myopathy 1	0.2837
	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens c	0.2840
	457290	AA465293	Hs.105069	ESTs	0.2841
	458244	AI929453	Hs.122489	Homo sapiens cDNA FLJ13289 fis, clone OV	0.2841
55	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842
	407938	AA905097	Hs.85050	phospholamban	0.2845
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.2846
	428212	AW444451	Hs.134812	ESTs	0.2853
	424433	H04607	Hs.9218	ESTs	0.2857
60	425195	AA352026	Hs.94319	VPS10 domain receptor protein	0.2857
	404769				0.2863
	411620	AW854536		gb:RC3-CT0255-200100-024-e08 CT0255 Homo	0.2868
	428746	AW503820	Hs.192861	Spl-B transcription factor (Spl-1/PU.1 r	0.2870
65	431822	AA516049		gbmg65d01.s1 NCL_CGAP_Lip2 Homo sapiens	0.2872
	441280	W27501	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.2874
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877
	421935	AA131632	Hs.109572	CMP-NeuAC:(beta)-N-acetylglucosaminide	0.2878
	447955	BE544271	Hs.288390	hypothetical protein FLJ22795	0.2880
	405364				0.2881
70	422165	AL041199	Hs.1481	histidine decarboxylase	0.2882
	431087	H12723	Hs.290791	ESTs	0.2882
	450610	AA010370	Hs.60386	nuclear RNA export factor 3	0.2882
	445627	AW818475	Hs.7363	ESTs	0.2883
	436144	AW881250	Hs.148367	ESTs	0.2886
75	445152	AI214667	Hs.283597	ESTs	0.2891
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.2891
	455614	AI693369	Hs.202274	ESTs	0.2899
	419683	AA248897	Hs.48784	ESTs	0.2900
80	411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904
	430770	AA765694	Hs.123296	ESTs	0.2913
	444459	AI680624	Hs.148676	ESTs	0.2913
	444918	AI202262	Hs.283362	ESTs	0.2915
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915
	435598	AA689470	Hs.163026	ESTs	0.2921

5	413056	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
	443998	AI620661	Hs.296276	ESTs	0.2924
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	0.2925
	421204	AW081587	Hs.165051	ESTs	0.2928
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	0.2938
	440507	H06994		gb:yl81b07.r1 Scores infant brain INIB H	0.2943
	445555	AW974013	Hs.260809	ESTs	0.2945
	438570	AW888554	Hs.84298	CD74 antigen (invariant polypeptide of m	0.2948
10	447195	T73745	Hs.279870	ESTs, Weakly similar to A46010 X-linked	0.2950
	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (fr	0.2956
	421920	BE551245	Hs.1438	gamma-aminobutyric acid (GABA) receptor,	0.2956
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	0.2959
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	0.2959
15	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	0.2969
	417935	R53697	Hs.170044	ESTs	0.2970
	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.2973
	413537	BE145856		gb:QV4-HT0222-211099-014-008 HT0222 Homo	0.2973
	445194	AI216667	Hs.175044	ESTs	0.2974
20	454135	AW153965	Hs.246783	ESTs	0.2976
	403418				0.2988
	457605	AV657778	Hs.3314	selenoprotein P, plasma, 1	0.2989
	408896	AI610447	Hs.48778	niban protein	0.2993
	448542	BE256176	Hs.278712	eukaryotic translation initiation factor	0.2994
25	417945	R29072		gb:F1-101D 22 week old human fetal liver	0.2994
	412518	BE047637	Hs.173739	hypothetical protein FLJ10297	0.2996
	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.2997
	430778	D90337	Hs.247916	natriuretic peptide precursor C	0.3000
	451531	AA018311	Hs.114762	ESTs	0.3003
30	444926	AI202492	Hs.212933	ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
	407368	AF026942		gb:Homo sapiens c1g33 mRNA, partial sequ	0.3012
	459456	AA486036	Hs.190124	ESTs	0.3012
	417111	AW016321	Hs.82306	desitin (actin depolymerizing factor)	0.3012
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
35	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	0.3012
	410482	AW772187	Hs.191859	ESTs	0.3013
	417700	M36542	Hs.1101	POU domain, class 2, transcription facto	0.3018
	404414				0.3019
	432247	AA531287	Hs.105805	ESTs	0.3023
40	453471	AL037887	Hs.208179	ESTs	0.3028
	417481	AA203281	Hs.21798	ESTs	0.3029
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	0.3032
	448744	AL135424	Hs.9469	pleckstrin homology domain-containing, f	0.3033
45	429223	BE264152	Hs.221994	ESTs	0.3034
	404501	AW247252	Hs.75514	nucleoside phosphorylase	0.3037
	406829	AW419128	Hs.84298	CD74 antigen (invariant polypeptide of m	0.3039
	438839	AW297945	Hs.128490	ESTs	0.3039
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.3042
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	0.3045
50	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fs, clone AD	0.3048
	443294	AI733625	Hs.133053	ESTs	0.3050
	447023	AA356784	Hs.17109	Integral membrane protein 2A	0.3052
	458583	AI479646	Hs.157081	hypothetical protein MGC4170	0.3056
	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	0.3057
55	445123	AI762911	Hs.145369	ESTs	0.3064
	412682	AW983772		gb:RC3-HN0002-060400-012-h09 HN0002 Homo	0.3065
	434361	AF129755	Hs.117772	ESTs	0.3071
	414026	BE241713		gb:TCAAP1E0472 Pediatric acute myelogeno	0.3072
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	0.3073
60	408350	AW183350	Hs.250127	ESTs	0.3074
	401042				0.3077
	422586	AA312704	Hs.59457	hypothetical protein FLJ22127	0.3077
	438692	AB007950	Hs.6360	KIAA0481 gene product	0.3077
	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.3083
65	444414	AW293214	Hs.8752	transmembrane protein 4	0.3085
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fs, clone L	0.3088
	430410	AF099144	Hs.250700	tryptase beta 1	0.3090
	419299	AI311085	Hs.62406	hypothetical protein FLJ22573	0.3091
	400672				0.3094
70	444010	AW976457	Hs.282887	ESTs	0.3096
	451699	AL118571	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	0.3096
	432471	BE244667	Hs.296155	CGI-100 protein	0.3105
	405277				0.3106
	456765	AI497800	Hs.33067	ESTs	0.3106
75	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fs, clone HE	0.3106
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	0.3108
	406592				0.3108
	423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo	0.3107
80	417919	AI928203	Hs.86379	ESTs	0.3110
	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	0.3110
	457439	AW410408	Hs.271167	L-pipecolic acid oxidase	0.3116
	426449	AL134009	Hs.169936	Homo sapiens mRNA; cDNA DKFZp586N1918 (f	0.3116
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.3119
	458544	AI631036	Hs.195843	ESTs	0.3119

5	447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypotheti	0.3121
	449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	0.3125
	429338	AW170591	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125
	451385	AA017656		gb:ze39h01.1 Scores retina N2b4HR Homo	0.3125
	446404	AA019961	Hs.26216	LOC50627	0.3130
10	446616	R55964	Hs.241569	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132
	409404	BE220053	Hs.129056	ESTs	0.3135
	417318	AW853937	Hs.12891	ESTs	0.3139
	443980	AI459140	Hs.299087	ESTs	0.3140
	459138	AI903291		gb:RC-BT029-080199-047 BT029 Homo sapien	0.3142
15	414807	AF738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.3143
	434704	AW135275	Hs.192311	ESTs	0.3143
	414214	D49958	Hs.75819	glycoprotein M6A	0.3145
	446378	AI905699	Hs.239760	citrate synthase	0.3145
	459233	AI939966		gb:MR0-CT0015-160799-002-b05 CT0015 Homo	0.3146
20	428193	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	0.3148
	426515	BE394222	Hs.231444	Homo sapiens, Similar to hypothetical pr	0.3150
	426597	AA382250	Hs.145601	ESTs	0.3153
	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157
	405071				0.3160
25	407457	AJ242724		gb:Homo sapiens mRNA for partial putativ	0.3162
	409922	AW505582	Hs.130732	KJAA1575 protein	0.3172
	438219	AI916151	Hs.257194	ESTs	0.3173
	412944	AA384110	Hs.197143	ESTs	0.3175
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.3178
30	426662	AA879474	Hs.122710	ESTs	0.3178
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	0.3179
	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	0.3181
	411084	T18987	Hs.125472	ESTs, Moderately similar to KJAA0877 pro	0.3183
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	0.3185
35	448812	H30775	Hs.22140	BM89 antigen	0.3188
	411288	AW835511		gb:QV0-LT0015-180200-127-d02 LT0015 Homo	0.3189
	422884	AW860975	Hs.13256	ESTs	0.3190
	405535				0.3195
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	0.3195
40	455353	W26786		gb:15d7 Human retina cDNA randomly prime	0.3195
	414540	BE379050	Hs.306969	Homo sapiens, clone MGC:10782, mRNA, com	0.3195
	428558	AC004755	Hs.184922	Homo sapiens chromosome 19, fosmid 37502	0.3195
	428106	BE620016	Hs.182470	PTD10 protein	0.3198
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	0.3202
45	445682	AW378397		gb:RC3-HT0220-031299-012-g06 HT0220 Homo	0.3205
	437568	AI954795	Hs.156135	ESTs	0.3205
	448943	AI608810	Hs.193288	ESTs	0.3205
	431999	AL133573	Hs.272312	Homo sapiens mRNA: cDNA DKFZp434J2235 (f	0.3207
	419279	AA235900	Hs.87500	ESTs	0.3208
50	405913				0.3209
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.3212
	424729	AF063012	Hs.152531	heart and neural crest derivatives expre	0.3212
	440020	AI480204	Hs.177131	ESTs	0.3213
	429082	AL135682	Hs.22452	Homo sapiens mRNA for KJAA1737 protein,	0.3215
55	433663	AF083131	Hs.229535	CATX-15 protein	0.3215
	400641				0.3216
	406140				0.3216
	415280	R56473	Hs.268715	ESTs	0.3217
	447635	AI669669	Hs.195362	ESTs	0.3217
60	401887				0.3217
	400767				0.3221
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
	448768	AB018311	Hs.21917	KJAA0768 protein	0.3222
	444750	AW242684	Hs.243623	ESTs	0.3223
65	411466	AW847669		gb:IL3-CT0213-280100-058-G10 CT0213 Homo	0.3226
	432749	NM_014438	Hs.278909	Interleukin 1, eta	0.3231
	408112	AW451982	Hs.248613	ESTs	0.3231
	433234	AB040928	Hs.65366	KJAA1495 protein	0.3231
	422831	R02504	Hs.332943	ESTs	0.3234
70	403215				0.3236
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypotheti	0.3236
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	0.3242
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	0.3254
	445848	AA774824	Hs.13377	Homo sapiens clone Z3649 and Z3765 unkno	0.3257
75	441143	AI027604	Hs.159650	ESTs	0.3257
	405138				0.3262
	412888	M88161		gb:EST02679 Hippocampus, Stratagene (cat	0.3262
	409662	AW452320	Hs.279726	ESTs	0.3262
	425438	T62216	Hs.270840	ESTs	0.3263
80	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.3263
	423512	AW844694	Hs.306752	Homo sapiens cDNA: FLJ21391 fis, clone C	0.3264
	436777	AA731199	Hs.293130	ESTs	0.3267
	431651	BE250915	Hs.266914	hypothetical protein FLJ10355	0.3287
	454117	BE410101	Hs.40368	adaptor-related protein complex 1, sigma	0.3288
	426048	AI768853	Hs.134478	ESTs	0.3269
	451096	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.3270
	426942	AA393551	Hs.97450	ESTs	0.3271

5	454947	AW846590	gb:QV0-CT0180-011099-025-d07 CT0180 Homo	0.3275
	413814	BE169692	gb:PM1-HT0527-290200-006-a05 HT0527 Homo	0.3275
	422818	AA404290	Hs.97848	0.3277
	423634	AW959908	Hs.1690	0.3278
	414002	NM_006732	Hs.75678	0.3278
	452164	AI863171	gb:tz44b02.x1 NCI_CGAP_Bm52 Homo sapien	0.3279
	458477	NM_000314	Hs.10712	0.3279
	433197	AB040889	Hs.281022	0.3280
	405701		KIAA1456 protein	0.3282
10	437782	AI370876	Hs.79090	0.3284
	459001	AI761313	Hs.204605	0.3285
	422783	AA598956	Hs.120439	0.3289
	417036	AF039918	Hs.80975	0.3290
	456041	BE270795	Hs.268864	0.3295
15	423310	AA325225	Hs.124023	0.3296
	427530	AA405093	Hs.126519	0.3296
	420172	AA601122	Hs.95655	0.3297
	445610	AI831648	Hs.143993	0.3297
20	411328	AW837063	gb:QV1-LT0037-150200-069-g08 LT0037 Homo	0.3300

Table 8B

	Pkey:	Unique Eos probeset identifier number	
25	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
30	409921	1159516_1	AW600239 AW600255 AW505332
	410626	1212621_1	BE407727
	410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283
	410950	1227728_1	AW811633 AW811652 AW811898
35	411288	1237709_1	AW835511 AW835517 AW835513
	411319	1238595_1	BE537094 AW836542
	411328	1238987_1	AW837063 AW935882 AW935957
	411468	1246771_1	AW847669 AW847667 BE145799
	411514	1248638_1	AW850178 AW850233 AW850445 AW850446
	411620	1252014_1	AW854536 AW854417 AW854495 AW854355
40	411880	1263110_1	AW872477 BE088101 T05990
	412474	129869_1	AI791451 AI791288 BE019234 BE296601 AA111939
	412506	1301336_1	AW957159 H09937 T75143
	412682	1321572_1	AW983772 AW983730 AW983769 AW983836 AW983835 AW983837
45	412888	1334784_1	M86151 BE061884 BE061883 BE061898 BE061882 BE061887 BE061891 BE061890 BE061896 BE061893 BE061895 BE061894 BE061885 BE007474
			BE007481 BE007553
	413056	1347545_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
	413537	1375441_1	BE146866 BE146865 BE146867
	413541	1375499_1	BE147036 BE146951 BE146958 BE146966 BE146976 BE146955
50	413814	1391574_1	BE169692 BE169421
	414026	1411109_1	BE241713 BE241912
	414193	1424706_2	BE260069
	414349	1437515_1	BE512968
	414484	1452830_1	BE314385
55	414539	1460320_1	BE379046 BE395459
	415154	1525577_1	D63176 D78984 D83269
	415160	1525768_1	T82802 D78670 R08505
	416035	1567254_1	H42314 H43080 H45217 H15384
	417945	1711126_1	R29072 R29717 R29699 R29709 R29751 R29609 R29060 R29718 R29057 R29591 R29683 R29575 R28913 R28910
60	419850	188485_1	F06844 F06845 Z45488 AW748501 AW748591 AW752021 AW748545 AW853362 AW853363 AW853427 AA251253
	422909	222858_1	AA533355 AW468427 R67736 AA778031 AA614088 AJ823404 AA318991 AA720986
	422954	223239_1	AW998605 AW993131 BE514709 AA319445
	423621	230314_1	BE002904 H64880 AA328679
	424648	241947_1	AA344576 AA732430 AA344601
65	426132	261431_1	AA370501 AW962784 AA370727
	426497	268121_1	AA379913 AA379981 AW963523
	430553	319868_1	AW392821 AW392809 AW843258 AW843049 AW603156 BE165658 AW821728
	431822	338082_1	AA516049 AW004922
	434098	380006_1	AA625499 AA625269 AA625184
70	437483	43756_1	AL390174 AW898817
	440507	495677_1	H06994 BE147898
	441042	50823_1	AA077735 AA078505 BE562497 Z17859
	441083	50904_1	BE562611 AA436054
	445682	647580_1	AW378397 AW378390 AW378358 AJ247957
75	446294	670076_1	AJ284935 AW409822 BE408182
	446901	697809_1	AJ347274 AW844024
	447787	73719_1	BE620108 BE312062 AW896316 BE262546
	451385	86787_1	AA017656 AA017374 AA019761
	452164	902091_1	AJ853171 BE047919
80	454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581
			BE141477 BE141520 BE141458 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
			BE141749 AW177598

454790 1234752_1 AW820852 AW820773 AW821088
 454947 1245953_1 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
 455353 1284289_1 W26786 AW998612 AW902272
 457115 286601_1 AA420712 AA469165 AA420737
 459138 918860_1 AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903346
 459233 944881_1 AI939966 AI939988 AI939951 AI939981 AI939976 AI939959

Table 8C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400541	8117693	Plus	4786-4992
400672	8118724	Minus	148067-148503
400767	8131627	Minus	80531-80629,82169-82278
400855	1945037	Minus	44482-45526
401024	8117489	Plus	60551-60802
401042	8117611	Plus	151364-151606
401371	9550602	Plus	80901-81283
401381	8570226	Minus	118629-119146,119392-119657
401465	6682292	Plus	25676-25800
401521	7705251	Plus	9127-9234
401753	9838183	Minus	155287-155529,159719-159997
401776	9966323	Plus	115535-115743,117746-117839,120290-120455
401887	7229981	Plus	93973-94120
401974	3126777	Plus	85330-85683
402076	8117410	Plus	128316-128627
402182	8575917	Minus	98298-98439
402425	9796347	Minus	50224-50395
402810	9926549	Minus	22955-23124
402695	8569871	Minus	159927-160055
403047	3540153	Minus	59793-59968
403215	7630945	Minus	177270-177971
403418	6862692	Minus	176202-176395
403548	8081591	Minus	38760-39352
403957	8076835	Minus	81649-81754
404070	2996642	Plus	7210-7414,10043-10195
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
404414	7382165	Plus	143127-143398
404605	8212566	Plus	125032-125291
404638	9796751	Minus	99433-99528,100035-100161
404696	9800109	Minus	60037-60144,62675-63081
404767	7882827	Minus	23244-23759
404769	8099713	Minus	176801-176823
404927	7342002	Plus	68680-69563
404958	7407841	Minus	2731-4531
405071	7708797	Minus	11115-11552
405073	7769921	Plus	31419-31774
405138	8576241	Plus	90303-90516
405277	3980473	Plus	23471-23572
405282	3810573	Minus	10482-10689
405334	3135285	Plus	139386-139856
405364	2281075	Minus	48325-48491,49136-49252
405385	6552772	Plus	48332-48454
405535	9795658	Plus	63384-63545
405610	5757553	Minus	71907-72080
405654	4895155	Minus	53624-53759
405691	4508112	Plus	171350-171739
405701	4263751	Plus	93243-93364
405880	6758747	Minus	55673-56287
405913	7712139	Minus	7484-7678
406140	9168231	Minus	49887-50219
406592	4567182	Plus	352560-352963

Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic function or of transducing an intracellular signal, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). In order to remove gene-specific

background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

Key: Unique Eos probaset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of tumor samples divided by the 70th percentile of normal body tissue samples, where the 15th percentile of normal body tissues was subtracted from the numerator and denominator

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
15	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	29.34
	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carc	25.56
	406667	M12523			20.28
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP)	18.84
20	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel	17.38
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intesti	16.61
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S384_H	16.42
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, eptitel	15.92
	407242	M18728		(locuslink)NM_002483:Homo sapiens carc	15.84
25	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease I	15.59
	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
	406685	M18728		(locuslink)NM_002483:Homo sapiens carc	14.54
	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	13.68
30	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.23
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	13.21
	453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	12.35
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.11
35	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	11.99
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, Li c	11.87
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carc	11.81
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	11.27
	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
40	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	10.82
	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.73
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.10
45	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	9.68
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	9.44
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	9.38
	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carc	9.34
50	427583	M82962	Hs.179704	NM_005588:Homo sapiens mepirin A, alpha (9.18
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.06
	406687	M31128	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.02
	409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	8.89
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.53
55	422654	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	8.23
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	8.10
	430569	AF241254	Hs.178058	NM_021804:Homo sapiens angiotensin I con	8.05
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
	406399				7.73
60	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	7.71
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	7.43
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	7.40
	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	7.29
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.25
65	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	7.19
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	7.18
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfat	7.03
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysl	7.00
70	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	6.92
	452194	AI694413	Hs.373599	Hs.373599:EST	6.88
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.59
	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	6.55
75	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	420344	BE483721	Hs.97101	NM_014373:Homo sapiens putative G protel	6.49
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	6.33
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	6.31
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (li iso)	6.30
80	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.29
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	6.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	6.27
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	6.26
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cyste)	6.23

5	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.23
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cysteine) protein kinase	6.23
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, beta	6.19
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier family 12 member 1	6.17
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible cytokine A1	6.17
10	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tyrosine kinase	6.17
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeobox domain	6.16
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding protein	6.14
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	6.13
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis	6.09
15	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	6.02
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading frame	5.95
	403220				5.90
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	5.87
20	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	5.79
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	5.79
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis transmembrane	5.77
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-coA	5.77
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible cytokine A1	5.76
25	431301	AA502384	Hs.151529	Hs.151529:ESTs	5.71
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 subunit	5.71
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	5.68
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	5.66
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical protein	5.61
30	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine deficient	5.57
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2, group	5.55
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-III	5.54
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1)	5.53
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.50
35	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagulation factor	5.38
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation factor V	5.33
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71)	5.32
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globulin) chain	5.32
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane protein	5.28
40	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation factor V	5.28
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-methylacyl-coA	5.27
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.26
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth factor	5.25
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	5.25
45	436251	BE515065	Hs.296565	(locuslink)NM_006392:Homo sapiens nucleoside	5.25
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransferase	5.23
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid inducible	5.22
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium channel	5.20
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-containing	5.18
50	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.13
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mRNA	5.12
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b receptor	5.11
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruit	5.08
	426174	AA547959	Hs.115838	Hs.115838:ESTs	5.07
55	403218				5.07
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGalNAc	5.00
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptidase	4.98
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	4.96
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolipoprotein	4.92
60	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif domain	4.91
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading frame	4.91
	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix protein	4.90
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	424010	AL080188	Hs.137558	NM_033100:Homo sapiens MT-protocadherin	4.86
65	428953	AA308610	Hs.348183	NM_003823:Homo sapiens tumor necrosis factor	4.86
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25-dihydroxy) vitamin	4.83
	425983	AK000226	Hs.165819	NM_031265:Homo sapiens mucin and cadherin	4.81
	428289	M26301	Hs.2253	Hs.2253:complement component 2	4.79
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	4.78
70	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tumorigen	4.77
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical protein	4.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	4.72
	430680	AW138724	Hs.168974	Hs.168974:ESTs	4.69
75	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidized low density	4.69
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ12425 f	4.67
	403221				4.65
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast cancer	4.65
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apoptotic	4.64
80	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	4.64
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility complex	4.64
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kinase	4.60
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene product	4.60
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H domain	4.60
80	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properdin	4.59
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.57
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryonic	4.56

5	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	4.55
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.55
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	4.55
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens statidase 1 (lyso	4.54
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.53
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.53
10	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	443484	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.49
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	4.48
	432378	AI493046	Hs.146133	Hs.146133:ESTs	4.48
	431958	X63829	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
15	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.47
	422511	AA076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.46
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
20	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.44
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	4.43
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	4.40
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.38
25	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.37
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	4.36
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.36
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.35
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	4.33
30	432575	AA553722	Hs.194346	Hs.194346:Spr-2 protein	4.33
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	4.33
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.32
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.32
35	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.30
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
40	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.29
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	4.28
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.28
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.27
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.27
45	414361	AI086138	Hs.204044	Hs.204044:ESTs	4.26
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.26
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.24
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.22
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
50	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.19
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.18
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	4.18
55	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	4.17
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.17
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.16
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.15
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA: cDNA DKFZp4	4.15
60	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.14
	403219				4.14
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.14
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.14
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
65	409956	AW103364	Hs.727	NM_002192:Homo sapiens Inhibin, beta A (4.12
	439559	AW970780	Hs.69483	Hs.69483:leucine-rich repeat-containing	4.12
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.12
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.11
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	4.10
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	4.09
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.07
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA: cDNA DKFZp6	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
75	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.05
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.04
	425280	U31519	Hs.1872	NM_002691:Homo sapiens phosphoenolpyruva	4.03
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.03
80	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.02
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.01
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78996	NM_002592: Homo sapiens proliferating cell	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819: Homo sapiens phosphoribosylg	3.98
	405484				3.98
5	409162	H25530	Hs.50868	Hs.50868: solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246: Homo sapiens lymphocyte antigen	3.97
	414695	BE439915	Hs.76913	Hs.76913: proteasome (prosome, macropain)	3.97
	411155	NM_000169	Hs.69089	NM_000169: Homo sapiens galactosidase, al	3.97
10	421975	AW961017	Hs.6459	(locuslink)NM_024531: Homo sapiens hypoth	3.96
	431836	AF178532	Hs.271411	NM_138992: Homo sapiens beta-site APP-cle	3.96
	412133	U83460	Hs.104557	NM_001859: Homo sapiens solute carrier fa	3.96
	412870	N22788	Hs.82407	NM_022059: Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833: interferon-stimulated protein, 15	3.95
15	400130		Hs.165560	NM_001746: Homo sapiens catenin (CANX),	3.93
	430696	AA531276	Hs.59509	Hs.59509: ESTs, Weakly similar to similar	3.93
	443802	AW504924	Hs.9805	Hs.9805: exportin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465: squalene epoxidase	3.92
	456629	AW891965	Hs.367942	Hs.367942: Homo sapiens, clone IMAGE:4701	3.92
20	421943	BE616520	Hs.343912	NM_033504: Homo sapiens CAC-1 (CAC-1), mR	3.91
	422293	X94453	Hs.114366	Hs.114366: pyrroline-5-carboxylate synthe	3.90
	419488	AA316241	Hs.90691	NM_006993: Homo sapiens nucleosomitu	3.89
	425123	AW205274	Hs.154695	NM_000303: Homo sapiens phosphomannomul	3.89
	447343	AA256641	Hs.236894	Hs.236894: ESTs, Highly similar to S02392	3.88
25	413254	U40272	Hs.75253	NM_004135: Homo sapiens isocitrate dehydr	3.88
	413950	AA249096	Hs.32793	Hs.32793: Homo sapiens cDNA FLJ31108 fis	3.88
	409453	AI885516	Hs.95612	Hs.95612: ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093: Homo sapiens ephrin-B2 (EFNB2)	3.86
	421910	NM_014586	Hs.109437	NM_014586: Homo sapiens hormonally upregu	3.86
30	434263	N34895	Hs.79187	Hs.79187: coxsackie virus and adenovirus	3.85
	444700	NM_003645	Hs.11729	NM_003645: Homo sapiens fatty-acid-Coenzy	3.85
	433662	W07162	Hs.150826	NM_020387: Homo sapiens RAB25, member RAS	3.84
	418526	BE019020	Hs.85838	NM_004207: Homo sapiens solute carrier fa	3.84
	425998	AU076629	Hs.165950	NM_002011: Homo sapiens fibroblast growth	3.84
35	422616	BE300330	Hs.118725	NM_012248: Homo sapiens selenophosphate s	3.83
	408056	AA312329	Hs.42331	Hs.42331: ephrin-A4	3.83
	407233	X16354	Hs.50964	(locuslink)NM_001712: Homo sapiens cardin	3.83
	426514	BE616633	Hs.170195	Hs.170195: bone morphogenetic protein 7 (3.82
	451541	BE279383	Hs.26557	NM_007183: Homo sapiens plakophilin 3 (PK	3.82
40	424441	X14850	Hs.147097	Hs.147097: H2A histone family, member X	3.81
	426378	U80082	Hs.169600	Hs.169600: KIAA0826 protein	3.81
	409636	AA305729	Hs.18272	(locuslink)NM_030674: Homo sapiens solute	3.81
	407786	AA687538	Hs.38972	NM_005727: Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11962	NM_030766: Homo sapiens apoptosis regulat	3.79
45	414561	AI064813	Hs.195155	Hs.195155: solute carrier family 38, memb	3.79
	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636: Homo sapiens transi	3.79
	400529				3.79
	412869	AA290712	Hs.82407	Hs.82407: chemokine (C-X-C motif) ligand	3.78
50	427239	BE270447	Hs.356512	Hs.356512: ESTs, Weakly similar to UBCA_A	3.78
	429638	AI916662	Hs.211577	(locuslink)NM_004986: Homo sapiens kinect	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051: Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741: klninogen	3.77
	443639	BE289042	Hs.9661	Hs.9661: proteasome (prosome, macropain)	3.76
55	400290	H18836	Hs.31608	(locuslink)NM_017636: Homo sapiens transi	3.76
	431350	AI192528	Hs.164537	Hs.164537: ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085: Homo sapiens serine (or cystei	3.75
	435099	AC004770	Hs.4756	NM_004111: Homo sapiens flap structure-sp	3.75
	418218	AA682240	Hs.283099	Hs.283099: AF15q14 protein	3.74
60	414907	X90725	Hs.77597	NM_000998: Homo sapiens ribosomal protein	3.74
	413063	AL035737	Hs.75184	Hs.75184: chitinase 3-like 1 (cartilage g	3.73
	420665	AW469240	Hs.371581	Hs.371581: ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663: ESTs	3.72
	444664	N26362	Hs.11615	NM_016086: Homo sapiens map kinase phosph	3.72
65	450334	AF035959	Hs.24879	Hs.24879: phosphatidic acid phosphatase t	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832: Homo sapiens hypoth	3.72
	449437	AF702038	Hs.100057	Hs.100057: serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069: serine hydroxymethyltransferase	3.71
	427490	Z95152	Hs.178695	NM_002754: Homo sapiens mitogen-activated	3.71
70	427333	AF067797	Hs.176658	NM_001169: Homo sapiens aquaporin 8 (AQP8	3.70
	434203	BE262677	Hs.283558	NM_018509: Homo sapiens hypothetical prot	3.70
	414805	D14694	Hs.77329	(locuslink)NM_014754: Homo sapiens phosph	3.70
	456362	AW973003	Hs.179909	(locuslink)NM_024831: Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936: Homo sapiens CGI-04 protein (L	3.69
75	437016	AU076916	Hs.53398	Hs.53398: guanine monophosphate synthetase	3.69
	430387	AW372884	Hs.240770	Hs.240770: nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530: Homo sapiens cDNA: FLJ23602 fi	3.69
	432593	AW301003	Hs.51483	Hs.51483: Homo sapiens, Similar to RIKEN	3.68
	413813	M96956	Hs.75561	NM_003212: Homo sapiens teratocarcinoma-d	3.68
80	428376	AF119665	Hs.184011	Hs.184011: pyrophosphatase (inorganic)	3.67
	431890	X17033	Hs.271986	NM_002203: Homo sapiens integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911: Homo sapiens solute carrier fa	3.67
	419378	R24922	Hs.90078	Hs.90078: nucleotide-sugar transporter sl	3.67
	448140	AF146761	Hs.20450	NM_020125: Homo sapiens B lymphocyte acti	3.67

5	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	A1375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.66
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	3.66
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.66
10	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spr-2 protein	3.64
	404826				3.63
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
15	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.63
	452098	AJ858183		BF755039:QV0-CT0583-181000-428-107 CT058	3.62
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protel	3.61
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.60
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
20	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	3.59
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcni	3.58
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	3.58
25	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	3.58
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.57
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosp	3.57
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	3.57
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.56
30	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.55
	421357	AK000609	Hs.103808	NM_017895:Homo sapiens chromosome 20 ope	3.55
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	3.55
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.55
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.55
35	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	3.55
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.54
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.54
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	3.54
40	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.53
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	3.53
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	3.53
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.53
45	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.53
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	3.52
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.52
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.51
50	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.51
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.51
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	3.51
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	3.51
55	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.51
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.51
	419593	AA133749	Hs.301350	Hs.301350:FXD domain-containing lon tra	3.51
	407971	AI469117	Hs.62918	Hs.62918:CDG91 cell division cycle 91-II	3.50
60	424865	AF011333	Hs.153663	NM_002349:Homo sapiens lymphocyte antige	3.50
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.50
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	3.50
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.50
65	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.50
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.49
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	3.49
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	3.48
70	407137	T97307			3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.48
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.47
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.47
75	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.45
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.45
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
80	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	3.44
	425209	ALD49761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.44
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.43
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.43
	437867	BE277414	Hs.5947	NM_005370:Homo sapiens mei transforming	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43

	414862	BE621310	Hs.923	Hs.923: single-stranded DNA binding prote	3.43
	400750				3.42
	413186	AU077141	Hs.374548	Hs.374548: solute carrier family 16 (mono	3.41
5	425263	NM_001197	Hs.155419	NM_001197: Homo sapiens BCL2-interacting	3.40
	453857	AL080235	Hs.35861	Hs.35861: Ras-induced senescence 1	3.40
	428474	AB023182	Hs.184523	Hs.184523: serine/threonine kinase 38 lik	3.39
	410315	AI638871	Hs.378965	Hs.378965: Homo sapiens cDNA FLJ37658 fis	3.39
	428206	AB020643	Hs.183006	Hs.183006: likely homolog of mouse hepari	3.39
10	450506	NM_004460	Hs.418	(locuslink)NM_004460: Homo sapiens fibrob	3.39
	413179	N99692	Hs.75227	NM_005002: Homo sapiens NADH dehydrogenas	3.38
	440876	NM_004987	Hs.112378	(locuslink)NM_004987: Homo sapiens LIM an	3.38
	400847				3.37
	431685	AW296135	Hs.267659	NM_006113: Homo sapiens vav 3 oncogene (V	3.37
15	410189	AW377424	Hs.205126	Hs.205126: Homo sapiens cDNA: FLJ22667 fi	3.37
	432633	AI796390	Hs.210567	Hs.210667: ESTs	3.36
	429344	R94038	Hs.374564	NM_005538: Homo sapiens inhibin, beta C (3.36
	424685	W21223	Hs.151734	Hs.151734: nuclear transport factor 2	3.38
	456950	AF111170	Hs.306165	Hs.306165: ESTs, Highly similar to unknow	3.35
20	418313	BE244231	Hs.84038	NM_015937: Homo sapiens CGI-06 protein (L	3.35
	453454	AW052006	Hs.374973	NM_004697: Homo sapiens PRP4 pre-mRNA pro	3.35
	400448				3.35
	424142	AI878727	Hs.378970	Hs.378970: Homo sapiens cDNA FLJ35102 fis	3.35
25	430720	U85768	Hs.247838	NM_002991: Homo sapiens small inducible c	3.35
	416412	NM_014742	Hs.79305	Hs.79305: KIAA0255 gene product	3.35
	429824	AA296363	Hs.121520	Hs.121520: Homo sapiens cDNA FLJ35792 fis	3.35
	412948	BE243313	Hs.334851	Hs.334851: LIM and SH3 protein 1	3.34
	451129	BE072881		BE072881: RC2-BT0548-200300-012-e09 BT054	3.34
	425322	U63630	Hs.155637	NM_006904: Homo sapiens protein kinase, D	3.34
30	446291	BE397753	Hs.14623	Hs.14623: Interferon, gamma-inducible pro	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051: Homo sapiens hypoth	3.34
	423198	M81933	Hs.1634	Hs.1634: cell division cycle 25A	3.34
	448093	AW977382	Hs.15898	Hs.15898: 2,4-dienoyl CoA reductase 2, pe	3.34
	414045	NM_002951	Hs.75722	NM_002951: Homo sapiens ribophorin II (RP	3.34
35	421190	U95031	Hs.102482	Hs.102482: mucin 5, subtype B, tracheobro	3.34
	419607	R52557	Hs.91579	NM_033416: Homo sapiens similar to HYPOTH	3.33
	435975	AL118990	Hs.373554	(locuslink)NM_130786: Homo sapiens alpha-	3.33
	418416	U11700	Hs.84999	NM_000053: Homo sapiens ATPase, Cu++ tran	3.33
	433570	AI580053	Hs.109007	Hs.109007: Homo sapiens, Similar to LOC16	3.33
40	441128	AA570256	Hs.348504	Hs.348504: hypothetical protein BC014072	3.33
	432320	AW411066	Hs.274351	NM_016032: Homo sapiens zinc finger, DHHC	3.33
	444019	BE173977	Hs.10098	NM_019082: Homo sapiens putative nucleola	3.32
	432680	T47364	Hs.278613	(locuslink)NM_005532: Homo sapiens Intarf	3.32
	410219	T98226	Hs.171952	Hs.171952: occludin	3.32
45	410663	AA194952	Hs.36093	Hs.36093: Homo sapiens cDNA FLJ12885 fis,	3.32
	402829				3.32
	445921	AW015211	Hs.153799	Hs.153799: Homo sapiens cDNA FLJ38333 fis	3.32
	414198	AW505308	Hs.75812	NM_004563: Homo sapiens phosphoenolpyruva	3.32
50	443425	AI068776	Hs.133397	Hs.133397: ESTs	3.32
	436485	X59135	Hs.156110	Hs.156110: immunoglobulin kappa constant	3.31
	410268	AA316181	Hs.61635	NM_012449: Homo sapiens six transmembrane	3.30
	425159	NM_004341	Hs.154868	NM_004341: Homo sapiens carbamoyl-phospha	3.30
	420614	AL110291	Hs.99364	Hs.99364: abhydrolase domain containing 1	3.30
	421814	L12350	Hs.108623	NM_003247: Homo sapiens thrombospondin 2	3.30
55	432215	AU076609	Hs.2934	NM_001033: Homo sapiens ribonucleotide re	3.30
	409402	AF208234	Hs.695	Hs.695: cystatin B (steifin B)	3.30
	421038	AL080192	Hs.101282	Hs.101282: Homo sapiens mRNA; cDNA DKFZp4	3.29
	424408	AI754813	Hs.146428	Hs.146428: collagen, type V, alpha 1	3.29
	448775	AB025237	Hs.388	NM_002452: Homo sapiens nudix (nucleoside	3.29
60	442821	BE391929	Hs.8752	Hs.8752: transmembrane protein 4	3.29
	459306	AW578452		AW578452: RC1-CT0252-030100-023-b07 CT025	3.28
	400846				3.28
	422256	M64673	Hs.1499	NM_005526: Homo sapiens heat shock transc	3.28
	408089	H59799	Hs.42644	Hs.42644: thioredoxin-like 2	3.28
65	432078	BE314877	Hs.24553	(locuslink)NM_022369: Homo sapiens hypoth	3.27
	435575	AF213457	Hs.44234	NM_018965: Homo sapiens triggering recept	3.27
	456534	X91195	Hs.100623	NM_138689: Homo sapiens protein phosphata	3.27
	447335	BE617695	Hs.286192	NM_032192: Homo sapiens protein phosphata	3.27
	414368	W70171	Hs.75939	NM_012474: Homo sapiens uridine monophosp	3.27
70	422599	BE387202	Hs.118638	Hs.118638: non-metastatic cells 1, protei	3.26
	437897	AA770561	Hs.146170	Hs.146170: hypothetical protein FLJ22969	3.26
	431183	NM_006855	Hs.250696	NM_006855: Homo sapiens KDEL (Lys-Asp-Glu	3.26
	457635	AV660978	Hs.3569	Hs.3569: chromosome 20 open reading frame	3.26
	432391	AI732374	Hs.339827	Hs.339827: ESTs, Weakly similar to protea	3.25
75	417640	D30857	Hs.82353	NM_006404: Homo sapiens protein C recepto	3.25
	440086	NM_005402	Hs.6906	NM_005402: Homo sapiens v-ral simian leuk	3.25
	401179				3.25
	411125	AA151647	Hs.68877	Hs.68877: cytochrome b-245, alpha polypep	3.25
	453323	AF034102	Hs.32951	NM_001532: Homo sapiens solute carrier fa	3.25
80	407236	W79485	Hs.173980	Hs.173980: nuclear matrix protein NMP200	3.25
	447250	AI878909	Hs.17883	NM_002707: Homo sapiens protein phosphata	3.25
	452875	BE275760	Hs.30928	NM_006114: Homo sapiens translocase of cu	3.24
	428390	AI640377	Hs.350077	NM_000982: Homo sapiens ribosomal protein	3.24
	425811	AL039104	Hs.159557	NM_002266: Homo sapiens karyopherin alpha	3.24

5	446356	A1816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.24
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.24
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.23
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-1	3.23
10	409586	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multid	3.23
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.23
	419705	AW368834	Hs.154331	Hs.154331:ESTs	3.22
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
	413835	A1272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	3.22
15	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.22
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.21
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.21
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
	420085	A1741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
20	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
	424954	NM_000546	Hs.1848	NM_000546:Homo sapiens tumor protein p53	3.21
	437741	BE581610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diff	3.20
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.20
25	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
	452203	X57622	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.20
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.19
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.19
	408716	A1567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
30	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfactant 4 (SURF4)	3.19
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.19
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.18
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.18
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	3.18
35	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.18
	420531	A1652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.18
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
	452700	A1859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.18
40	433604	NM_013442	Hs.3439	Hs.3439:stomatol (EPB72)-like 2	3.18
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.18
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.18
	447698	A1420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.17
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
45	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.17
	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.17
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
50	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
	447151	A1022813	Hs.92679	(locuslink)NM_145754:Homo sapiens knesi	3.15
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.15
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
55	423599	A1805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.15
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (3.14
	420190	A1816209	Hs.85867	(locuslink)NM_024112:Homo sapiens chromo	3.14
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.14
60	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXD d	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.13
65	426841	A1052358	Hs.131741	Hs.131741:ESTs	3.13
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
	420576	AA434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
	438444	A1064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE3456	3.12
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.12
70	412326	R07568	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens sro family associ	3.12
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
	421779	A1879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.11
75	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.11
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.11
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phos	3.11
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.11
	433179	AW362945	Hs.162459	Hs.162459:ESTs	3.11
80	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.10
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.10
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.10
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

5	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.10
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neur	3.10
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.10
10	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201078	Hs.201078:ESTs	3.09
	427648	AJ376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.08
	404240				3.08
	408989	AW361668	Hs.49500	Hs.49500:KIAA0746 protein	3.08
15	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.08
	402260				3.08
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.08
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
20	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.07
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosyl	3.07
	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.07
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.07
25	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.07
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.07
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.07
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.07
30	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.06
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.06
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.06
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.06
35	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, similar to RIKEN	3.06
	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.06
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.06
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.05
40	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.05
	408806	AW847814	Hs.75608	Hs.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.05
	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.05
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.05
45	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
	406363				3.05
	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannosyl-P-dolicho	3.05
50	431738	AW237728	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-4	3.04
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	3.04
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.04
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.04
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.04
55	430281	AI876842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.04
	452865	AI924046	Hs.119567	Hs.119567:ESTs, weakly similar to ALU1_H	3.04
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor CX	3.04
	444301	AK000135	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.04
60	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antimicr	3.03
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis	3.03
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.03
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
65	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	3.03
	440659	AF134160	Hs.7327	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.03
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.02
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.02
70	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.02
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.02
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens Interleukin 13 re	3.02
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.02
75	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.01
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.01
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.01
	410293	AK000047	Hs.61950	NM_018992:Homo sapiens hypothetical prot	3.01
80	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 8A	3.00
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.00
	414249	AI797994	Hs.279929	(locuslink)NM_017610:Homo sapiens gp25L2	3.00
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Hs.90572:PTK7 protein tyrosine kinase 7	3.00
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

5	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	2.99
	437763	AA469369	Hs.5831	Hs.5831:tissue inhibitor of metalloprote	2.99
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, rbo	2.99
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
10	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
	432396	AW295856	Hs.11900	(locuslink)NM_032527:Homo sapiens hypoth	2.98
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	2.98
	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.98
15	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	2.98
	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	2.98
	452124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	2.97
20	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	2.97
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	2.97
25	430354	AA954810	Hs.239784	Hs.239784:scribble	2.97
	417079	U65590	Hs.81134	(locuslink)NM_000577:Homo sapiens interl	2.97
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostatic)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
30	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinesin	2.96
	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.96
35	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	2.96
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	2.96
40	429597	NM_003816	Hs.2442	Hs.2442:alpha disintegrin and metalloprotein	2.95
	421179	U72684	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.95
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alph	2.95
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	2.95
45	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	2.94
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.94
50	419152	L12711	Hs.89643	(locuslink)NM_001084:Homo sapiens transk	2.94
	444824	AA843575	Hs.12056	NM_001671:Homo sapiens estroglycoprotein	2.94
	431629	AU077025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	2.94
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.93
55	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	2.93
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AI689496	Hs.108932	Hs.108932:ESTs	2.93
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
60	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.92
	417944	AU077196	Hs.82985	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(locuslink)NM_145294:Homo sapiens simila	2.92
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
65	451608	AA384525	Hs.28745	NM_016499:Homo sapiens HSPC244 (MGC:1337	2.92
	434608	AA805443	Hs.179909	NM_024831:Homo sapiens nuclear receptor	2.92
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
70	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	2.91
	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	2.91
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	2.91
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	2.91
75	450167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
	408815	AW957974	Hs.25485	(locuslink)NM_024599:Homo sapiens hypoth	2.91
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262889	Hs.12045	Hs.12045:C2f protein	2.91
80	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	2.90
	432710	AA505685	Hs.278672	NM_005898:Homo sapiens membrane componen	2.80
	405203				2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	2.80
	412926	AI878076	Hs.75061	Hs.75061:macrophage myristoylated alanin	2.90

	455967	L12535	Hs.75551	(locustlink)NM_012425:Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locustlink)NM_002004:Homo sapiens farnes	2.90
	442739	NM_007274	Hs.86779	(locustlink)NM_007274:Homo sapiens cyto	2.90
5	456157	AW979153	Hs.336881	Hs.336881:ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274:Homo sapiens a disintegrin and	2.89
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	2.89
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	2.89
	438543	AA810141	Hs.192182	Hs.192182:ESTs	2.89
10	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	2.89
	441455	AJ271671	Hs.7854	NM_014437:Homo sapiens solute carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797:Homo sapiens proteasome (proso	2.89
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.89
15	418062	AW630656	Hs.83383	NM_005406:Homo sapiens peroxidoreductin 4 (2.89
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yamaguchi sarcoma viral	2.89
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	2.88
20	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	2.88
	411030	BE387193	Hs.67896	(locustlink)NM_007346:Homo sapiens oploid	2.88
	413822	R08950	Hs.272044	Hs.272044:ESTs, Weakly similar to hypoth	2.88
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	2.88
	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	2.88
25	440490	AW513684	Hs.7218	Hs.7218:acetyl-Coenzyme A synthetase 2 (2.87
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	2.87
	423570	AW838306	Hs.129819	NM_018344:Homo sapiens hypothetical prot	2.87
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	2.87
	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	2.87
30	442643	U82758	Hs.374973	(locustlink)NM_004697:Homo sapiens PRP4 p	2.87
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419:zinc finger protein	2.87
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	2.87
35	416448	L13210	Hs.79339	NM_005567:Homo sapiens lactin, galactosi	2.87
	453145	R63438	Hs.183454	Hs.183454:Homo sapiens cDNA FLJ14883 fis	2.86
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D80001	Hs.152629	Hs.152629:KIAA0179 protein	2.86
	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	2.86
40	450273	AW298454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	2.86
	407082	Z47055			2.86
	450038	AA005159	Hs.188489	Hs.188489:ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.85
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rb-related antige	2.85
45	417824	AA084798	Hs.82646	NM_006145:Homo sapiens DnaJ (Hsp40) homo	2.85
	426989	A1815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (2.85
	434916	AF161383	Hs.284207	Hs.284207:hypothetical protein BC003515	2.85
	412664	AA421404	Hs.346868	NM_006824:Homo sapiens EBNA1 binding pro	2.85
	414172	AW954324	Hs.75790	(locustlink)NM_002642:Homo sapiens phosph	2.85
50	409504	AA304961	Hs.699	Hs.699:peptidylprolyl isomerase B (cyclo	2.84
	439920	H05430	Hs.288433	NM_016522:Homo sapiens neurotrophin (HNT)	2.84
	418462	BE001596	Hs.85266	Hs.85266:integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879:Homo sapiens etoposide-induced	2.84
	406710	AJ708347	Hs.184014	Hs.184014:ribosomal protein L31	2.84
	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Tc translation el	2.84
55	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	2.84
	448730	AB032883	Hs.21894	Hs.21894:KIAA1157 protein	2.84
	433027	AF191018	Hs.279923	(locustlink)NM_014366:Homo sapiens putati	2.84
	449090	AK001735	Hs.22983	NM_020121:Homo sapiens UDP-glucose ceram	2.84
60	439737	AJ751438	Hs.41271	Hs.41271:Homo sapiens mRNA full length i	2.84
	403912				2.84
	423225	AA852604	Hs.125359	NM_006288:Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9069	Hs.9069:KIAA0962 protein	2.84
	429211	AF052693	Hs.198249	NM_005268:Homo sapiens gap junction prot	2.84
65	452518	AA280722	Hs.24768	Hs.24768:Homo sapiens cDNA FLJ32068 fis,	2.84
	418127	BE243982	Hs.83532	(locustlink)NM_002389:Homo sapiens membra	2.83
	448489	AI523875		R45782:Ha616-4 Adult heart, Clontech Hom	2.83
	426194	T50872	Hs.2001	NM_001061:Homo sapiens thromboxane A syn	2.83
	422129	AU076635	Hs.1478	NM_000185:Homo sapiens serine (or cystei	2.83
70	437651	BE560672	Hs.13543	(locustlink)NM_145214:Homo sapiens tripar	2.83
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	2.83
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	2.83
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	2.83
75	439720	AI935202	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.83
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	2.83
	425907	AA365752	Hs.155965	Hs.155965:ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	2.82
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	2.82
80	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	2.82
	415697	AI365603	Hs.279696	Hs.279696:DKFZP5661024 protein	2.82
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	2.82
	430040	AW503115	Hs.227823	NM_014287:Homo sapiens pM5 protein (PM5)	2.82
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004596:Homo sapiens small nuclear rib	2.82
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	2.82
	400845				2.81
5	419501	AW843822	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.81
	418140	BE613836	Hs.83551	(locuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201931	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
10	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	2.81
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433061	AW068033	Hs.296422	(locuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.81
15	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fis,	2.81
	410240	AL157424	Hs.61289	Hs.61289:synaptotagmin 2	2.80
	423880	BE278111	Hs.134200	Hs.134200:DKFZP564C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:neuronal protein 17.3	2.80
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	2.80
20	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
	456602	AA411607	Hs.118964	NM_017660:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	2.80
	426437	BE076537	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	2.79
25	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	2.79
	409531	BE384319	Hs.54702	(locuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021987:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
	419846	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren s	2.79
30	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Nal56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	2.79
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(locuslink)NM_005723:Homo sapiens tetras	2.79
35	448752	AA593887	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	2.79
	419235	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrophin (HNT)	2.78
	407754	AA527348	Hs.288957	Hs.288957:Homo sapiens, similar to RIKEN	2.78
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AK000476	Hs.76798	NM_016470:Homo sapiens chromosome 20 ope	2.78
40	418869	AW516555		AA229762:nc49101.r1 NCI_CGAP_Pr3 Homo sa	2.78
	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
45	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
	447402	H54520	Hs.351327	(locuslink)NM_017828:Homo sapiens hypoth	2.78
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422051	AW327546	Hs.111024	(locuslink)NM_006984:Homo sapiens solute	2.78
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
50	419757	AA773820	Hs.63970	Hs.63970:ESTs	2.77
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206939	Hs.42287	NM_001952:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
55	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	2.77
	444207	AI665004	Hs.374415	Hs.374415:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fis	2.77
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE253927	Hs.24983	Hs.24983:hypothetical protein from EUROI	2.77
60	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12280 fis	2.77
	412890	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
65	427509	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	2.76
	450770	AA019924	Hs.28803	Hs.28803:ESTs	2.76
	419594	AA013051	Hs.91417	(locuslink)NM_007027:Homo sapiens topois	2.76
	450878	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	2.76
	417767	BE242241	Hs.82542	NM_001637:Homo sapiens acylcoxyacyl hydro	2.76
70	439968	AA224760	Hs.153	NM_000971:Homo sapiens ribosomal protein	2.76
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	2.75
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
75	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	2.75
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	2.75
	435025	T08990	Hs.4742	Hs.4742:GPAAP1P anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
80	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
	408196	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.75
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containing	2.74

5	423527	AI206965	Hs.105861	(locuslink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	2.74
	450247	AF123303	Hs.24713	NM_013385:Homo sapiens hypothetical prot	2.74
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquitin-cytochr	2.74
10	440457	BE387593	Hs.21321	(locuslink)NM_145808:Homo sapiens granul	2.74
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	2.73
15	421921	H83353	Hs.355993	NM_012456:Homo sapiens translocase of in	2.73
	403217				2.73
	423871	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to chol	2.73
	416733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
	400275		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synthe	2.73
20	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
	422009	AI742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
25	436995	AI160015	Hs.125489	Hs.125489:KIAA1961 protein	2.73
	400509				2.73
	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
	445899	AI263738	Hs.145626	Hs.145626:Homo sapiens, Similar to hypot	2.72
	453557	AA522464	Hs.285996	NM_024956:Homo sapiens hypothetical prot	2.72
30	446859	AM94299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA579535	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5855	Hs.5855:Homo sapiens mRNA; cDNA DKFZp434	2.72
	428466	AF151063	Hs.184456	NM_016486:Homo sapiens hypothetical prot	2.71
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic I	2.71
35	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protel	2.71
	429359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.71
	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
40	426263	AI908774	Hs.259785	Hs.259785:carbamoyl palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.71
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
45	424965	AW956282	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412973	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
	410113	AW996564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 fi	2.70
	413092	AA126856	Hs.118655	Hs.118655:ESTs	2.70
50	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	2.70
	450493	M93718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endot	2.70
	413745	AW247252	Hs.76514	NM_000270:Homo sapiens nucleoside phosph	2.70
	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
	436042	AF284422	Hs.119178	(locuslink)NM_020246:Homo sapiens caton	2.70
55	432981	NM_002733	Hs.3136	Hs.3136:protein kinase, AMP-activated, g	2.70
	431341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43666	NM_007079:Homo sapiens protein tyrosine	2.70
	415770	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
	447507	H59696	Hs.18747	NM_005837:Homo sapiens POP7 (processing	2.70
60	424500	AF040704	Hs.149443	(locuslink)NM_007022:Homo sapiens putat	2.69
	414237	BE536554	Hs.278270	Hs.278270:inactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
65	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04.s1 NCL CGAP_Pr2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
	449957	D31365	Hs.24220	(locuslink)NM_016479:Homo sapiens scotin	2.69
	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA)	2.69
70	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domai	2.69
	429544	BE299343	Hs.2430	NM_005997:Homo sapiens transcription fac	2.68
	428582	BE336699	Hs.185055	Hs.185055:BEENE protein	2.68
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	2.68
	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
75	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEAD(H) (Asp-Glu-Ala-Asp/His) b	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntaxin 4A (plac	2.68
	409533	AW969543	Hs.144509	NM_080652:Homo sapiens similar to RIKEN	2.68
	433184	AA147979	Hs.285005	NM_020243:Homo sapiens translocase of ou	2.68
80	455303	AW892049		BE066891:PM3-BT0338-211299-002-e12 BT033	2.68
	452600	AI910842	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.68
	415410	AF037332	Hs.276569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxonase 2 (PO	2.67
	435049	AL122067	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450528	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO0461 protein (2.67
	433339	AF019226	Hs.8036	NM_004283:Homo sapiens RAB3D, member RAS	2.67
	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

5	451798	BE297587	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67
	427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67
	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67
	415116	AA160383	Hs.269956	Hs.269956:ESTs	2.67
	425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66
	418706	U73524	Hs.87465	NM_006831:Homo sapiens ATP/GTP-binding p	2.66
	410165	BE560228	Hs.71869	NM_013258:Homo sapiens apoptosis-associ	2.66
	410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66
10	430066	AI929559	Hs.237825	Hs.237825:signal recognition particle 72	2.66
	425910	AAB30797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66
	427954	J03060	Hs.247551	NM_002455:Homo sapiens metaxdn 1 (MTX1)	2.66
	439971	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fis	2.66
	438449	AK001333	Hs.6216	Hs.6216:DnaJ (Hsp40) homolog, subfamily	2.66
	435906	AI686379	Hs.110796	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
15	433387	L76528	Hs.3260	NM_000021:Homo sapiens presenilin 1 (Alz	2.66
	447191	NM_014521	Hs.17667	(locuslink)NM_014521:Homo sapiens SH3-do	2.66
	444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66
	418529	AW005695	Hs.250897	Hs.250897:TRK-fused gene	2.65
20	426025	AW138330	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.65
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	2.65
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65
	444395	N66148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65
25	431222	X56777	Hs.273790	NM_007155:Homo sapiens zona pellucida g1	2.65
	406790	AA293303	Hs.356342	Hs.356342:ESTs, Highly similar to 211320	2.65
	440708	AF038962	Hs.7391	Hs.7391:voltage-dependent anion channel	2.65
	416526	H61082	Hs.14743	Hs.14743:ESTs	2.65
	413995	BE048148	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (brai	2.65
30	424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.65
	452882	AW972990	Hs.196270	NM_030780:Homo sapiens folate transporte	2.65
	406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31233	2.64
	451295	AI557212	Hs.17132	Hs.17132:ESTs	2.64
35	448428	AF282874	Hs.21201	NM_015480:Homo sapiens necln 3 (DKFZP56	2.64
	426611	BE178050	Hs.171271	NM_001904:Homo sapiens catenin (cadherin	2.64
	426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fis,	2.64
	407223	H96850		H96850:cw03b12.s1 Soares melanocyte 2NbH	2.64
	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	2.64
40	420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64
	428471	X57348	Hs.184510	Hs.184510:stratillin	2.64
	451544	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64
	413245	BE244334	Hs.75249	Hs.75249:ADP-ribosylation factor-like 6	2.64
	415020	BE249915	Hs.293533	Hs.293533:Homo sapiens cDNA FLJ37093 fis	2.64
45	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64
	418694	U82987	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
	410688	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	2.64
	436183	AI146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64
	441226	BE563042	Hs.118820	Hs.118820:hypothetical protein BC007882	2.64
50	432788	AA521091	Hs.178499	Hs.178499:HSPC063 protein	2.64
	432746	AA564512	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3948	2.64
	450377	AB033091	Hs.355925	Hs.355925:KIAA1265 protein	2.64
	434633	AI189587	Hs.120915	Hs.120915:ESTs	2.64
	424707	BE061914	Hs.10844	Hs.10844:leucine-rich alpha-2-glycoprote	2.64
55	427600	AW630918	Hs.179774	Hs.179774:proteasome (prosome, macropain	2.63
	446522	NM_003876	Hs.15198	NM_003876:Homo sapiens putative receptor	2.63
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility comp1	2.63
	410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63
	410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63
60	406716	AW148546	Hs.169476	Hs.169476:glyceraldehyde-3-phosphate deh	2.63
	430308	BE540865	Hs.238990	NM_004064:Homo sapiens cyclin-dependent	2.63
	431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	2.63
	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63
65	435958	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens Integr	2.63
	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	2.63
	447528	AI612027	Hs.76277	NM_138393:Homo sapiens hypothetical prot	2.63
	406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63
	439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63
70	435311	W86610	Hs.185738	Hs.185738:ESTs	2.63
	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	2.62
	410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fis	2.62
	414839	X63692	Hs.77462	(locuslink)NM_001379:Homo sapiens DNA (c	2.62
	443217	NM_001545	Hs.9078	Hs.9078:immature colon carcinoma transcr	2.62
75	448749	AW859679	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62
	450009	AI399947	Hs.166486	Hs.166486:Homo sapiens cDNA FLJ11432 fis	2.62
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	2.62
	442232	AI357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62
	419625	U91618	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62
80	416114	AI695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62
	439437	AI207788	Hs.343628	Hs.343628:sialyltransferase 4B (beta-gal	2.61
	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	2.61
	443142	AI696513	Hs.108705	Hs.108705:protein phosphatase 2 (bomert	2.61
	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61

	419687	AU077005	Hs.92208	NM_003815:Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876:hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.61
	403399				2.61
5	419579	W49529	Hs.296200	NM_023948:Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481:ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984:Homo sapiens small inducible c	2.61
	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.61
	446488	AB037782	Hs.15119	Hs.15119:KIAA1361 protein	2.61
10	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	2.60
	448204	AA751124	Hs.170561	Hs.170561:ESTs	2.60
	449175	AJ005892	Hs.23170	(locuslink)NM_012280:Homo sapiens FtsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509:ESTs, Weakly similar to C3HU com	2.60
	424805	AF230904	Hs.153260	NM_031892:Homo sapiens SH3-domain kinase	2.60
15	425421	L11669	Hs.157145	Hs.157145:tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	(locuslink)NM_004069:Homo sapiens adapto	2.60
	450858	C18458	Hs.25597	Hs.25597:elongation of very long chain f	2.59
	443185	BE148235	Hs.193063	Hs.193063:Homo sapiens cDNA FLJ14201 fis	2.59
	430504	H52761	Hs.44095	Hs.44095:cyclin M3	2.59
20	439578	AW263124	Hs.350547	NM_024665:Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	(locuslink)NM_024647:Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239:zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001521:Homo sapiens general transcrip	2.59
25	422140	BE295918	Hs.112193	(locuslink)NM_025259:Homo sapiens chromo	2.59
	452817	AA322659	Hs.284275	Hs.284275:p21 (CDKN1A)-activated kinase	2.59
	413353	AW293542	Hs.75309	Hs.75309:eukaryotic translation elongat	2.59
	421700	BE515018	Hs.107014	NM_016641:Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66493	NM_016430:Homo sapiens Down syndrome cri	2.59
	440511	AF132959	Hs.7236	NM_015953:Homo sapiens eNOS interacting	2.59
30	407887	AA579668	Hs.41072	(locuslink)NM_004568:Homo sapiens serine	2.59
	423556	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.59
	408102	U48351	Hs.621	Hs.621:lectin, galactoside-binding, solu	2.59
	417952	AI192838	Hs.173135	Hs.173135:dual-specificity tyrosine-(Y)-	2.59
	433053	BE301909	Hs.279952	NM_015917:Homo sapiens glutathione S-tra	2.59
35	450935	BE514743	Hs.379039	NM_005851:Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	(locuslink)NM_021959:Homo sapiens protel	2.59
	438364	AK000860	Hs.6191	NM_020441:Homo sapiens coronin, actin-bi	2.59
	430976	AA505112	Hs.282990	NM_033550:Homo sapiens chromosome 20 ope	2.58
40	444838	AV651680	Hs.208558	Hs.208558:ESTs	2.58
	416435	AI431301	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452:solute carrier family 20 (phosp	2.58
	452222	AW806287	Hs.21432	Hs.21432:SEX gene	2.58
	400541				2.58
45	444309	U83236	Hs.10803	Hs.10803:calcium and Integrin binding 1	2.58
	416116	H51847	Hs.99858	Hs.99858:ribosomal protein L7a	2.58
	418629	BE247550	Hs.86859	(locuslink)NM_005310:Homo sapiens growth	2.58
	432995	AF105025	Hs.279901	Hs.279901:PTD009 protein	2.57
	426781	AL048967	Hs.172207	(locuslink)NM_007363:Homo sapiens non-PO	2.57
50	452636	BE615074	Hs.145279	Hs.145279:SET translocation (myeloid leu	2.57
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	2.57
	447674	BE270840	Hs.19192	NM_001798:Homo sapiens cyclin-dependent	2.57
	445647	AV654627	Hs.271808	Hs.271808:Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	2.57
	402861				2.57
55	450069	AI698139	Hs.202093	Hs.202093:ESTs	2.57
	414029	BE297731	Hs.75709	NM_002355:Homo sapiens mannose-6-phospha	2.57
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.57
	449961	AW265634	Hs.133100	Hs.133100:ESTs	2.56
60	449378	AW684026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	2.56
	442599	AF078037	Hs.324051	(locuslink)NM_006663:Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21635	NM_001070:Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844:Homo sapiens protein tyrosine	2.56
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	2.56
65	451664	AJ076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	2.56
	457601	AF041429	Hs.284265	(locuslink)NM_145169:Homo sapiens simila	2.56
	439630	AA313607	Hs.58633	Hs.58633:Homo sapiens cDNA: FLJ22145 fis	2.55
	419587	S62907	Hs.91343	NM_000807:Homo sapiens gamma-aminobutyl	2.55
	448279	BE250564	Hs.283655	Hs.283655:lysophospholipase II	2.55
70	453350	AI917771	Hs.61790	(locuslink)NM_024658:Homo sapiens import	2.55
	423720	AL044191	Hs.23388	NM_030817:Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087:Homo sapiens angio-associated,	2.55
	420856	BE513294	Hs.205736	Hs.205736:KIAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584:ribosomal protein S6 kinase, 9	2.55
75	434848	BE256304	Hs.32148	NM_018445:Homo sapiens AD-015 protein (L	2.55
	424488	AK000413	Hs.149227	(locuslink)NM_017806:Homo sapiens hypoth	2.55
	449089	O78850	Hs.250465	Hs.250465:Homo sapiens mRNA; cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673:Homo sapiens SEC13-like 1 (S.	2.55
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	2.55
80	407755	AI151353	Hs.29742	Hs.29742:Homo sapiens cDNA FLJ32147 fis	2.55
	446573	NM_016361	Hs.15871	NM_016381:Homo sapiens LPAP for lysophos	2.55
	411766	AA399871	Hs.71969	Hs.71969:Homo sapiens mRNA; cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943:natural killer cell transcript 4	2.55
	436495	BE258948	Hs.290874	Hs.290874:Homo sapiens, clone MGC:31984	2.55

5	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.55
	443358	H55417	Hs.17757	(locuslink)NM_021622:Homo sapiens plecks	2.55
	452349	A8028944	Hs.29189	Hs.29189:ATPase, Class VI, type 11A	2.55
	427721	A1582843	Hs.180455	NM_005053:Homo sapiens RAD23 homolog A (2.54
	407559	AA313352	Hs.280858	Hs.280858:Homo sapiens cDNA FLJ32370 fis	2.54
10	413426	U88837	Hs.75354	Hs.75354:GCN1 general control of amino-a	2.54
	425465	L18964	Hs.1904	Hs.1904:protein kinase C, tota	2.54
	444152	A1125694	Hs.149305	Hs.149305:hypothetical protein MGC2603	2.54
	451820	AW058357	Hs.199248	NM_000958:Homo sapiens prostaglandin E r	2.54
	441356	BE384361	Hs.182885	(locuslink)NM_004556:Homo sapiens nuclea	2.54
15	444410	BE387360	Hs.33719	Hs.33719:Homo sapiens, similar to data s	2.54
	415200	AL040328	Hs.78202	NM_003072:Homo sapiens SWI/SNF related,	2.54
	403955				2.54
	430361	A1033965	Hs.239926	Hs.239926:sterol-C4-methyl oxidase-like	2.54
	432401	NM_013330	Hs.274479	NM_013330:Homo sapiens NME7 (NME7), mRNA	2.54
20	446719	W39500	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.54
	439941	A1392640	Hs.18272	NM_030674:Homo sapiens solute carrier fa	2.54
	436685	W28661	Hs.5288	Hs.5288:Homo sapiens mRNA; cDNA DKFZp434	2.54
	424522	AL134847	Hs.149957	Hs.149957:ribosomal protein S6 kinase, 9	2.54
	442904	AW575008	Hs.11355	Hs.11355:thymopoietin	2.54
25	422605	H16646	Hs.118666	Hs.118666:hypothetical protein PP591	2.54
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cDNA FLJ32174 fis	2.54
	447362	AW176120	Hs.9061	NM_024099:Homo sapiens hypothetical prot	2.53
	416305	AU076628	Hs.79187	NM_001338:Homo sapiens coxsackie virus a	2.53
	422624	BE616678	Hs.76152	NM_006854:Homo sapiens KDEL (Lys-Asp-Glu	2.53
30	447298	BE617527	Hs.239818	NM_006219:Homo sapiens phosphoinositide-	2.53
	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.53
	404854				2.53
	415761	AA132665	Hs.78802	(locuslink)NM_002093:Homo sapiens glycog	2.53
	431104	AW970859	Hs.313503	Hs.313503:ESTs	2.53
35	439180	A1393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukem	2.53
	424260	AF073310	Hs.143648	NM_003749:Homo sapiens Insulin receptor	2.53
	452878	AW081128	Hs.246374	Hs.246374:Homo sapiens cDNA FLJ31250 fis	2.53
	415742	BE410243	Hs.78769	NM_003249:Homo sapiens thimet oligopepti	2.53
	404140				2.53
40	407255	AA012992	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.53
	422509	AA258513	Hs.117865	Hs.117865:solute carrier family 17 (anlo	2.53
	434866	AW002565	Hs.355460	Hs.355460:Homo sapiens cDNA: FLJ21763 fi	2.53
	429743	AA804398	Hs.288995	(locuslink)NM_017961:Homo sapiens hypoth	2.53
	433047	M86135	Hs.279946	NM_004990:Homo sapiens methionine-tRNA s	2.53
45	418945	BE246762	Hs.89499	Hs.89499:arachidonate 5-lipoxygenase	2.52
	445926	AF054284	Hs.334826	NM_012433:Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784	Hs.279784:prolactin regulatory element b	2.52
	448252	BE622791	Hs.12199	NM_030577:Homo sapiens hypothetical prot	2.52
	447365	BE383878	Hs.334	(locuslink)NM_005435:Homo sapiens Rho gu	2.52
50	414844	AA296874	Hs.77494	NM_080916:Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093	NM_015945:Homo sapiens ovarian cancer ov	2.52
	416149	AA311965	Hs.79058	NM_003168:Homo sapiens suppressor of Ty	2.52
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ31263 fis,	2.52
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.52
55	445625	BE246743	Hs.353181	(locuslink)NM_025092:Homo sapiens hypoth	2.52
	431555	AF161470	Hs.260622	Hs.260622:butyrate-induced transcript 1	2.52
	410179	W27723	Hs.59498	(locuslink)NM_003718:Homo sapiens cell d	2.52
	431476	BE612705	Hs.256697	(locuslink)NM_005340:Homo sapiens histid	2.52
	406672	M26041	Hs.198253	(locuslink)NM_002122:Homo sapiens major	2.52
60	418180	BE618087	Hs.83724	Hs.83724:hypothetical protein MGC5466	2.52
	428248	A1126772	Hs.40479	Hs.40479:Homo sapiens cDNA FLJ25802 fis,	2.52
	419935	A8020580	Hs.93832	Hs.93832:putative membrane protein	2.52
	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.52
	426691	NM_006201	Hs.171834	(locuslink)NM_006201:Homo sapiens PCTAIR	2.51
65	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726	NM_003651:Homo sapiens cold shock domain	2.51
	428921	Z43809	Hs.194638	Hs.194638:polymerase (RNA) II (DNA direc	2.51
	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.51
	422607	Z45471	Hs.118684	NM_006923:Homo sapiens stromal cell-deri	2.51
70	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515	NM_002224:Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861	NM_015959:Homo sapiens CG1-31 protein (L	2.51
	438393	AA351815	Hs.50740	Hs.50740:Homo sapiens mRNA; cDNA DKFZp76	2.51
	418360	AW296974	Hs.84264	NM_006401:Homo sapiens acidic (leucine-r	2.50
75	401061				2.50
	426559	AB001914	Hs.170414	Hs.170414:paired basic amino acid cleavi	2.50
	412204	A1125507	Hs.24937	Hs.24937:transformer-2 alpha (htra-2 alp	2.50
	448950	AF288687	Hs.9275	NM_020410:Homo sapiens CG1-152 protein (2.50
	409936	AK001691	Hs.57655	(locuslink)NM_018234:Homo sapiens dudul	2.50
80	414675	R79015	Hs.288968	Hs.288968:RAS22A, member RAS oncogene fa	2.50
	409983	D50922	Hs.57729	(locuslink)NM_012289:Homo sapiens Kelch-	2.50
	450914	A1743761	Hs.142528	Hs.142528:ESTs	2.50
	444630	A1753230	Hs.323562	(locuslink)NM_032121:Homo sapiens hypoth	2.50
	401353				2.50
80	441680	AW444598	Hs.7940	(locuslink)NM_021159:Homo sapiens RAP1,	2.50
	408860	AA876469		AA876469:oe48b04.s1 NCL_CGAP_Pr25 Homo s	2.50
	449163	AW161356	Hs.23119	NM_003492:Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimerin (chimaerin) 2	2.50
430600	AW950967	Hs.274348	NM_004639:Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173:hypothetical protein FLJ10803	2.50

5 TABLE 9B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

10	Pkey	CAT Number	Accession
	406685	0_0	M18728
	452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AB58183
	451129	1495511_1	BE072881 A1762181 BE072946
15	459306	223120_4	AW578452
	448489	2189115_1	R45782 R45781
	418869	12789_14	AA229762 AA230035
	418546	242836_1	T59708 AA224827 T59843 BE156903
20	455303	1152492_1	BE066891 BE066895 AW892049 BE066897 BE903884
	406860	0_0	AA876469

TABLE 9C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

30	Pkey	Ref	Strand	NL_position
	406399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
	403218	7630969	Plus	58039-58149
35	403221	7630969	Plus	68294-66438,66936-67124
	403219	7630969	Plus	61858-61995
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
40	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
	400529	9796988	Plus	138232-138423
	404826	6572184	Plus	47726-48046
	400750	8119067	Plus	198991-199168,199316-199548
	400847	9188605	Plus	44643-44835
45	400448	9887687	Minus	177372-177674
	402829	8918414	Plus	101532-101852,102008-102263
	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	404240	5002624	Minus	116132-118407,116653-116922
50	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	406363	9256114	Plus	14403-14602,17000-17147,17241-17368
	405203	7230116	Plus	125295-125463
	402104	8119072	Plus	122409-122600
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
55	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	403483	9966188	Minus	144546-144854
	400509	9796539	Minus	157909-158430
	403399	6684178	Plus	61841-62145,62367-62756
60	400541	7574902	Plus	126235-126380,126478-126597
	402861	2814366	Minus	14933-15231,15387-15627
	403955	7770475	Minus	54527-54740
	404854	7143420	Plus	14260-14537
	404140	9843520	Plus	37761-38147
65	401061	3242744	Minus	99468-99549,100707-100848,100918-101107,
	401353	9931295	Minus	50831-51352

70 Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75 TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

80 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 UnigenTitle: Unigene gene title
 Rt: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	435749	AA584890	Hs.5302	NM_006149:Homo sapiens lactin, galactosi	15.54
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	14.52
	446787	U87187	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	14.04
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S384_H	14.02
	423541	AA286922	Hs.129778	NM_014471:Homo sapiens serine protease I	13.72
10	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	13.44
	418406	X73501	Hs.84905	Hs.84905:cryotokeratin 20	12.70
	406667	M12523			12.42
	416768	AA383733	Hs.1032	NM_006507:Homo sapiens regenerating iste	11.98
	437835	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	11.58
15	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	11.50
	418888	AU076801	Hs.89436	NM_004083:Homo sapiens cadherin 17, U c	10.16
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	9.77
20	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	9.69
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	9.48
	453863	X02544	Hs.572	Hs.572:corosomucoid 1	9.20
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.18
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
25	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	8.69
	430178	AW449612	Hs.152475	Hs.152475:ESTs	8.51
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	8.43
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	8.17
	409683	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
30	431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small i	8.08
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	8.06
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (7.95
	436624	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid bindin	7.74
	410407	X68839	Hs.63287	NM_001216:Homo sapiens carbonic anhydras	7.48
35	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	7.41
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	7.40
	412374	X01388	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-	7.34
	407244	M10014			7.31
	419741	NM_007019	Hs.93002	Hs.93002:ubiquitin-conjugating enzyme E2	7.31
40	406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	7.26
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	7.21
	404519				7.18
	413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	7.13
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	7.10
45	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	7.02
	430828	AI763257	Hs.86327	Hs.86327:homeo box B9	6.83
	433927	AI557019	Hs.116467	NM_032391:Homo sapiens small nuclear pro	6.81
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	6.78
	423538	AW603823	Hs.146268	Hs.146268:ESTs, Weakly similar to C71400	6.53
50	434206	AW136973	Hs.362915	Hs.362915:Homo sapiens cDNA FLJ34876 fis	6.37
	409041	AB033025	Hs.50081	Hs.50081:KIAA1199 protein	6.33
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.19
	436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (re	6.01
55	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	6.00
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	5.97
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	5.94
	420823	AF097021	Hs.273321	NM_005418:Homo sapiens differentially ex	5.94
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homcl	5.90
60	420802	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	5.89
	431727	AW293464	Hs.162031	Hs.162031:ESTs	5.85
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	5.84
	432023	AW273128	Hs.300268	Hs.300268:EST	5.75
65	447033	AJ357412	Hs.157601	Hs.157601:ESTs	5.69
	411734	AW374954	Hs.71779	Hs.71779:ESTs, Weakly similar to S24C_AR	5.69
	406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	5.55
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	5.48
	443247	BE614387	Hs.333893	Hs.333893:cell division cycle associated	5.45
70	409153	W03754	Hs.50813	NM_017625:Homo sapiens Intelectin (ITLN)	5.44
	449388	H53191	Hs.36723	Hs.36723:ESTs, Weakly similar to C05G5.5	5.38
	428046	AW812795	Hs.337534	Hs.337534:Homo sapiens cDNA FLJ25241 fis	5.38
	433013	AI697690	Hs.127337	(locuslink)NM_004655:Homo sapiens axin 2	5.38
	419079	AW014838	Hs.18844	Hs.18844:ESTs	5.37
75	428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	6.35
	422956	BE545072	Hs.122579	(locuslink)NM_018098:Homo sapiens epithe	6.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysl	5.30
	450543	AJ394037	Hs.170296	Hs.170296:Homo sapiens cDNA: FLJ22090 fi	5.30
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	5.30
80	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	5.28
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	5.28
	427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 ope	5.26
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	5.26
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	5.21
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	5.16

5	447208	BE315291	Hs.237971	NM_024096:Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004863:Homo sapiens guanylate cyclase	5.12
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.07
	447342	A1199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	5.06
	452194	A1694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	4.99
	406399				4.98
10	403220				4.94
	408380	AF123050	Hs.44532	NM_006398:Homo sapiens ubiquitin D (UBD)	4.92
	415214	A1445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPH2), tr	4.92
	431330	X69532	Hs.2777	NM_002215:Homo sapiens Inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protol	4.84
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	4.81
15	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
	444666	BE293347	Hs.11638	(locuslink)NM_016234:Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78619	(locuslink)NM_003878:Homo sapiens gamma-	4.80
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	4.80
	455630	AV655701	Hs.75183	NM_000773:Homo sapiens cytochrome P450,	4.78
20	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	4.78
	423337	NM_004655	Hs.127337	NM_004655:Homo sapiens adn 2 (conductin	4.75
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	4.73
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	4.70
25	423936	U77629	Hs.135639	NM_005170:Homo sapiens achaete-scute com	4.70
	404661				4.68
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (l iso)	4.61
30	427506	AK000134	Hs.179100	NM_016768:Homo sapiens hypothetical prot	4.60
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	4.59
	453884	AA355925	Hs.36232	NM_021067:Homo sapiens KIAA0186 gene pro	4.55
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.54
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	4.54
35	449032	AA045573	Hs.22900	NM_004289:Homo sapiens nuclear factor (e	4.54
	434540	NM_016045	Hs.3945	NM_016045:Homo sapiens chromosome 20 ope	4.54
	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	4.53
	458748	A1381530	Hs.371132	Hs.371132:ESTs	4.53
	408298	A1745325	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.51
40	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	4.50
	411975	A1916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	4.49
	425371	D49441	Hs.165981	NM_005823:Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
45	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
	430294	A1538226	Hs.32976	(locuslink)NM_004485:Homo sapiens guanin	4.42
	411248	AA551538	Hs.69321	Hs.69321:KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083:Homo sapiens glutathione perox	4.37
50	434414	A1799376		AF134163:Homo sapiens Human endogenous r	4.36
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	4.35
	422539	AJ009938	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	4.33
	450531	AW301032	Hs.203800	Hs.203800:ESTs	4.33
	403055				4.31
55	414809	A1434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	4.31
	400965				4.30
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	4.29
	432978	AF126743	Hs.278884	NM_013238:Homo sapiens DNAJ domain-conta	4.29
60	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:225881	4.28
	430832	A1073913	Hs.100686	Hs.100686:anterior gradient protein 3	4.28
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	4.27
	414617	A1339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	4.27
65	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	4.27
	439211	A1890347	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.27
	459299	BE094291	Hs.155651	NM_021784:Homo sapiens hepatocyte nuclea	4.25
	449720	AA311152	Hs.288708	(locuslink)NM_025113:Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc6S-betaGa	4.24
70	421777	BE562088	Hs.108196	NM_016095:Homo sapiens HSPC037 protein (4.21
	418395	BE268326	Hs.90280	Hs.90280:5-aminomidazole-4-carboxamide	4.20
	443211	A1128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading tra	4.19
75	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	4.19
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	4.19
	421408	A1688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.18
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	4.18
	440869	NM_014297	Hs.7488	NM_014297:Homo sapiens protein expressed	4.17
80	441075	U11862	Hs.75741	NM_001091:Homo sapiens amiloride binding	4.17
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125608	Hs.125608:ESTs	4.16
	445584	AB028957	Hs.12896	Hs.12896:KIAA1034 protein	4.16
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	4.12

	401868			Hs.264428:tissue specific transplanta	9.11
	431611	U58766	Hs.264428	Hs.158989:Homo sapiens cDNA FLJ37836 fis	4.10
	430187	A1799309	Hs.158989	NM_000506:Homo sapiens coagulation facto	4.10
	414590	NM_000506	Hs.76530	NM_032756:Homo sapiens hypothetical prot	4.08
	449281	A1808699	Hs.162717	Hs.23960cystin B1	4.08
	449722	BE280074	Hs.23960	NM_004616:Homo sapiens transmembrane 4 s	4.08
	418318	UA7732	Hs.84702	NM_001363:Homo sapiens dyskeratosis cong	4.06
	435066	BE261750	Hs.4747	NM_006437:Homo sapiens ADP-ribosyltransf	4.05
	414753	AF158255	Hs.77225		4.04
10	403221				4.04
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.03
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.03
	431657	A1345227	Hs.105448	Hs.105448:protein kinase, lysine deficite	4.01
	439759	A1359055	Hs.67709	Hs.67709:Homo sapiens mRNA full length l	4.00
	441362	BE614410	Hs.23044	NM_080668:Homo sapiens similar to RIKEN	3.99
	417900	BE250127	Hs.82906	Hs.82906:CDCC20 cell division cycle 20 ho	3.99
	428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.89
	456877	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
	445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGCI14141	3.98
	432164	AK000032	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, bs	3.97
	422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	3.97
	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
25	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	3.86
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.95
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
	408243	Y00787	Hs.624	NM_000584:Homo sapiens Interleukin 8 (IL	3.94
	408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 fts	3.94
	412610	X90908	Hs.74126	NM_001445:Homo sapiens fatty acid bindin	3.94
30	433323	AA805132	Hs.159142	Hs.159142:lunatic fringe homolog (Drosop	3.94
	422515	AW500470	Hs.117950	Hs.117950:phosphoribosylaminoimidazole c	3.92
	436543	NM_002212	Hs.5215	Hs.5215:intrin beta 4 binding protein	3.91
	418113	A1272141	Hs.83484	Hs.83484:SRY (sex determining region Y)-	3.91
35	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	3.90
	431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE:4341	3.90
	453439	A1572438	Hs.32976	NM_004485:Homo sapiens guanine nucleotid	3.89
	441888	A1733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
40	425234	AW152225	Hs.165909	Hs.165909:ESTs, Weady similar to hypoth	3.89
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	3.87
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	3.85
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	3.85
	422424	A186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
45	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in ml	3.84
	416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic arre	3.83
	430680	AW138724	Hs.168974	Hs.168974:ESTs	3.83
50	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplaslin 1,	3.82
	436481	AA379597	Hs.5199	NM_014176:Homo sapiens HSPC150 protein s	3.82
	453700	AB009426	Hs.5650	NM_001644:Homo sapiens apolipoprotein B	3.81
	410619	BE512730	Hs.65514	Hs.65514:keralatin 18	3.81
55	409420	Z15008	Hs.54451	NM_005662:Homo sapiens laminin, gamma 2	3.79
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ0256	3.79
	432179	F57208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	3.78
	453987	AW009677	Hs.232947	Hs.232947:ESTs	3.78
	426106	AI678765	Hs.21812	Hs.21812:ESTs	3.78
	434170	AA626509	Hs.159642	(locuslink)NM_001490:Homo sapiens glucos	3.78
60	418322	AA284168	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	3.78
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	3.78
	419229	AJ827237	Hs.362919	Hs.362919:ESTs	3.74
	437156	AJ916600	Hs.121194	Hs.121194:Homo sapiens cDNA: FLJ21569 fi	3.74
	452833	BE559681	Hs.30736	(locuslink)NM_015201:Homo sapiens block	3.73
65	426831	BE296216	Hs.176273	NM_000687:Homo sapiens S-adenosylthiomocys	3.73
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid Ind	3.72
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	3.71
	408832	AW085690	Hs.63428	Hs.63428:Homo sapiens cDNA FLJ34457, SHAPY,	3.71
	440300	N39760	Hs.8859	NM_138793:Homo sapiens apyrase (SHAPY),	3.71
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	3.71
	432575	AA553722	Hs.194346	Hs.194346:Sp1-2 protein	3.71
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	3.71
70	417001	AU076848	Hs.80741	NM_000282:Homo sapiens propionyl Coenzym	3.69
	421225	AA463998	Hs.102696	Hs.102696:MCT-1 protein	3.69
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	3.69
75	428330	L22524	Hs.2256	NM_002423:Homo sapiens matrix metallopro	3.67
	447472	AW207347	Hs.211101	Hs.211101:ESTs	3.67
	423349	AF010258	Hs.127428	NM_002142:Homo sapiens homoo box A9 (HOX	3.67
	422206	U80736	Hs.110826	Hs.110826:trnucleotide repeat containin	3.66
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	3.66
80	417720	AA205625	Hs.201865	Hs.208067:ESTs	3.66
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	3.66
	421515	Y11339	Hs.105352	(locuslink)NM_018144:Homo sapiens GalNAc	3.65
	433675	AW977653	Hs.75319	Hs.75319:ribonucleotide reductase M2 pol	3.65

5	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	3.65
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	3.64
	412140	AA219691	Hs.73625	NM_005733:Homo sapiens RAB6 interacting,	3.64
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	3.63
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	3.63
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	3.62
	428862	NM_000346	Hs.2316	Hs.2316:SRF (sex determining region Y)-b	3.62
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	3.62
10	412056	T28160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
	401519				3.60
	428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
	421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens protin	3.58
15	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	3.58
	424544	M88700	Hs.150403	NM_000790:Homo sapiens dopa decarboxylas	3.58
	431563	AI027643	Hs.120912	Hs.120912:ESTs	3.57
	435602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
	434369	AI650383	Hs.118462	Hs.118462:ESTs	3.57
20	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	3.56
	447334	AA515032	Hs.91109	Hs.91109:ESTs, Weakly similar to putativ	3.56
	422150	AI867118	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	3.56
	450663	H43540	Hs.25292	Hs.25292:ribonuclease H2, large subunit	3.56
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
25	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	3.55
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	3.55
	422532	AL008726	Hs.118126	(locuslink)NM_000308:Homo sapiens proteo	3.55
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
	442053	R35343	Hs.24968	Hs.24968:hypothetical protein BC016683	3.55
30	437386	W52452	Hs.356766	Hs.356766:Homo sapiens mRNA; cDNA DKFZp7	3.54
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	3.53
	446372	AB020644	Hs.14945	Hs.14945:fatty-acid-Coenzyme A ligase, I	3.53
	432378	AI493046	Hs.146133	Hs.146133:ESTs	3.53
	434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
35	428479	Y00272	Hs.334582	NM_001786:Homo sapiens cell division cyc	3.52
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	3.51
	414918	AI219207	Hs.72222	Hs.72222:fer-1-like 4 (C. elegans)	3.51
	440340	AW895503	Hs.125276	Hs.125276:Homo sapiens cDNA FLJ25833 fis	3.51
	418384	AW149266	Hs.25130	Hs.25130:Homo sapiens cDNA FLJ14923 fis,	3.51
40	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	3.51
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	3.51
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	3.50
	431567	N51357	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.50
	453883	AI638516	Hs.347524	Hs.347524:Homo sapiens, clone MGC:24665	3.50
45	442700	AA377818	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
	410237	AI760589	Hs.61258	Hs.61258:argininosuccinate lyase	3.50
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
	436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
	442923	AW248322	Hs.95835		3.49
50	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	3.48
	448993	AI471630	Hs.355952	Hs.355952:ESTs, Weakly similar to 090320	3.48
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23556	3.48
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	3.47
55	420996	AK001927	Hs.100895	(locuslink)NM_018099:Homo sapiens hypoth	3.47
	439580	AF086401	Hs.293847	Hs.293847:ESTs	3.46
	422158	L10343	Hs.112341	NM_002638:Homo sapiens protease inhibito	3.46
	418256	AW845318	Hs.12271	(locuslink)NM_012162:Homo sapiens F-box	3.46
	400157		Hs.356473	NM_006713:Homo sapiens activated RNA pol	3.46
60	406709	AI355761	Hs.242463	Hs.242463:keratin 8	3.46
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
	421526	AL080121	Hs.105460	NM_015393:Homo sapiens DKFZP564O0823 pro	3.45
	415164	AW084352	Hs.157123	Hs.157123:ESTs	3.45
	405451				3.44
65	414361	AI086138	Hs.204044	Hs.204044:ESTs	3.44
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.44
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	3.43
	450983	AA305384	Hs.25740	NM_014584:Homo sapiens ERO1-like (S. cer	3.43
70	421828	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.42
	418588	BE387040	Hs.182476	NM_031295:Homo sapiens Williams Beuren s	3.42
	417348	AI940507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
	423554	M90516	Hs.1674	NM_002056:Homo sapiens glutamine-fructos	3.42
	451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 cpe	3.41
75	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	3.41
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
	437575	AW954355	Hs.36529	NM_024320:Homo sapiens hypothetical prot	3.40
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alpha	3.40
	439955	AW203959	Hs.149532	Hs.149532:ESTs	3.40
80	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	3.40
	435745	AW967059	Hs.374342	Hs.374342:Homo sapiens clone 24711 mRNA	3.40
	403532				3.39
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.39
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	3.39

	424956	AF006005	Hs.154104	NM_002657:Homo sapiens plasmaloma aden	3.38
	402944				3.37
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 f	3.37
5	427528	AU077143	Hs.179565	NM_002388:Homo sapiens MCM3 minichromosome	3.37
	426711	AA383471	Hs.343800	(locuslink)NM_033255:Homo sapiens epithel	3.37
	439186	AI697274	Hs.105435	Hs.105435:GDP-mannose 4,6-dehydratase	3.36
	444783	AK001468	Hs.62180	NM_018685:Homo sapiens anillin, actin bi	3.36
	426174	AA547959	Hs.115838	Hs.115838:ESTs	3.36
10	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	3.36
	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	3.36
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	3.34
15	458946	T29678	Hs.166068	Hs.166068:villin 1	3.33
	425580	L11144	Hs.1907	Hs.1907:gelsolin	3.33
	412605	AW410734	Hs.74111	Hs.74111:RNA binding protein (autoantige	3.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 f	3.33
	416782	L35035	Hs.79886	(locuslink)NM_144563:Homo sapiens ribose	3.33
20	426761	AI015709	Hs.172089	Hs.172089:pro-oncogene receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_004131	Hs.1051	NM_004131:Homo sapiens granzyme B (granz	3.31
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	3.31
	431192	AI870058	Hs.137274	Hs.137274:ESTs, Weakly similar to hypo	3.30
25	431836	AF17532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 f	3.30
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	3.29
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 f	3.29
30	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403381				3.28
	434031	BE384165	Hs.23723	(locuslink)NM_025215:Homo sapiens pseudo	3.28
35	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.28
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Hs.75113:general transcription factor II	3.28
	443162	T49951	Hs.9029	(locuslink)NM_015515:Homo sapiens type I	3.28
40	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	3.28
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	3.28
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Hs.90073:CSE1 chromosome segregation 1-I	3.27
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.27
	444371	BE540274	Hs.239	Hs.239:forkhead box M1	3.27
45	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kD	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens aldehyde 1 (lyso	3.27
	403485				3.27
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	3.26
50	421943	BE516520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-tRN	3.26
	404684				3.25
55	447188	H65423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Hs.146109:ESTs, Weakly similar to T28937	3.24
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.24
	424243	AI949359	Hs.143600	Hs.143600:glut1 phosphoprotein 4	3.24
60	435014	BE560898	Hs.10026	NM_022061:Homo sapiens ribosomal protein	3.24
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 f	3.24
	416065	BE267831	Hs.78996	NM_002692:Homo sapiens proliferating cel	3.23
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	3.23
	432035	AA524725	Hs.162108	Hs.162108:ESTs	3.23
65	408868	AW292286	Hs.255058	Hs.255058:ESTs	3.23
	429504	X99133	Hs.204238	Hs.204238:lipocalin 2 (oncogene 24p3)	3.22
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 f	3.22
	426991	AK001536	Hs.214410	Hs.214410:Homo sapiens cDNA FLJ31573 f	3.22
70	408901	AK001330	Hs.48855	(locuslink)NM_018101:Homo sapiens hypoth	3.22
	439979	AW600291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Hs.62711:Homo sapiens, clone IMAGE:33512	3.22
	457465	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
	414639	X87055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	3.21
75	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inositol triphosph	3.20
	444261	AA298958	Hs.10724	Hs.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box HB9 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	3.20
80	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	3.19
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX)	3.19
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.19
	400290	H18836	Hs.31608	(locuslink)NM_017638:Homo sapiens transl	3.18

5	419239	AA468183	Hs.335788	(locuslink)NM_033103:Homo sapiens rhophi	3.18
	426215	AW963419	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (3.18
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	3.17
	413313	NM_002047	Hs.293885	NM_002047:Homo sapiens glycyl-tRNA synth	3.17
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015869:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1350	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
10	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	3.16
	416984	H38765	Hs.80706	NM_000903:Homo sapiens NAD(P)H dehydrog	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mesenchymal stem	3.16
	406708	AI282759		AI282759:qt84a01.x1 NCL CGAP_Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
15	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.15
20	446595	T57448	Hs.15467	NM_017943:Homo sapiens hypothetical prot	3.15
	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.15
25	436391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.14
	432370	AA308334	Hs.274424	NM_018946:Homo sapiens N-acetylnearmini	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	3.14
	417791	AW965339	Hs.44269	Hs.44269:Homo sapiens cDNA FLJ37972 fis,	3.14
30	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	3.13
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomulas	3.13
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.13
	446386	AI032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AF228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.11
40	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA: cDNA DKFZp5	3.11
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	425427	M86699	Hs.169840	Hs.169840:TTK protein kinase	3.11
	409162	H25630	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (3.10
45	434861	AA208153	Hs.4209	NM_018491:Homo sapiens mitochondrial rib	3.10
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	3.10
	414808	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
50	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
	421470	R27496	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW582256	Hs.91011	NM_006408:Homo sapiens anterior gradient	3.09
	418691	AW752389	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fis,	3.08
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	3.08
55	447760	AI431328	Hs.348605	NM_052963:Homo sapiens mitochondrial top	3.08
	405508				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410168	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
60	422880	AF228704	Hs.193974	Hs.193974:glutathione reductase	3.08
	442013	AA506476	Hs.376009	Hs.376009:Homo sapiens mRNA: cDNA DKFZp6	3.08
	431722	AF161528	Hs.268049	(locuslink)NM_016101:Homo sapiens hypoth	3.08
	421508	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439492	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to T06291	3.07
65	417866	AW087903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
	412530	AA766268	Hs.266273	(locuslink)NM_024918:Homo sapiens chromo	3.07
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW951952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12683 fis	3.06
	424971	AA478005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	3.05
	439273	AW139099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ25668 fis	3.05
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.05
	435703	AW630133	Hs.83313	(locuslink)NM_020192:Homo sapiens GK003	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fis	3.04
75	403739				3.04
	444664	N26382	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.04
	409152	AA176585	Hs.194346	Hs.194346:Spr-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015938:Homo sapiens CGI-04 protein (L	3.04
	406545				3.03
80	450553	AW850613	Hs.8715	Hs.8715:hypothetical protein MGC3232	3.03
	418867	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434523	AA703709	Hs.23410	(locuslink)NM_016539:Homo sapiens skt1	3.03
	440088	BE559877	Hs.183232	NM_024839:Homo sapiens hypothetical prot	3.02

	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.02
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	3.02
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
5	422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
	417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
10	436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (3.01
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens displa	3.01
	417678	X06560	Hs.82396	(locuslink)NM_002534:Homo sapiens 2',5'-	3.01
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.00
	429983	W92620	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.00
15	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.00
	414732	AW410976	Hs.77152	Hs.77152:MCM7 minichromosome maintenance	3.00
	409614	BE297412	Hs.55189	NM_016489:Homo sapiens 5'-nucleotidase,	3.00
	439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
	411096	U80034	Hs.68583	NM_005932:Homo sapiens mitochondrial int	2.99
20	433312	AI241331	Hs.131765	Hs.131765:ESTs, Moderately similar to l3	2.99
	420767	AF072711	Hs.99918	Hs.99918:carboxyl ester lipase (bile sal	2.99
	429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
	423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
	420552	AK000492	Hs.98806	Hs.98806:hypothetical protein FLJ20485	2.99
25	413380	AI904232	Hs.75323	Hs.75323:prohibitin	2.99
	421533	N71826	Hs.105465	NM_003095:Homo sapiens small nuclear rib	2.99
	439352	BE614347	Hs.169615	NM_023080:Homo sapiens hypothetical prot	2.98
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	2.98
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.98
30	457211	AW972565	Hs.32399	(locuslink)NM_145240:Homo sapiens simila	2.98
	410467	AF102546	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
	422066	AW249275	Hs.343521	Hs.343521:malate dehydrogenase 2, NAD (m	2.97
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
	453012	T95804	Hs.31334	NM_012469:Homo sapiens chromosome 20 ope	2.97
35	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
	413813	M96956	Hs.75581	NM_003212:Homo sapiens teratocarcinoma-d	2.97
	418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
40	417911	AA333387	Hs.82916	Hs.82916:chaperonin containing TCP1, sub	2.96
	413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (2.96
	445462	AA378776	Hs.288649	(locuslink)NM_024061:Homo sapiens hypoth	2.96
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	2.96
	408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
45	421959	AW751497	Hs.98370	NM_030822:Homo sapiens cytochrome P450,	2.96
	459306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	2.96
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
50	406863	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.95
	432843	BE250865	Hs.279529	NM_013237:Homo sapiens p19-like protein	2.95
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	2.95
	410006	AW732308	Hs.57783	NM_003751:Homo sapiens eukaryotic transl	2.94
	442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	2.94
55	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
	427779	AA906997	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	2.94
	414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
	410817	AI262789	Hs.93659	(locuslink)NM_004911:Homo sapiens protei	2.93
60	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter sl	2.93
	426376	AF119565	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
	414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
	434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
65	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.93
	429048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	2.92
	422397	AJ223368	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
	426715	AB037855	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
	429539	AK001839	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
70	443715	AI583187	Hs.9700	NM_001238:Homo sapiens cyclin E1 (CCNE1)	2.92
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transl	2.92
	433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
	422558	NM_006420	Hs.118249	Hs.118249:ADP-ribosylation factor guanin	2.92
75	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
	429626	U36787	Hs.211571	NM_005333:Homo sapiens holocytochrome c	2.92
	413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
	442159	AW163390	Hs.278554	NM_007276:Homo sapiens chromobox homolog	2.92
80	400133		Hs.184693	NM_005648:Homo sapiens transcription elo	2.91
	419381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	2.91
	426108	AA522037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
	436278	BE396290	Hs.5097	Hs.5097:synaplogyrin 2	2.91
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

5	433487	U31814	Hs.3352	NM_001527: Homo sapiens histone deacetylase	2.91
	416933	BE561850	Hs.80506	NM_003090: Homo sapiens small nuclear rib	2.90
	430287	AW182459	Hs.125759	Hs.125759: likely ortholog of mouse RING	2.90
	434026	R15486	Hs.285218	(locuslink)NM_021213: Homo sapiens phosph	2.90
	447698	AI420156	Hs.326733	NM_052858: Homo sapiens similar to RUKEN	2.90
	411263	BE297802	Hs.69360	NM_006845: Homo sapiens kinesin-like 6 (m	2.90
	432754	BE241691	Hs.3100	Hs.3100: chyl-IRNA synthetase	2.90
	437016	AU076916	Hs.5398	Hs.5398: guanine monophosphate synthetase	2.90
10	446228	NM_016046	Hs.14415	NM_016046: Homo sapiens exosomal core pro	2.90
	420421	AF281133	Hs.343589	Hs.343589: exosome component Rrp41	2.89
	428385	AF112213	Hs.184062	Hs.184062: chromosome 20 open reading fra	2.89
	414420	AA043424	Hs.76095	NM_052815: Homo sapiens immediate early r	2.89
	457284	AF102850	Hs.227933	NM_013338: Homo sapiens Alg5, S. cerevisi	2.89
	401405				2.89
15	453111	AB014598	Hs.31720	NM_014799: Homo sapiens hephassin (HEPH)	2.89
	400247		Hs.356473	NM_006713: Homo sapiens activated RNA pol	2.89
	421910	NM_014586	Hs.109437	NM_014586: Homo sapiens hormonally upregu	2.89
	413610	AL117554	Hs.119908	NM_015934: Homo sapiens nucleolar protein	2.89
20	413588	AA971014	Hs.75432	NM_000884: Homo sapiens IMP (inosine mono	2.89
	418661	NM_001949	Hs.1189	NM_001949: Homo sapiens E2F transcription	2.88
	427490	Z95152	Hs.178695	NM_002754: Homo sapiens mitogen-activated	2.88
	417634	W27202	Hs.82327	NM_000178: Homo sapiens glutathione synth	2.88
	435099	AC004770	Hs.4756	NM_004111: Homo sapiens flap structure-sp	2.88
25	425811	AL039104	Hs.159557	NM_002266: Homo sapiens karyopherin alpha	2.88
	446849	AU076617	Hs.16251	(locuslink)NM_016207: Homo sapiens cleava	2.88
	412974	R18978	Hs.75105	NM_006579: Homo sapiens emopamil binding	2.88
	413179	N99692	Hs.75227	NM_005002: Homo sapiens NADH dehydrogenas	2.88
	407770	AW607831	Hs.38738	NM_014343: Homo sapiens claudin 15 (CLDN1	2.88
30	408847	AW290997	Hs.190153	Hs.190153: Homo sapiens cDNA FLJ33988 fis	2.87
	448250	NM_016034	Hs.20776	(locuslink)NM_016034: Homo sapiens mitoch	2.87
	428810	AF068236	Hs.193788	NM_000625: Homo sapiens nitric oxide synt	2.87
	427505	AA361562	Hs.178761	Hs.178761: 26S proteasome-associated pad1	2.87
	418443	NM_005239	Hs.85146	Hs.85146: v-ets erythroblastosis virus E2	2.87
35	447343	AA256641	Hs.236894	Hs.236894: ESTs, Highly similar to S02392	2.87
	409262	AK000631	Hs.52256	Hs.52256: hypothetical protein FLJ20624	2.87
	443323	BE560621	Hs.9222	Hs.9222: estrogen receptor binding site a	2.87
	450378	AW249181	Hs.154796	Hs.154796: Homo sapiens cDNA FLJ37976 fis	2.86
	411761	A1733848	Hs.71935	NM_021220: Homo sapiens zinc finger prote	2.86
40	415691	AW963979	Hs.24723	Hs.24723: ESTs	2.86
	417715	AW969587	Hs.86366	Hs.86366: ESTs	2.86
	452099	BE612992	Hs.27931	Hs.27931: hypothetical protein FLJ10607 s	2.86
	436138	H53323	Hs.25717	Hs.25717: Homo sapiens cDNA: FLJ23454 fis	2.86
	432858	BE618609	Hs.279591	Hs.279591: Homo sapiens, Similar to RNA p	2.86
45	434457	AF141332	Hs.200333	NM_018690: Homo sapiens apolipoprotein B4	2.86
	444237	AA336878	Hs.9842	Hs.9842: ESTs	2.85
	456362	AW973003	Hs.179909	(locuslink)NM_024831: Homo sapiens nuclea	2.85
	411393	AW797437	Hs.69771	NM_001710: Homo sapiens B-factor, properd	2.85
50	424270	AK001818	Hs.144407	NM_018283: Homo sapiens hypothetical prot	2.85
	414396	BE548266	Hs.76057	(locuslink)NM_000403: Homo sapiens galact	2.85
	426120	AA325243	Hs.166887	Hs.166887: xopline I	2.85
	446663	BE614599	Hs.356501	(locuslink)NM_032335: Homo sapiens hypoth	2.85
	443802	AW504924	Hs.9805	Hs.9805: exportin 5	2.85
	445863	R12234	Hs.13396	Hs.13396: Homo sapiens clone 25028 mRNA s	2.85
55	434808	AF155108	Hs.256150	Hs.256150: NY-REN-41 antigen	2.85
	440334	BE276112	Hs.7165	NM_003904: Homo sapiens zinc finger prote	2.85
	449057	AB037784	Hs.22941	Hs.22941: KIAA1363 protein	2.85
	432680	T47384	Hs.278613	(locuslink)NM_005532: Homo sapiens Interf	2.84
60	446421	BE297434	Hs.15071	Hs.15071: chaperonin containing TCP1, sub	2.84
	427239	BE270447	Hs.356512	Hs.356512: ESTs, Weakly similar to UBCCA_A	2.84
	425649	U30930	Hs.158540	(locuslink)NM_003360: Homo sapiens UDP gl	2.84
	429638	AI916662	Hs.211577	(locuslink)NM_004986: Homo sapiens kinect	2.84
	435777	AW419202	Hs.286192	NM_032192: Homo sapiens protein phosphata	2.84
	424441	X14850	Hs.147097	Hs.147097: H2A histone family, member X	2.84
65	407833	AW955632	Hs.66666	Hs.66666: chromosome 7 open reading frame	2.84
	415083	AI632683	Hs.27179	Hs.27179: Homo sapiens cDNA FLJ12933 fis,	2.83
	421462	AF016495	Hs.104624	NM_020980: Homo sapiens aquaporin 9 (AQP9	2.83
	443572	AA025810	Hs.9605	Hs.9605: cleavage and polyadenylation spe	2.83
70	443180	R15875	Hs.258576	NM_012129: Homo sapiens claudin 12 (CLDN1	2.83
	417573	U17760	Hs.75517	NM_000228: Homo sapiens lamlnr, beta 3 (2.83
	453028	AB006532	Hs.31442	NM_004260: Homo sapiens RecQ protein-like	2.83
	425047	U34038	Hs.154299	NM_005242: Homo sapiens coagulation facto	2.83
	432593	AW301003	Hs.51483	Hs.51483: Homo sapiens, Similar to RIKEN	2.83
	410197	NM_005518	Hs.59889	(locuslink)NM_005518: Homo sapiens 3-hydr	2.83
75	413095	AA494359	Hs.30715	Hs.30715: potassium voltage-gated channel	2.83
	417677	NM_016055	Hs.82389	NM_016055: Homo sapiens mitochondrial rib	2.83
	425263	NM_001197	Hs.155419	NM_001197: Homo sapiens BCL2-interacting	2.82
	437430	WA4871	Hs.124	NM_014628: Homo sapiens gene predicted fr	2.82
	428289	M26301	Hs.2253	Hs.2253: complement component 2	2.82
80	407137	T97307			2.82
	400750				2.82
	428788	AF082283	Hs.193516	NM_003921: Homo sapiens B-cell CLL/lympho	2.82
	432633	AI796390	Hs.210667	Hs.210667: ESTs	2.82
	432816	N38913	Hs.221575	Hs.221575: ESTs	2.82

5	410045	AA806930	Hs.58189	Hs.58189:eukaryotic translation Initiat	2.82
	454144	BE280478	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81
	434583	AA095761	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	2.81
10	428093	AW594506	Hs.104830	Hs.104830:ESTs	2.81
	416047	BE439894	Hs.78991	NM_012080:Homo sapiens DNA segment, nume	2.81
	447495	AW401884	Hs.18720	NM_004208:Homo sapiens programmed cell d	2.81
	452199	BE255643	Hs.110695	Hs.110695:hypothetical protein MGC3133	2.81
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	2.80
15	445921	AW015211	Hs.153789	Hs.153789:Homo sapiens cDNA FLJ38333 fis	2.80
	422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
	417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	2.80
	418731	AI264688	Hs.1197	NM_002157:Homo sapiens heat shock 10kD p	2.80
20	432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
	428028	U52112	Hs.182018	Hs.182018:Interleukin-1 receptor-associa	2.80
	441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
	409463	AI458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	2.79
	450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
25	418960	NM_004494	Hs.89525	(locuslink)NM_004494:Homo sapiens hepato	2.79
	401179				2.79
	419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
	434750	BE019254	Hs.4112	Hs.4112:complex 1	2.79
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
30	400529				2.79
	436414	BE264633	Hs.143638	NM_033681:Homo sapiens WD repeat domain	2.79
	436291	BE568452	Hs.344037	(locuslink)NM_003981:Homo sapiens protei	2.79
	427863	AK042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (2.79
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	2.79
35	413880	AI600842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	2.79
	442468	N77737	Hs.8349	NM_138933:Homo sapiens epobec-1 compleme	2.79
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
	413278	BE563085	Hs.833	Hs.833:Interferon-stimulated protein, 15	2.79
	430120	AW675298	Hs.233694	(locuslink)NM_018396:Homo sapiens putat	2.79
40	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	2.79
	417164	AA338283	Hs.81361	Hs.81361:heterogeneous nuclear ribonucle	2.79
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
	409638	AA305729	Hs.18272	(locuslink)NM_030874:Homo sapiens solute	2.78
	447619	AI174800	Hs.19054	(locuslink)NM_018530:Homo sapiens hypoth	2.78
45	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.78
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	2.78
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.78
	430612	AF182294	Hs.241578	NM_016200:Homo sapiens U6 snRNA-associat	2.78
50	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
	414697	BE266134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
	420665	AW469240	Hs.371581	Hs.371581:ESTs	2.78
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
55	443343	BE409809	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	2.77
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	2.77
	432543	AA552690	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fi	2.77
60	423271	W47225	Hs.126256	NM_000576:Homo sapiens interleukin 1, be	2.77
	410595	AW629223	Hs.64794	NM_006978:Homo sapiens zinc finger prote	2.77
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	2.77
	457757	AA434109	Hs.12271	NM_012162:Homo sapiens F-box and leucine	2.77
	420188	NM_015925	Hs.95697	Hs.95697:diver-specific bHLH-Zip transcr	2.77
65	410094	BE147897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
	403817				2.77
	459125	AA811383	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
	432705	AI879473	Hs.157123	Hs.157123:ESTs	2.77
	446658	AI440137	Hs.184989	NM_138492:Homo sapiens hypothetical prot	2.76
70	419485	AA489023	Hs.99807	Hs.99807:Homo sapiens mRNA; cDNA DKFZp31	2.76
	432866	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
	428438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
	414767	BE541381	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
	406830	AI829848	Hs.342389	Hs.342389:peptidylprolyl isomerase A (cy	2.76
75	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	2.76
	430450	R23553	Hs.241489	(locuslink)NM_015913:Homo sapiens hypoth	2.76
	433808	NM_014062	Hs.3566	Hs.3566:ART-4 protein	2.75
	431890	X17033	Hs.271986	NM_002203:Homo sapiens Integrin, alpha 2	2.75
	433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
80	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	2.75
	432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
	424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
	433862	D86960	Hs.3610	NM_014873:Homo sapiens KIAA0206 gene pro	2.75
	417080	BE392846	Hs.1063	Hs.1063:small nuclear ribonucleoprotein	2.75
	428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
	416188	BE157260	Hs.79070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75

5	419489	AW411280	Hs.90693	NM_013400:Homo sapiens replication Init	2.75
	407971	AM69117	Hs.62918	Hs.62918: CDC91 cell division cycle 91-B	2.75
	432403	AA550815	Hs.124840	(locuslink)NM_138456:Homo sapiens hypoth	2.75
	410775	AB014460	Hs.66196	NM_002528:Homo sapiens ntlh endonuclease	2.75
	444197	BE266947	Hs.10590	NM_016883:Homo sapiens zinc finger prote	2.75
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	2.75
	406806	AW088535	Hs.350108	Hs.350108:ribosomal protein, large, P0	2.75
	411580	AL080088	Hs.70877	NM_015421:Homo sapiens DKFZP564K2062 pro	2.75
10	433652	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	2.74
	426235	AI631964	Hs.34447	Hs.34447:Homo sapiens cDNA FLJ38512 fis,	2.74
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	2.74
	419713	AW968058	Hs.92381	NM_019094:Homo sapiens nudix (nucleosida	2.74
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	2.74
15	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	2.74
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	2.74
	452767	AW014195	Hs.61472	Hs.61472:Homo sapiens, clone IMAGE:51841	2.74
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	2.73
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	2.73
20	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	2.73
	444706	AK000398	Hs.11747	(locuslink)NM_017788:Homo sapiens chromo	2.73
	423908	AJ006422	Hs.135183	NM_008869:Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199:Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	2.73
25	452461	N78223	Hs.108106	Hs.108106:ubiquitin-like, containing PHD	2.73
	407699	AA825974	Hs.32646	NM_024622:Homo sapiens hypothetical prot	2.73
	412258	AA376768	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.73
	450256	AA286887	Hs.24724	Hs.24724:Homo sapiens cDNA FLJ39185 fis,	2.72
	443905	AI215948	Hs.143969	Hs.143969:ESTs	2.72
30	413274	NM_004893	Hs.75258	NM_004893:Homo sapiens H2A histone famil	2.72
	408885	C02741	Hs.48712	NM_017948:Homo sapiens hypothetical prot	2.72
	424585	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	2.72
	424692	AA429834	Hs.151791	NM_014679:Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_002014:Homo sapiens FK506 binding pro	2.72
35	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	2.72
	450164	AI239923	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.71
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.71
	450897	W16741	Hs.351629	NM_014017:Homo sapiens HSPC003 protein (2.71
	447349	AI375546		BE743847:601577765F1 NIH_MGC_9 Homo sapi	2.71
40	445413	AA151342	Hs.12677	(locuslink)NM_016077:Homo sapiens CGI-14	2.71
	448826	AI580252	Hs.255565	Hs.255565:Homo sapiens cDNA FLJ33892 fis	2.71
	406871	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	2.71
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	2.71
	441020	W79283	Hs.35962	Hs.35962:Homo sapiens mRNA; cDNA DKFZp68	2.70
45	458933	AI638429	Hs.24763	NM_002882:Homo sapiens RAN binding prote	2.70
	423787	AJ295745	Hs.236204	Hs.236204:nuclear pore complex protein	2.70
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	2.70
	439556	AW138241	Hs.160602	Hs.160602:Homo sapiens cDNA FLJ36008 fis	2.70
	425236	AW067800	Hs.155223	NM_003714:Homo sapiens stanniocalcin 2 (2.70
50	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	2.70
	448296	BE622756	Hs.10949	Hs.10949:Homo sapiens cDNA FLJ14162 fis,	2.70
	430200	BE613337	Hs.234896	Hs.234896:geminin	2.70
	424308	AW975531	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.70
	423453	AW450737	Hs.128791	NM_015939:Homo sapiens CGI-09 protein (L	2.70
55	421344	AW631030	Hs.103665	(locuslink)NM_015873:Homo sapiens villin	2.70
	446507	AI691065	Hs.155780	Hs.155780:ESTs	2.70
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9880	NM_006347:Homo sapiens peptidyl prolyl	2.70
	413794	AF234532	Hs.61638	NM_012334:Homo sapiens myosin X (MYO10),	2.70
60	451481	AA300228	Hs.295866	(locuslink)NM_030974:Homo sapiens hypoth	2.70
	458820	BE552151	Hs.108118	Hs.108118:hypothetical protein FLJ22474	2.70
	425905	AB032959	Hs.318584	NM_032173:Homo sapiens hypothetical prot	2.69
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	2.69
	431201	AA678405	Hs.8854	Hs.8854:Pv11 oncogene homolog, MYC activ	2.69
65	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.69
	441703	AW390054	Hs.192843	NM_022145:Homo sapiens leucine zipper pr	2.69
	433916	AW732839	Hs.3631	NM_001551:Homo sapiens immunoglobulin (C	2.69
	422516	BE258862	Hs.117950	NM_006452:Homo sapiens phosphoribosylami	2.69
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.69
70	427464	BE262956	Hs.178292	Hs.178292:protein O-fucosyltransferase 1	2.69
	453876	AW021748	Hs.110406	Hs.110406:ESTs	2.69
	424373	AJ133758	Hs.146219	NM_014427:Homo sapiens copine VII (CPNE7	2.69
	411619	AI418609	Hs.71040	NM_017816:Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117:interleukin enhancer binding fa	2.69
75	420062	AW411096	Hs.94785	(locuslink)NM_021809:Homo sapiens TGF-beta	2.69
	446077	BE251048	Hs.22579	Hs.22579:Homo sapiens clone CDABP0036 mR	2.68
	446269	AW263155	Hs.14559	NM_018131:Homo sapiens hypothetical prot	2.68
	428728	NM_016625	Hs.191381	Hs.191381:hypothetical protein LOC51319	2.68
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	2.68
80	421933	R98881	Hs.109555	NM_006746:Homo sapiens sex comb on middle	2.68
	417750	AI287720	Hs.260523	Hs.260523:neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	2.68
	421720	AF155096	Hs.107213	Hs.107213:formin binding protein 3	2.68
	425601	AW629485	Hs.140720	NM_012083:Homo sapiens frequently rearm	2.68

5	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepar	2.68
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (2.68
	427719	AJ393122	Hs.134726	(locuslink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
10	413142	M81740	Hs.75212	(locuslink)NM_002539:Homo sapiens ornith	2.67
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	2.67
	432391	AJ732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
15	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	2.67
	439586	AA922936	Hs.110039	Hs.110039:ESTs	2.67
	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108809	NM_006429:Homo sapiens chaperonin contai	2.67
	400448				2.67
20	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu+++ tran	2.67
	445304	BE613206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	2.67
	417601	NM_014735	Hs.82292	NM_014735:Homo sapiens KIAA0215 gene pro	2.66
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AJ869564	Hs.351863	(locuslink)NM_003312:Homo sapiens thiosu	2.66
25	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	2.66
	456248	AL035786	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427691	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
30	419705	AW388634	Hs.154331	Hs.154331:ESTs	2.66
	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coat protein gamm	2.66
	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40369 fis	2.66
	446356	AJ816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	2.66
	432435	BE218886	Hs.282070	Hs.282070:ESTs	2.66
35	433020	AJ375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
	436106	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
	431127	U66618	Hs.250581	Hs.250581:SWI/SNF related, matrix associ	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
	430508	AJ015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
40	414761	AU077228	Hs.77256	NM_004456:Homo sapiens enhancer of zeste	2.65
	412738	N34731	Hs.74562	NM_078480:Homo sapiens fuse-binding prot	2.65
	409893	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenanc	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.64
	428072	BE266602	Hs.182366	NM_016292:Homo sapiens heat shock protel	2.64
45	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGC2574	2.64
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	2.64
	409214	AW405967	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	2.64
50	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	2.64
	408633	AW963372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (2.64
	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432864	AF118395	Hs.279865	NM_014317:Homo sapiens trans-prenyltrans	2.63
	444855	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
55	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
	408137	AI694131	Hs.29002	Hs.29002:KIAA1708 protein	2.63
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37054	Hs.37054:ephra-A3	2.63
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	2.63
	406122				2.63
60	420988	AW006352	Hs.159643	Hs.159643:ESTs, Weakly similar to putati	2.63
	436433	AW631437	Hs.5184	(locuslink)NM_016397:Homo sapiens TH1-II	2.63
	417129	AJ381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410397	AF217517	Hs.63042	NM_018457:Homo sapiens DKFZp564J157 prot	2.63
65	419420	AA355435	Hs.30724	(locuslink)NM_001516:Homo sapiens genera	2.63
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	2.63
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	2.63
	436199	R38946	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 fis	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.63
70	442025	AW887434	Hs.11810	NM_032028:Homo sapiens CDA11 protein (CD	2.62
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.62
	409703	NM_006187	Hs.56009	Hs.56009:2'-5'-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens Integral membrane	2.62
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	2.62
75	451926	AW134519	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.62
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (I	2.62
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-29 protein (L	2.62
	429491	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
80	453335	AW857376	Hs.169238	NM_000149:Homo sapiens fucosyltransferas	2.62
	441126	NM_000429	Hs.323715	(locuslink)NM_000429:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locuslink)NM_007350:Homo sapiens plects	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10888	2.62
	446766	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis antagon	2.62

5	437033	AW248364	Hs.5409	(locuslink)NM_004875:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
	433037	NM_014158	Hs.279938	NM_014158:Homo sapiens HSPC057 protein (2.61
	414438	AJ879277	Hs.76136	(locuslink)NM_003329:Homo sapiens thione	2.61
	16221	BE513171	Hs.79086	(locuslink)NM_007208:Homo sapiens mitoch	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
10	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448625	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410686	AJ733735	Hs.114905	NM_033266:Homo sapiens ER to nucleus sig	2.60
	411400	AA311919	Hs.69851	NM_018983:Homo sapiens nucleolar protein	2.60
15	429770	AJ766047	Hs.99738	Hs.99738:hypothetical protein MGC39350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	430237	AJ272144	Hs.236522	Hs.236522:DKFZP434P106 protein	2.60
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	2.60
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	2.60
	457234	AW968360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis,	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
25	438533	AJ440266	Hs.170673	NM_138969:Homo sapiens retinal short cha	2.60
	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of Invas	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372280	Hs.178576	(locuslink)NM_030877:Homo sapiens cateni	2.60
	453949	AU077146	Hs.36927	(locuslink)NM_006644:Homo sapiens heat s	2.59
30	451110	AJ955040	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.59
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	442990	AA197226	Hs.19347	NM_032351:Homo sapiens mitochondrial rib	2.59
35	424197	AF096834	Hs.142989	NM_015982:Homo sapiens germ cell specifi	2.59
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T98226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	2.59
	441153	BE562826	Hs.601336534F1	BE562826:601336534F1 NIH_MGC_44 Homo sap	2.59
40	410570	AJ133096	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	410315	AJ638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
45	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.58
	449019	AJ949095	Hs.67776	Hs.67776:Homo sapiens, clone IMAGE:54556	2.58
	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.357942	Hs.357942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AJ244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
	416330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
50	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	2.58
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
55	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	2.58
	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21766	Hs.21766:ESTs, Weakly similar to hypothe	2.57
	447418	AA063074	Hs.18552	Hs.18552:E2f2 protein	2.57
60	424142	AJ578727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
	428342	AJ739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31753 fis	2.57
	427254	AL121523	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (2.57
	425689	W16480	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis,	2.57
	452700	AJ859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	2.57
65	427678	BE267756	Hs.180312	NM_016065:Homo sapiens mitochondrial rib	2.57
	444656	AJ277924	Hs.145199	Hs.145199:ESTs, Weakly similar to hypothe	2.57
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	2.56
	427648	AJ376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	2.56
70	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.56
	409964	AW368228	Hs.67928	Hs.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774:hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcription fac	2.56
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
75	419423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.56
	437623	D63880	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.282990	(locuslink)NM_033560:Homo sapiens chromo	2.56
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	2.56
80	425368	AB014595	Hs.155976	(locuslink)NM_003588:Homo sapiens cullin	2.56
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	2.56
	427876	AJ494291	Hs.369171	Hs.369171:ESTs	2.56
	418862	BE550564	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	2.56
	416432	BE391787	Hs.79322	(locuslink)NM_005051:Homo sapiens glutam	2.55

5	458814	AM98957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
	457400	AF032908	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ)	2.55
10	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2)	2.55
	402829				2.55
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	2.55
	400895				2.55
	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
15	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fls485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1268 protein	2.55
	410012	AW015832	Hs.67898	(locuslink)NM_017819:Homo sapiens hypoth	2.55
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
20	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	2.55
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	2.55
	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
	421612	AF161254	Hs.106186	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
25	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	2.54
	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
	425268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
30	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cyste	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCTA00142	2.54
	456031	AA335996	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
35	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_015956:Homo sapiens mitochondrial rib	2.53
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	2.53
	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
40	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105683	Hs.6947	(locuslink)NM_014159:Homo sapiens Humlin	2.53
	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FLJ14075	2.53
	417933	X02308	Hs.82962	NM_001071:Homo sapiens thymidylate synth	2.53
45	426812	AF105355	Hs.172613	NM_006598:Homo sapiens solute carrier fa	2.53
	452313	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA826401	Hs.122393	Hs.122393:ESTs	2.53
	409299	AA045650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	2.53
50	412525	AA581439	Hs.152328	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
	427581	NM_014789	Hs.179703	NM_014788:Homo sapiens tripartite moti-	2.53
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	2.53
	434274	AA628539	Hs.57783	Hs.57783:eukaryotic translation initiati	2.53
55	400282		Hs.289101	NM_005313:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	2.53
	453344	BE349075	Hs.44571	Hs.44571:ESTs	2.53
	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.52
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
60	439012	BE383814	Hs.6455	NM_006666:Homo sapiens RuvB-like 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	2.52
	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.52
65	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
	433001	AF217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
70	440773	AA352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440587	AL138461	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	2.52
	424259	AK001776	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.52
75	453204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453665	AA626250	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016558	Hs.274411	NM_016558:Homo sapiens SCAN domain conta	2.52
	433271	BE621697	Hs.14317	NM_018648:Homo sapiens nucleolar protein	2.51
	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exoninucle	2.51
80	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
	429669	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0020 gene pro	2.51
	434474	AL042938	Hs.211571	(locuslink)NM_005333:Homo sapiens holocy	2.51
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_018386:Homo sapiens hypoth	2.51

5	421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily 1B	2.51
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
	452101	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alph	2.51
	436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	2.51
	435677	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor interac	2.51
	406363				2.51
	452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
10	409591	AA532983	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
	421837	AJ878857	Hs.109706	NM_016185:Homo sapiens hematological and	2.51
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
	434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
15	426053	U68105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
	432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
	452390	AJ864142	Hs.29288	(locuslink)NM_022759:Homo sapiens endo-b	2.50
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inact)	2.50
	400076				2.50
20	420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
	422244	Y08890	Hs.113503	NM_002271:Homo sapiens karyopherin (impo	2.50
	410723	AA100683	Hs.372108	Hs.372108:ESTs	2.50
	435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
25	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	2.50
	433626	AF078859	Hs.86347	NM_013341:Homo sapiens hypothetical prot	2.50
	448391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

30	Pkey:	Unique Eos probeset Identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
35	Pkey	CAT Number	Accession
	406685	0_0	M18728
	434414	35978_1	AF134164 BF809407 AA218567 BF842863 A1267168 BF876178 BG999253 AW861851 AW858362 A1817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 A1694265 AA045564 BG950256 A1829309 BG987850 BE093175 BF854337
40	432407	MH1429_12	BG036675 BF772005 BF771868 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817991 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 B1861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 A1075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 B1055728 BF242843 AA207189 BF770412 BF771157 BG430030 AA055592
45	406708	0_0	A1282759
	459306	223120_4	AW578452
	447349	1063443_1	BE743847 AW809603 BM469626 A1375546
50	441153	264480_3	BE562826 BE378727

TABLE 10C

55

Pkey:

Ref:

Strand:

NL_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

60

Pkey

Ref

Strand

NL_position

404519

8152000

Plus

12817-13000

406399

9256288

Minus

63448-63554

65

403220

7630969

Plus

64338-64517

404661

9797073

Plus

33374-33675,33769-34008

402496

9797769

Minus

8615-9103

403055

8748904

Minus

109532-110225

400965

7770576

Minus

173043-173564

70

403218

7630969

Plus

58039-58149

401866

8018106

Plus

73126-73623

403221

7630969

Plus

66294-66438,66936-67124

401519

6649315

Plus

157315-157950

405451

7622517

Minus

145949-146227

75

403532

8076842

Minus

81750-81901

402944

9368423

Plus

110411-110716,111173-111640

403219

7630969

Plus

61858-61995

403381

9438267

Minus

26009-26178

403485

9966528

Plus

2888-3001,3198-3532,3655-4117

80

405484

5922025

Plus

199214-199579,199672-199920,200262-20049

404684

9797403

Minus

110881-111020

402474

7547175

Minus

53526-53628,55755-55920,57530-57757

405506

6466489

Plus

80014-80401,80593-81125

403739

7630882

Plus

44563-44768,48209-48483,52255-52495

5	406545	7711510	Plus	145662-145781,147854-147984,148098-14824
	401405	7768126	Minus	69276-69452,69548-69958
	400750	8119067	Plus	198991-199168,199316-199548
	401179	9438647	Plus	113477-113893
	400529	9796988	Plus	138232-138423
	403817	8962065	Plus	110297-111052
	400448	9887687	Minus	177372-177674
	406122	9144087	Minus	30940-31386
10	406180	7283201	Minus	38923-39107
	402829	8918414	Plus	101532-101852,102006-102263
	400995	8099094	Plus	141188-141601
	404826	6572184	Plus	47726-48048
15	406363	9256114	Plus	14403-14602,17000-17147,17241-17368

Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 69680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

35	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	37.18
	406690	M29540	Hs.220529	(locustlink)NM_004363:Homo sapiens carcin	31.24
	407242	M18728		(locustlink)NM_002483:Homo sapiens cardin	24.81
	406685	M18728		(locustlink)NM_002483:Homo sapiens cardin	20.54
40	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S384_H	20.38
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	20.13
	406687	M12523			19.89
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	19.88
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	19.55
45	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease 1	18.33
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	17.47
	414388	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	17.37
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	15.15
50	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	14.23
	407243	AA058357	Hs.74466	(locustlink)NM_006890:Homo sapiens carc	14.12
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	13.64
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.48
55	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	13.43
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, U c	13.20
	453863	X02544	Hs.572	Hs.572:corosomucoid 1	13.06
	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	12.58
60	436217	T63925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.34
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	11.72
	409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	11.72
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	11.49
	406399				11.25
65	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	11.12
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	11.01
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.70
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	10.69
70	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (10.48
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
	406741	AA058357	Hs.74466	(locustlink)NM_006890:Homo sapiens carcin	10.20
	422424	AI186431	Hs.295638	Hs.295638:prostate differentiation facto	10.19
75	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	9.72
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	9.70
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	9.65
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.52
80	426355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	9.47
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.41
	413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	9.39
	422664	AA315833	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	9.31
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	9.30

5	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cysteal	8.99
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	8.71
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	8.47
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfat	8.47
	422310	AA316822	Hs.98370	(locuslink)NM_030522:Homo sapiens cytoch	8.43
10	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysl	8.12
	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	8.09
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	7.92
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	7.89
15	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	7.87
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cysteal	7.71
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	7.58
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.48
20	451035	AU076785	Hs.430	NM_002670:Homo sapiens plasmin 1 (1 isof	7.31
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
	425978	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	7.29
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
25	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	7.12
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	7.12
	414617	A1339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypo	7.10
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.06
	452194	AI694413	Hs.373599	Hs.373599:EST	7.02
30	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.96
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
	403220				6.96
35	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	6.80
	415214	AA445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
	411976	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
40	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis I	6.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	6.59
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
	431657	A1345227	Hs.105448	Hs.105448:protein kinase, lysine deficite	6.54
45	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	6.50
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.47
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	6.45
50	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.41
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	6.41
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	6.20
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
55	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
	414809	AK434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	6.18
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
60	426174	AA547959	Hs.115838	Hs.115838:ESTs	6.10
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.07
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
	409453	AI885516	Hs.95612	Hs.95612:ESTs	6.06
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	6.03
65	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.99
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif	5.95
	430204	AA618335	Hs.356684	Hs.356684:hypothetical protein FLJ32334	5.92
	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.90
70	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	5.88
	408908	BE286227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.86
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	5.82
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
75	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	5.75
	403218				5.74
80	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	5.72
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	5.72
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

5	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63
	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	5.60
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	5.59
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.56
10	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitam	5.56
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	5.54
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	5.53
	403221				5.52
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisoma prolif	5.52
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.48
	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.42
	438251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.41
20	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	5.38
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	5.32
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.31
25	430680	AW138724	Hs.168974	Hs.168974:ESTs	5.25
	432378	AI493046	Hs.146133	Hs.146133:ESTs	5.25
	419693	AA133749	Hs.301350	Hs.301350:FXFD domain-containing lon tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	5.21
30	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	5.21
	418203	X54942	Hs.83768	NM_001827:Homo sapiens CDC28 protein kin	5.20
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
35	446051	BE048061	Hs.37054	Hs.37054:ephritin-A3	5.15
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	5.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pro-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
40	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
	432575	AA553722	Hs.194346	Hs.194346:Spr-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	5.07
45	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	5.06
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	5.06
	414361	AI086138	Hs.204044	Hs.204044:ESTs	5.04
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	5.01
50	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.99
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.98
55	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.98
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.97
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014781	Hs.184339	NM_014781:Homo sapiens maternal embryoni	4.95
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
60	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.91
65	414108	AI267692	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
	422539	AJ009936	Hs.118138	NM_003013:Homo sapiens nuclear receptor	4.89
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
70	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.88
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ecodysplaslin 1,	4.87
	413763	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.87
	405484				4.87
75	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.87
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	4.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_005002:Homo sapiens ubiquitin carboxy	4.79
80	417115	AW952782	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.78
	453751	R38762	Hs.101282	Hs.101282:Homo sapiens mRNA: cDNA DKFZp4	4.77
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76

	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	4.75
	400529				4.75
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	4.75
	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
5	447968	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	4.72
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	405558				4.70
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
10	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	4.65
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
15	403739				4.61
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.60
20	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432160	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	4.59
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
25	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.57
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 8 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:ephrin-AA	4.55
	409964	AW368226	Hs.67928	Hs.67928:ESTs	4.54
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	4.54
30	432407	AA221036		AF134164:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTKS protein tyro	4.53
	403219				4.53
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.52
35	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-BR-M (murine)	4.51
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomut	4.51
40	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.49
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.48
	434263	N34895	Hs.79187	Hs.79187:coxsa virus and adenovirus	4.47
45	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW206330	Hs.355663	Hs.355663:ESTs	4.46
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
50	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	4.46
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase 1	4.45
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis	4.44
	433662	Y07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
55	419559	Y07828	Hs.91095	NM_007028:Homo sapiens tripartite motif	4.44
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	4.43
	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.43
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	4.43
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.42
	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.41
60	431350	AI192528	Hs.164537	Hs.164537:ESTs	4.39
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	4.39
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
65	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
	422293	X94453	Hs.114366	Hs.114366:pyroline-5-carboxylate synth	4.38
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.37
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	4.36
70	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	4.36
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.34
	424865	AF011333	Hs.163563	NM_002349:Homo sapiens lymphocyte antigen	4.34
75	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	4.33
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	4.32
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
80	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.29
	429638	AI916662	Hs.211577	(locuslink)NM_004988:Homo sapiens kinact	4.29

5	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	4.29
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	4.29
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	4.28
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.27
	409636	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	4.27
	408989	AW361666	Hs.49500	Hs.49500:KIAA0746 protein	4.27
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23502 fi	4.27
	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	4.24
10	431685	AW296135	Hs.267659	NM_008113:Homo sapiens vav 3 oncogene (V	4.24
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (4.24
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.23
	436856	AI469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	4.23
15	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	4.23
	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	4.23
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.22
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	4.22
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	4.21
20	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	4.21
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	4.21
	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	4.19
25	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	4.19
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens displa	4.19
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.19
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	4.18
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	4.17
30	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	4.17
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	4.17
	404826				4.17
	414198	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	4.17
35	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	4.17
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	4.16
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	4.16
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	4.15
	446686	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	4.15
	400130		Hs.155560	NM_001748:Homo sapiens calnexin (CANX),	4.14
40	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	4.14
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	4.13
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	4.13
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	4.13
45	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	4.12
	428471	X57348	Hs.184510	Hs.184510:stratifin	4.12
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	4.11
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	4.10
50	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transl	4.10
	409152	AA176585	Hs.194346	Hs.194346:Spr-2 protein	4.10
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	4.10
	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	4.09
	444654	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	4.09
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	4.09
55	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	4.09
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	4.08
	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	4.08
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	4.06
60	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	4.04
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	4.04
65	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	4.04
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	4.04
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	4.02
	436278	BE396290	Hs.5097	Hs.5097:synaptophysin 2	4.02
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	4.02
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.02
70	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.01
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	4.00
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	4.00
	455362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.99
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	3.98
75	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	3.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	3.98
	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	3.98
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.97
80	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.96
	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.96
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.95
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.94
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.94

	420162	BE378432	Hs.95577	NM_052984: Homo sapiens cyclin-dependent	3.94
	443180	R15875	Hs.258576	NM_012129: Homo sapiens claudin 12 (CLDN1	3.93
	418738	AW388633	Hs.6682	Hs.6682: solute carrier family 7, (cation	3.93
5	409463	AI458165	Hs.17286	NM_023930: Homo sapiens hypothetical prot	3.92
	447495	AW401864	Hs.18720	NM_004208: Homo sapiens programmed cell d	3.92
	448093	AW977382	Hs.15898	Hs.15898: 2,4-dienoyl CoA reductase 2, pe	3.91
	428698	AA852773	Hs.334838	Hs.334838: KIAA1866 protein	3.90
	438485	W57578	Hs.378718	Hs.378718: Homo sapiens cDNA FLJ33433 fis	3.89
10	436827	H72187	Hs.356668	(locuslink)NM_005274: Homo sapiens guanine	3.89
	407971	AI469117	Hs.62918	Hs.62918: CDC91 cell division cycle 91-I	3.89
	400750				3.89
	448140	AF146761	Hs.20450	NM_020125: Homo sapiens B lymphocyte acti	3.89
	413880	AI660842	Hs.110915	NM_021258: Homo sapiens interleukin 22 re	3.89
15	453258	AW293134	Hs.32597	NM_005977: Homo sapiens ring finger prote	3.89
	428788	AF082283	Hs.193516	NM_003921: Homo sapiens B-cell CLL/lympho	3.88
	443044	N28522	Hs.8935	NM_014298: Homo sapiens quinolinate phosph	3.88
	413095	AA494359	Hs.30715	Hs.30715: potassium voltage-gated channel	3.88
	417129	AI381800	Hs.300684	Hs.300684: calcitonin gene-related peptid	3.87
20	410268	AA316181	Hs.61635	NM_012449: Homo sapiens six transmembrane	3.87
	425047	U34038	Hs.154299	NM_005242: Homo sapiens coagulation facto	3.87
	416084	L16991	Hs.79008	NM_012145: Homo sapiens deoxythymidylate	3.86
	449667	AB023227	Hs.23860	Hs.23860: KIAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635: six transmembrane epithelial an	3.85
25	407770	AW078331	Hs.38738	NM_014343: Homo sapiens claudin 15 (CLDN1	3.85
	418313	BE244231	Hs.84038	NM_015937: Homo sapiens CGI-06 protein (L	3.85
	413380	AI904232	Hs.75323	Hs.75323: prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296: ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884: Homo sapiens IMP (inosine mono	3.85
30	433658	L03878	Hs.156110	Hs.156110: immunoglobulin kappa constant	3.84
	428474	AB023182	Hs.184523	Hs.184523: serine/threonine kinase 38 lik	3.84
	430237	AI272144	Hs.236522	Hs.236522: DKFZP434P106 protein	3.84
	414862	BE621310	Hs.923	Hs.923: single-stranded DNA binding prote	3.84
	437967	BE277414	Hs.5947	NM_005370: Homo sapiens mel transforming	3.84
35	427318	AF186081	Hs.175783	NM_014579: Homo sapiens solute carrier fa	3.83
	459306	AW578452		AW578452: RC1-CT0252-030100-023-b07 CT025	3.83
	446342	BE298665	Hs.14846	Hs.14846: Homo sapiens mRNA; cDNA DKFZp56	3.83
	432886	BE159028	Hs.279704	Hs.279704: chromatin accessibility comple	3.82
	434845	BE267057	Hs.325321	Hs.325321: WD repeat domain 18	3.82
40	426514	BE616633	Hs.170195	Hs.170195: bone morphogenetic protein 7 (3.82
	410315	AI638871	Hs.378965	Hs.378965: Homo sapiens cDNA FLJ37658 fis	3.82
	421905	AI660247	Hs.32699	Hs.32699: Homo sapiens, Similar to RIKEN	3.81
	421481	AW391972	Hs.104696	Hs.104696: KIAA1324 protein	3.81
	445921	AW016211	Hs.153799	Hs.153799: Homo sapiens cDNA FLJ38333 fis	3.80
45	414368	W70171	Hs.75939	NM_012474: Homo sapiens uridine monophosp	3.80
	457284	AF102850	Hs.227933	NM_013338: Homo sapiens Alg5, S. cerevisi	3.80
	413813	M96956	Hs.75561	NM_003212: Homo sapiens teratocarcinoma-d	3.80
	414602	AW630088	Hs.76550	NM_052886: Homo sapiens mal, T-cell diffe	3.80
	410219	T98226	Hs.171952	Hs.171952: occludin	3.80
50	407137	T97307			3.78
	430462	AI584156	Hs.105640	Hs.105640: hypothetical protein BC007772	3.78
	432680	T47364	Hs.278613	(locuslink)NM_005532: Homo sapiens interl	3.78
	450010	AW293801	Hs.255052	Hs.255052: ESTs	3.78
55	440334	BE276112	Hs.7165	NM_003904: Homo sapiens zinc finger prote	3.78
	440676	NM_004987	Hs.112378	(locuslink)NM_004987: Homo sapiens LIM an	3.77
	428072	BE258602	Hs.182368	NM_016292: Homo sapiens heat shock protei	3.77
	407722	BE252241	Hs.38041	NM_003681: Homo sapiens pyridoxal (pyrido	3.77
	426459	AF151812	Hs.169992	NM_015966: Homo sapiens serologically def	3.77
60	443323	BE560821	Hs.9222	Hs.9222: estrogen receptor binding site a	3.76
	406621	X57809	Hs.181125	Hs.181125: immunoglobulin lambda locus	3.76
	423198	M81933	Hs.1634	Hs.1634: cell division cycle 25A	3.76
	428206	AB020643	Hs.183008	Hs.183008: likely homolog of mouse hepari	3.75
	447200	BE543146	Hs.281434	Hs.281434: Homo sapiens cDNA FLJ31373 fis	3.74
	425209	AL049761	Hs.155140	NM_001895: Homo sapiens casein kinase 2,	3.74
65	411950	T28407	Hs.81564	NM_002619: Homo sapiens platelet factor 4	3.74
	418681	AA287786	Hs.23449	Hs.23449: insulin receptor tyrosine kinas	3.74
	421532	AW138207	Hs.146170	NM_022842: Homo sapiens hypothetical prot	3.74
	446291	BE397753	Hs.14623	Hs.14623: interferon, gamma-inducible pro	3.74
	435886	BE265839	Hs.12126	NM_018487: Homo sapiens hepatocellular ca	3.73
70	417286	AA122237	Hs.81874	NM_002413: Homo sapiens microsomal glutat	3.73
	421743	T35958	Hs.107614	Hs.107614: DKFZP564I1171 protein	3.73
	400419	AF084545		AF084545: Homo sapiens versican Vint Isof	3.73
	421357	AK000609	Hs.103808	NM_017896: Homo sapiens chromosome 20 ope	3.73
	420665	AW469240	Hs.371581	Hs.371581: ESTs	3.73
75	418703	NM_014448	Hs.87435	Hs.87435: Rho guanine exchange factor (GE	3.73
	452679	Z42387	Hs.83883	(locuslink)NM_020182: Homo sapiens transm	3.72
	419743	AW408762	Hs.5957	Hs.5957: Homo sapiens clone 24416 mRNA se	3.72
	435730	AB020635	Hs.4984	Hs.4984: KIAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795: lactate dehydrogenase A	3.72
80	444008	BE395085	Hs.334762	(locuslink)NM_032832: Homo sapiens hypoth	3.72
	442875	BE623003	Hs.23625	Hs.23625: Homo sapiens clone TCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348: Homo sapiens ubiquitin-conjuga	3.71
	413950	AA249096	Hs.32793	Hs.32793: Homo sapiens cDNA FLJ31108 fis,	3.71
	411125	AA151647	Hs.68877	Hs.68877: zytocrome b-245, alpha polypep	3.71

5	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.53563	NM_001853:Homo sapiens collagen, type IX	3.70
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
	400846				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
10	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.69
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.69
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (3.69
15	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.68
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
20	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.67
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-rat simian leuk	3.66
	409402	AF208234	Hs.695	Hs.695:crystallin B (stefin B)	3.66
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.66
	432633	AI796390	Hs.210667	Hs.210667:ESTs	3.66
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.66
25	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.65
	432320	AW411068	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
30	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.63
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.62
35	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.62
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
	400847				3.60
40	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
45	453331	AI240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ31066 fis	3.60
	441406	Z45967	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.59
	419607	R52657	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
50	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
	431236	AV656840	Hs.285115	NM_001580:Homo sapiens interleukin 13 re	3.59
	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN),	3.58
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
55	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
	424241	AW995948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, I	3.57
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.56
60	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.56
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.56
	439407	AI457122	Hs.129673	Hs.129673:eukaryotic translation Initiat	3.56
	413859	AW992358	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, I	3.56
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.55
65	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.55
	411704	AI499220	Hs.71573	(locuslink)NM_017988:Homo sapiens hypoth	3.55
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.54
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.54
70	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.54
	452488	N74921	Hs.184389	Hs.184389:ESTs, Moderately similar to S1	3.54
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.54
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.53
75	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	3.53
	446147	AL133064	Hs.14051	(locuslink)NM_145698:Homo sapiens endoze	3.53
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.52
	450825	AC006954	Hs.25527	(locuslink)NM_014428:Homo sapiens light	3.52
80	442007	AA301116	Hs.142838	NM_032390:Homo sapiens MKI67 (FHA domain	3.52
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens BD6 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay acceleratin	3.50

	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.50
	452852	AW378065	Hs.8687	Hs.8687:ESTs	3.50
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
	404240				3.50
5	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
	445937	AA52943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.49
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.49
10	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-assoca	3.49
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.49
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.49
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.49
	439841	AF038951	Hs.6710	NM_004870:Homo sapiens mannose-P-doficho	3.49
15	428390	AA640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.48
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-alph	3.48
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.48
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protel	3.48
20	457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.48
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	402829				3.47
	451707	AW051061	Hs.60973	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
25	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.47
	420085	AJ741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.47
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.47
	439223	AW238299	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.46
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.46
30	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	3.46
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.46
	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	3.46
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.45
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite molif-	3.45
35	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfactant 4 (SURF4)	3.45
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.45
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC18	3.45
	410836	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.45
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.44
40	432391	AJ732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.44
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.44
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.44
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (3.44
	425274	BE281191	Hs.155462	Hs.155462:MCMB minichromosome maintenanc	3.44
45	448913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	3.44
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.44
	420168	AW732278	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	3.44
	412420	AL035668	Hs.73853	NM_001200:Homo sapiens bone morphogeneti	3.43
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.43
50	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prolactin)	3.43
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	3.43
	428093	AW594508	Hs.104830	Hs.104830:ESTs	3.43
	428293	BE250944	Hs.183558	Hs.183558:solute carrier family 1 (neutr	3.42
55	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.42
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.42
	427648	AJ376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.41
	428734	BE303044	Hs.192023	NM_003767:Homo sapiens eukaryotic transl	3.41
60	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	3.41
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	3.41
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	3.41
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	3.41
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	3.41
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.40
65	422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.40
	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.40
	400205		Hs.81848	NM_008265:Homo sapiens RAD21 homolog (S.	3.40
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.39
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
70	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.39
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
	406363				3.39
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	3.39
	423309	BE006775	Hs.126782	NM_014467:Homo sapiens sushi-repeat prot	3.38
75	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	3.38
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.38
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.38
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.38
	400125		Hs.125078	(locuslink)NM_004152:Homo sapiens ornith	3.38
80	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	3.37
	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.37
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.37
	423599	AI805564	Hs.31731	(locuslink)NM_012094:Homo sapiens perox	3.37
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.37

5	446715	AK37735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.36
	429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.36
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.36
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	3.36
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
10	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	3.36
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
	425725	NM_012243	Hs.159322	(locustlink)NM_012243:Homo sapiens solute	3.35
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.35
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.35
15	457329	AI634860	Hs.359682	(locustlink)NM_016442:Homo sapiens type 1	3.35
	432169	Y00971	Hs.2910	NM_002765:Homo sapiens phosphoribosyl py	3.35
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.35
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	3.35
20	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.34
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	3.34
	450506	NM_004460	Hs.418	(locustlink)NM_004460:Homo sapiens fibrob	3.34
25	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
	431731	BE266322	Hs.211374	(locustlink)NM_145051:Homo sapiens hypoth	3.34
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.34
	427349	AA360154	Hs.177415	(locustlink)NM_001997:Homo sapiens Finkel	3.34
	439246	AI498072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.34
30	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.34
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	3.34
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
	444706	AK000398	Hs.11747	(locustlink)NM_017798:Homo sapiens chromo	3.34
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	3.33
35	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.33
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
	414271	AK000275	Hs.75871	(locustlink)NM_012408:Homo sapiens protei	3.33
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
40	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.32
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	3.32
	430393	BE185030	Hs.241305	(locustlink)NM_006470:Homo sapiens tripar	3.32
45	402104				3.32
	446620	AA128808	Hs.178902	(locustlink)NM_022109:Homo sapiens CDw92	3.32
	443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.31
50	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.31
	451564	AU076698	Hs.132760	(locustlink)NM_001467:Homo sapiens glucos	3.31
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	3.31
	441866	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.31
55	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fls485 (LOC51066)	3.31
	446506	AI123118	Hs.15159	(locustlink)NM_016326:Homo sapiens chemok	3.31
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cyto	3.31
	449644	AW950707	Hs.148324	Hs.148324:ESTs	3.31
	422611	AA158177	Hs.118722	(locustlink)NM_004480:Homo sapiens fucosy	3.31
60	417640	D30857	Hs.82353	NM_008404:Homo sapiens protein C recepto	3.30
	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.30
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquitin-cytochr	3.30
65	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	3.30
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.29
	424756	AW504657	Hs.152931	(locustlink)NM_002296:Homo sapiens lamin	3.29
	442772	AW503680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.29
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
70	420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cystei	3.29
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	3.29
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	3.28
	427308	D26067	Hs.174905	Hs.174905:KIAA0033 protein	3.28
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
75	449199	AI990122	Hs.196968	Hs.196968:ESTs	3.28
	442739	NM_007274	Hs.8679	(locustlink)NM_007274:Homo sapiens cyto	3.28
	422051	AW327546	Hs.111024	(locustlink)NM_005984:Homo sapiens solute	3.28
	452714	AW770694	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
	431884	AA521248	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.28
80	402260				3.28
	409686	AK000002	Hs.55879	(locustlink)NM_033450:Homo sapiens multid	3.28
	409267	NM_012453	Hs.62515	NM_012453:Homo sapiens transducin (beta)	3.28
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogen	3.27
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.27

	429571	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.27
	434521	NM_002267	Hs.3886	Hs.3886:karyopherin alpha 3 (importin al	3.27
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27
5	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27
	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	3.26
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	3.26
	440286	U29589	Hs.7138	NM_000740:Homo sapiens cholinergic recep	3.26
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	3.26
10	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	3.26
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	3.26
	427640	AF058293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	3.26
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25
15	416448	L13210	Hs.79339	NM_005587:Homo sapiens lectin, galactosi	3.25
	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.25
	424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25
	426784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.25
20	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	3.24
	419216	AU076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	3.24
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24
25	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	3.23
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	3.23
30	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
	432731	R31178	Hs.287820	Hs.287820:fibronectin 1	3.23
	410340	AW182833	Hs.112188	(locuslink)NM_021826:Homo sapiens hypoth	3.23
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23
35	425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	3.22
	403912				3.22
	429782	NM_005754	Hs.220689	Hs.220689:Ras-GTPase-activating protein	3.22
40	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	3.22
	409591	AA532863	Hs.9100	Hs.9100:hypothetical gene supported by A	3.22
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	3.22
45	450770	AA019924	Hs.28803	Hs.28803:ESTs	3.22
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	3.22
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	3.21
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	3.21
	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.21
50	454358	AW972876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	3.21
	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21
	400836				3.20
55	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	3.20
	414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle me	3.20
	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	3.20
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.20
	407738	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.20
60	400845				3.20
	407082	Z47055			3.20
	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kines	3.20
	403217				3.20
65	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.19
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.19
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19
	457274	AW674193	Hs.227152	NM_018391:Homo sapiens hypothetical prot	3.19
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XII	3.19
70	430280	AA361258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19
	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	3.19
	422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere protel	3.18
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18
	449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18
	426925	NM_001196	Hs.172894	Hs.172894:BH3 interacting domain death a	3.18
75	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	3.18
	405387				3.18
	444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
80	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.17
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.17
	410663	AA184952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17

	415402	AA184687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	3.17
	451032	W03692	Hs.323079	Hs.323079:Homo sapiens mRNA: cDNA DKFZp5	3.17
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	3.17
5	417018	M16038	Hs.80887	Hs.80887:v-yes-1 Yemaguchi sarcoma viral	3.16
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.16
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	3.16
	432728	NM_006979	Hs.278721	NM_006979:Homo sapiens HLA class II regi	3.16
10	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	3.16
	418462	BE001596	Hs.85266	Hs.85266:Integrin, beta 4	3.16
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	3.16
	429556	AW139399	Hs.314807	Hs.314807:hypothetical protein MGC2655	3.15
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	3.15
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	3.15
15	435958	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens Integr	3.15
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.15
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	3.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.14
20	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	3.14
	407961	AW672939	Hs.41694	Hs.41694:origin recognition complex, sub	3.14
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-II	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	3.14
25	450295	AF765732	Hs.210628	Hs.210628:ESTs	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	452695	AW780189	Hs.30327	NM_003668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.13
30	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (renal a	3.13
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	3.13
	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	3.12
35	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	424727	AW590378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.12
	435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.12
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	3.12
	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
40	409220	BE243323	Hs.61233	(locuslink)NM_003842:Homo sapiens tumor	3.12
	428699	AW578262	Hs.190161	Hs.190161:LR8 protein	3.12
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	3.12
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	3.12
45	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	3.12
	410240	AL157424	Hs.61289	Hs.61289:synaptojanin 2	3.12
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	406865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	3.11
	405203				3.11
50	441028	AI333650	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
	421684	BE281591	Hs.106768	NM_018120:Homo sapiens hypothetical prot	3.11
	428824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.11
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	3.11
55	408806	H69912	Hs.48269	NM_003384:Homo sapiens vaccinia related	3.10
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	3.10
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	3.10
60	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.10
	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
	433409	AI278802	Hs.25661	Hs.25661:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.10
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic I	3.10
	436908	H95990	Hs.181244	Hs.181244:major histocompatibility compl	3.10
70	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.10
	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	3.09
	408160	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA: cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-4	3.09
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
75	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
	400278		Hs.2280	NM_002950:Homo sapiens riboporphin I (RPN	3.09
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	3.09
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	3.09
	430066	AI929559	Hs.237825	Hs.237825:signal recognition particle 72	3.09
80	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	3.09
	426989	AI815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	3.08
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	3.08

	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	3.08
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
	419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
5	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	3.08
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
	453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisph	3.08
	420187	AK001714	Hs.95744	NM_018028:Homo sapiens hypothetical prot	3.08
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	3.07
10	411423	AW845987	Hs.58864	(locuslink)NM_139248:Homo sapiens membra	3.07
	449954	AA641638	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to chol	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antiser	3.07
15	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	3.07
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	3.07
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	3.07
	436553	AW407157	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.08
	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
20	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
	418052	AW630656	Hs.83383	NM_006406:Homo sapiens peroxiredoxin 4 (3.06
	407223	H96850		H96850:ycw03b12.s1 Soares melanocyte 2Nbh	3.06
	418841	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXCD e	3.06
25	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	3.06
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	3.06
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.05
	440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
30	446770	AV660309	Hs.154986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	3.05
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	3.05
	453830	AA534296	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
35	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
	408524	D87942	Hs.48328	Hs.48328:fucosyltransferase 2 (secretor	3.05
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	3.05
	430508	AJ015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	3.04
40	432281	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
	423570	AW838308	Hs.129819	NM_018344:Homo sapiens hypothetical prot	3.04
	443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	3.04
45	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
	453450	AW797627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
50	412708	R26830	Hs.106137	Hs.106137:Homo sapiens mRNA for OK/SW-CL	3.04
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	3.04
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	3.03
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
	444309	U83236	Hs.10803	Hs.10803:calcium and Integrin binding 1	3.03
55	412969	AJ373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
	430354	AA954810	Hs.239784	Hs.239784:scribble	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
60	451798	BE297667	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	3.02
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.02
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.02
	417898	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
65	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	3.02
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	3.01
	414421	AI521130	Hs.355126	(locuslink)NM_144686:Homo sapiens hypoth	3.01
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Nci58 (D. melanog	3.01
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	3.01
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens trpser	3.01
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	3.00
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protel	3.00
	415697	AI365603	Hs.279696	Hs.279696:DKFZP5661024 protein	3.00
	437459	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
75	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	3.00
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.00
	406868	AA505445	Hs.300697	Hs.300697:immunoglobulin heavy constant	3.00
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	3.00
80	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rh-related antigen	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	406685	0_0	M18728
10	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AIT32411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG968155 AK057283 B1861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AJ075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592 AW578452
15	459306	223120_4	BG028348 BF772844 H83066 AW817969 H90585 BF755039 AI858183
	452098	161393_1	BE072881 A1762181 BE072946
	451129	1495511_1	

TABLE 11C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:469-495.
 Strand: Indicates DNA strand from which exons were predicted.
 N1_position: Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	N1_position
	406399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
30	403218	7630969	Plus	58039-58149
	403221	7630969	Plus	66294-66438,66936-67124
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	400529	9796988	Plus	138232-138423
35	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	403219	7630969	Plus	61858-61995
	404826	6572184	Plus	47726-48046
	400750	8119057	Plus	198991-199168,199316-199548
40	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	400847	9188605	Plus	44643-44835
	404854	7143420	Plus	14260-14537
	400448	9887687	Minus	177372-177674
45	404240	5002624	Minus	116132-116407,116653-116922
	402829	8918414	Plus	101532-101852,102006-102263
	408363	9256114	Plus	14403-14602,17000-17147,17241-17368
	402104	8119072	Plus	122409-122600
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
50	403912	7710730	Minus	72000-72290,72431-72700,72929-73189
	400836	8954179	Plus	677-1188
	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	405387	6587915	Minus	3769-3833,6708-6895
55	405203	7230116	Plus	125295-125463

Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the 93rd percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 93rd percentile value amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

70	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	402075	U19557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
75	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial coll	38.9
	435094	AI560129	Hs.329062	EST	30.3
	439506	W79123	Hs.58561	G protein-coupled receptor 87	28.8
80	452240	AI591147	Hs.61232	ESTs	27.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin bi	26.0
	417034	NM_006183	Hs.80962	neurotensin	25.5
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

5	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine proteinase inhibitor 13 (P113; serpin	20.1
	452461	N78223	Hs.108106	transcription factor	19.8
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	16.3
10	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA808229	Hs.167771	ESTs	15.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	15.4
	441459	AI919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	13.8
15	412719	AW016610	Hs.129911	ESTs	13.4
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comitin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AI023799	Hs.163242	ESTs	13.1
20	404996			Target Exon	13.1
	443211	AI128388	Hs.143655	ESTs	12.9
	414764	AW013887	Hs.72047	ESTs	12.9
	428618	AA885360	Hs.160199	Target CAT	12.7
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
25	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.6
	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
30	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415989	AI267700	Hs.317584	ESTs	11.5
	452838	U55011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	11.3
35	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
	449260	AA741180	Hs.29879	ESTs	11.0
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
40	439926	AW014875	Hs.137007	ESTs	10.2
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homeo box A13	10.2
	442660	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
45	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057		NM_007057: Homo sapiens ZW10 Interactor (ZW1N	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
50	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	9.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	9.1
55	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT2RP40	9.1
	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.0
	426427	M86699	Hs.169840	TTK protein kinase	9.0
60	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
	446232	AI281848	Hs.194691	retinoic acid induced 3	8.9
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.9
65	430486	BE082109	Hs.241551	chloride channel, calcium activated, family m	8.7
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178963		gb:MR0-ST0032-200899-001-b11 ST0032 Homo sapi	8.7
	422420	U03398	Hs.1624	tumor necrosis factor (ligand) superfamily, m	8.7
70	458027	L49054	Hs.85195	myeloid leukemia factor 1	8.4
	424086	AI351010	Hs.102267	lysyl oxidase	8.3
	420092	AA814043	Hs.88045	ESTs	8.3
	449034	AI624049		gb:ts41a09.x1 NCLCGAP_U11 Homo sapiens cDNA	8.3
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human, odont	8.2
75	418478	U38945	Hs.11174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440834	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
80	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
	429228	AI553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

	435159	AA668879	Hs.116649	ESTs	7.7
	439232	N48590	Hs.46693	ESTs	7.7
	437616	AI797163	Hs.207954	ESTs	7.6
	405554			Target Exon	7.4
5	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
	424088	AF077374	Hs.139322	small proline-rich protein 3	7.3
	418134	AA397769	Hs.86617	ESTs	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
10	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast	7.1
	414148	BE084049		gb:PMO-BT0651-270400-003402 BT0651 Homo sapi	7.0
	429548	AW138872	Hs.135288	ESTs	7.0
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	7.0
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.0
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila ho	6.9
	431941	AK000108	Hs.272227	Homo sapiens cDNA FLJ20099 fs, clone COL0454	6.9
	427821	AA470158	Hs.98202	ESTs	6.9
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
	425761	AW664214	Hs.198729	ESTs	6.9
20	450028	AI912012	Hs.200737	ESTs	6.8
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	6.8
	413573	AI733859	Hs.149089	ESTs	6.8
	422330	D30783	Hs.115263	epiregulin	6.8
25	454988	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo sapi	6.8
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
	403471			Target Exon	6.7
	409041	AB033025	Hs.50081	KIAA1199 protein	6.7
	407839	AA045144	Hs.161566	ESTs	6.6
30	415652	T79213	Hs.272073	ESTs	6.6
	420900	AL045633	Hs.44269	ESTs	6.6
	444271	AW452569	Hs.149804	ESTs	6.6
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.5
35	431622	AW979271	Hs.293184	ESTs	6.5
	457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202	6.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fs, clone NT2RP20	6.4
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	6.3
40	446435	AW206737	Hs.253582	ESTs	6.3
	421948	L42583	Hs.334309	keratin 6A	6.3
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	6.3
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
	406747	AI925153	Hs.217493	annexin A2	6.2
45	453884	AA355925	Hs.36232	KIAA0186 gene product	6.2
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens c	6.2
	421773	W69233	Hs.112457	ESTs	6.2
	457435	AW972024	Hs.142653	ret finger protein	6.1
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fs, clone HEMBB10	6.1
50	427043	AA397679	Hs.3991	ESTs	6.1
	409723	AW885757	Hs.257862	ESTs	6.1
	459462	AA481398	Hs.105167	ESTs	6.1
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	6.0
	427217	AA399272	Hs.144341	ESTs	6.0
55	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein [Hs	6.0
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferritin a	6.0
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein [Hs	5.9
	413385	M34455	Hs.840	Indoleamine-pyrrole 2,3 dioxygenase	5.9
60	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced prote	5.9
	414299	AA142989	Hs.71730	ESTs	5.8
	439292	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin (140	5.8
	413625	AW451103	Hs.71371	ESTs	5.8
65	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	5.8
	415064	AA159804	Hs.149305	hypothetical protein MGC2603	5.7
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
	415900	Z43758	Hs.26037	ESTs	5.7
70	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
	449611	AI970394	Hs.197075	ESTs	5.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapi	5.7
	438639	AI278360	Hs.31409	ESTs	5.7
	414972	BE263782	Hs.77695	KIAA0008 gene product	5.7
75	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fs, clone COL0042	5.6
	407746	AK001862	Hs.38114	hypothetical protein FLJ11100	5.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
	432239	X81334	Hs.2836	matrix metalloproteinase 13 (collagenase 3)	5.5
80	451307	AW293207	Hs.211516	ESTs	5.5
	441531	AW291239	Hs.271111	ESTs	5.5
	418663	AK001100	Hs.41690	desmocollin 3	5.5
	410659	AI080175	Hs.68826	ESTs	5.5
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo sapi	5.5

	431255	AA497043	Hs.115685	ESTs	5.5
	407366	AF026942		gb:Homo sapiens c1g33 mRNA, partial sequence.	5.5
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
5	418502	R99288	Hs.35152	ESTs	5.4
	440320	AA879294		gb:znr66e09.s1 NCL CGAP_Pr12 Homo sapiens cDNA	5.4
	439579	AF086400		gb:Homo sapiens full length insert cDNA clone	5.4
	420783	AJ659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (gate)	5.4
	408536	AW381532	Hs.135188	ESTs	5.4
10	408758	NM_003686	Hs.47504	exonuclease 1	5.4
	451411	AA017492	Hs.135655	EST	5.4
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.3
	407853	AA336797	Hs.40499	clckkopl (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabbkinesin 6)	5.2
15	420028	AJ831190	Hs.166676	ESTs	5.2
	427356	AW023482	Hs.97849	ESTs	5.2
	420440	NM_002407	Hs.97644	mammaglobin 2	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
	445259	AJ798994	Hs.152923	ESTs	5.2
20	457345	AJ699933	Hs.192175	ESTs	5.2
	453161	AA628608	Hs.61656	ESTs	5.2
	445019	AJ205540	Hs.281295	ESTs	5.2
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	5.2
25	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	5.2
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	5.2
	443179	AJ928402	Hs.6933	hypothetical protein FLJ12684	5.2
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, choline, al	5.2
	441020	W79283	Hs.35962	ESTs	5.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	5.1
30	419520	AB009303	Hs.90800	matrix metalloproteinase 16 (membrane-insert)	5.1
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
	405547			NM_018833*:Homo sapiens transporter 2, ATP-bi	5.1
	435206	AJ432364	Hs.160594	ESTs	5.1
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	5.1
35	439223	AW238299	Hs.250618	UL16 binding protein 2	5.1
	413251	AJ932903	Hs.211535	ESTs	5.1
	426320	W47595	Hs.169300	transforming growth factor, beta 2	5.1
	458829	AJ557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3'	5.0
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
	432473	AJ202703	Hs.152414	ESTs	5.0
	418738	AJ388633	Hs.6682	solute carrier family 7, (cationic amino acid	5.0
	423634	AW959908	Hs.1690	heparin-binding growth factor binding protein	5.0
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016936	Hs.233364	ESTs	5.0
45	449448	D60730	Hs.57471	ESTs	5.0
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (from c	4.9
	405657			C7000246:glj72477 pirj DVHY1C multidrug resis	4.9
	429882	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1	4.9
50	446704	AJ337228	Hs.197083	ESTs	4.9
	434376	AA631492	Hs.23921	hypothetical protein DKFZp547A023	4.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypothetic	4.9
	421155	H87879	Hs.102267	lysyl oxidase	4.9
	443335	T89697	Hs.16645	ESTs	4.9
55	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell growt	4.8
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.8
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elast	4.8
	441720	AJ348487	Hs.28739	ESTs	4.8
	442980	AA857025	Hs.8878	kinesin-like 1	4.8
60	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.8
	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosome seg	4.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosyltran	4.8
	418939	AW630803	Hs.89497	lamin B1	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
65	411958	AA099020		gb:zn45h01.s1 Stratagene HeLa cell s3 937216	4.7
	433858	N69243	Hs.192974	hypothetical protein FLJ12735	4.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	4.7
	418379	AA218940	Hs.137516	fidgetin-like 1	4.7
	401747			Homo sapiens keratin 17 (KRT17)	4.7
70	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA clo	4.7
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	4.7
	457465	AW301344	Hs.122908	DNA replication factor	4.6
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.6
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapi	4.6
	401137			Target Exon	4.6
75	401575			Target Exon	4.6
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL0667	4.6
	421978	AJ243662	Hs.110196	NICE-1 protein	4.6
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PLACE10	4.6
80	450510	AA010056	Hs.242998	ESTs	4.6
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.6
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184501	solute carrier family 7 (cationic amino acid	4.5
	449416	AJ651016	Hs.246311	ESTs	4.5

5	416168	H23587	gb:yn72d12r1 Soares adult brain N2b5HB55Y Ho	4.5
	447033	AI357412	Hs.157601	4.5
	446353	AI290919	Hs.153661	4.5
	443715	AI583187	Hs.9700	4.5
	454707	AW814989	cyclin E1	4.5
	435435	T89473	gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapi	4.5
	412099	U84198	ESTs	4.5
	409731	AA125985	interleukin 12 receptor, beta 2	4.4
10	422809	AK001379	thymosin, beta, identified in neuroblastoma c	4.4
	430919	AA489041	hypothetical protein FLJ10549	4.4
	435313	AI769400	ESTs	4.4
	425071	NM_013989	ESTs	4.4
	433322	H50621	deiodinase, iodothyronine, type II	4.4
15	416111	AA033813	ESTs, Weakly similar to I38022 hypothetical p	4.4
	408908	BE296227	chromatin assembly factor 1, subunit A (p150)	4.4
	444781	NM_014400	serine/threonine kinase 15	4.4
	429170	NM_001394	GPI-anchored metastasis-associated protein ho	4.4
	414035	Y00630	dual specificity phosphatase 4	4.4
20	418216	AA662240	serine (or cysteine) proteinase inhibitor, cl	4.4
	446252	AI283125	AF15q14 protein	4.4
	447519	U46258	ESTs	4.4
	425916	NM_006786	ESTs	4.4
	409420	Z15008	urotensin 2	4.3
25	416320	H47867	laminin, gamma 2 (nicotin (100kD), kalinin (10	4.3
	431808	M30703	ESTs	4.3
	441582	BE550200	amphiregulin (schwannoma-derived growth facto	4.3
	414132	AI801235	ESTs	4.3
	424012	AW368377	ESTs	4.3
30	411835	U29343	tumor protein 63 kDa with strong homology to	4.3
	433330	AW207084	hyaluronan-mediated motility receptor (RHAMM)	4.3
	428613	AB037749	hypothetical protein MGC14801	4.3
	425921	NM_007231	KIAA1328 protein	4.3
	447078	AW885727	solute carrier family 6 (neurotransmitter tra	4.3
35	434699	AA643687	ESTs	4.3
	428758	AA433988	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	4.3
	405708		hypothetical protein FLJ14303	4.3
	433405	AW157566	Target Exon	4.3
	456443	AW967500	ESTs	4.3
40	428479	Y00272	ESTs	4.2
	448621	AI097144	cell division cycle 2, G1 to S and G2 to M	4.2
	412608	AA247995	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	4.2
	406687	M31126	Homo sapiens clone TCCCTA00151 mRNA sequence	4.2
	455365	AW948343	pregnancy specific beta-1-glycoprotein 9	4.2
45	452930	AW195285	gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
	430134	BE380149	ESTs, Weakly similar to I38022 hypothetical p	4.2
	423035	AW449679	ESTs, Weakly similar to T33188 hypothetical p	4.2
	427666	AI791495	H.sapiens XG mRNA (clone PEP11)	4.2
	444602	AI174456	calmodulin-like skin protein	4.2
50	417791	AW965339	ESTs, Moderately similar to I38022 hypothetic	4.2
	444266	AI424984	ESTs	4.2
	439394	AA149250	ESTs	4.2
	457336	AW969657	ESTs	4.2
	429125	AA446854	ESTs, Weakly similar to I38022 hypothetical p	4.2
55	404440		NM_021048:Homo sapiens melanoma antigen, fam1	4.2
	449228	AJ403107	protein related with psoriasis	4.2
	437144	AL049466	ESTs	4.2
	448599	AW860912	gb:QV0-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
60	431810	X67155	kinasin-like 5 (mitotic kinasin-like protein	4.2
	419991	AJ000098	eyes absent (Drosophila) homolog 1	4.2
	444361	W76027	hypothetical protein FLJ11105	4.2
	458116	AW977549	KIAA1785 protein	4.1
	444105	AW189097	ESTs	4.1
	426010	AA136563	hypothetical protein FLJ21007	4.1
65	409632	W74001	serine (or cysteine) proteinase inhibitor, cl	4.1
	408096	BE250162	dihydrofolate reductase	4.1
	457620	AA602711	EST	4.1
	402048		Target Exon	4.1
	427025	AA397589	ESTs	4.1
70	423515	AA327017	ESTs	4.1
	423891	AK002042	Homo sapiens cDNA FLJ11180 fis, clone PLACE10	4.1
	455310	AW893961	gb:RC4-NN0027-060400-011-d11 NN0027 Homo sapi	4.1
	418696	AW959433	hypothetical protein FLJ12581	4.1
	426642	AW068223	ubiquitin C-terminal hydrolase UCH37	4.1
75	423738	AB002134	airway trypsin-like protease	4.1
	448243	AW369771	integrin, beta 8	4.1
	411559	BE144081	gb:MRO-HT0165-030200-007-d06 HT0165 Homo sapi	4.1
	423553	AA405635	ESTs, Weakly similar to DYX_HUMAN CYTOPLASMI	4.1
	457030	AI301740	dihydropyrimidinase-like 2	4.1
80	424115	AA335497	ESTs, Weakly similar to I38022 hypothetical p	4.1
	432374	W68815	Homo sapiens cDNA FLJ11346 fis, clone PLACE10	4.1
	424745	AA214618	activator of S phase kinase	4.0
	433384	AI021992	ESTs	4.0
	448995	AI613276	guanine nucleotide binding protein (G protein	4.0

5	448504	A1858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
	424794	M85646	Hs.210696	ESTs	4.0
	432184	AW971125		gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0
	408321	AW405882	Hs.44205	cortistatin	4.0
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.0
10	447724	AW298375	Hs.24477	ESTs	4.0
	446155	A1553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H06382	Hs.21400	ESTs	4.0
15	415857	AA856115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
	438390	A1422017		gb:tt45f12.x1 NCLCGAP_Bm23 Homo sapiens cDN	4.0
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	4.0
	429900	AA460421	Hs.30875	ESTs	4.0
	421270	H66037	Hs.108146	ESTs	3.9
20	430733	AW975920	Hs.283361	ESTs	3.9
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE581665	Hs.177677	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
25	404959			NM_025001*:Homo sapiens hypothetical protein	3.9
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.9
	428536	A1143139	Hs.2288	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H.sapi	3.9
	432757	AF113013	Hs.278919	PRO0808 protein	3.9
30	418686	Z36830	Hs.87268	annexin A8	3.9
	437845	AA769678	Hs.90488	ESTs	3.9
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.9
	419312	AA831850	Hs.58149	hypothetical protein MGC14136	3.9
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	3.9
35	410553	AW016824	Hs.255527	hypothetical protein MGC14128	3.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.9
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB10	3.9
	442163	AT91749	Hs.128896	ESTs	3.9
	438656	H85310	Hs.209456	ESTs, Weakly similar to NG22 [H.sapiens]	3.9
40	406560			ENSP00000016943*:CDNA	3.8
	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33)	3.8
	404132			Target Exon	3.8
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	ESTs	3.8
45	433289	AF005258		gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8
	436149	AJ764308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bindl	3.8
	405545			(MDR/TAP) (TAP2)	3.8
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
	409687	T51125	Hs.8493	ESTs	3.8
	407291	AA001464		gb:z45b01.r1 Soares retina N2b4HR Homo sapie	3.8
	415532	R14780	Hs.12826	ESTs	3.8
	402047	AK001921	Hs.169575	hypothetical protein MGC2550	3.8
55	415317	Z43388		gb:HSC1AF121 normalized infant brain cDNA Hom	3.8
	438777	AA825487	Hs.142179	ESTs	3.8
	422938	NM_001809	Hs.1694	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bu	3.7
	405943			Target Exon	3.7
60	430886	NM_001942	Hs.2633	desmoglein 1	3.7
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone Z3578 mRNA sequence	3.7
	418582	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
65	433849	BE465884	Hs.280728	ESTs	3.7
	449592	A1655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435812	AA693537	Hs.321411	ESTs	3.7
	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clone 22d	3.7
70	418735	N48769	Hs.44609	ESTs	3.7
	444707	A188613	Hs.41690	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450813	A1702055		gb:tg20g10.x1 NCLCGAP_U11 Homo sapiens cDNA	3.7
	418969	V33181	Hs.28907	hypothetical protein FLJ20258	3.7
75	432837	AA310693	Hs.87329	HSPC072 protein	3.7
	442353	BE378594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	A1806335	Hs.200829	ESTs, Weakly similar to T30171 ninein - mouse	3.7
80	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapi	3.7
	409582	R27430	Hs.271555	ESTs	3.6
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	455575	BE080825		gb:QV1-BT0631-180200-078-c08 BT0631 Homo sapi	3.6
5	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	GE36 gene	3.6
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.6
10	420373	AW968228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
15	434321	AA629368		gb:z78a11.s1 Soares_testis_NHT Homo sapiens	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
	427335	AA448542	Hs.251677	G antigen 7B	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	3.6
20	426749	AI623718	Hs.105618	ESTs	3.6
	443899	AW842283	Hs.79933	cyclin I	3.6
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H.sapi	3.6
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin 1	3.5
25	408667	AA437199	Hs.656	cell division cycle 26C	3.5
	428508	BE252383	Hs.184668	SBBI31 protein	3.5
	431120	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557::Homo sapiens keratin 16 (focal non	3.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
30	456671	AB011142	Hs.114293	KIAA0570 gene product	3.5
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP10 (HT	3.5
	435244	N77221	Hs.187824	ESTs	3.5
	436246	AW450963	Hs.119991	ESTs	3.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.5
35	443113	AI040686	Hs.132908	ESTs	3.5
	443341	AW631480	Hs.8668	ESTs	3.5
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
	418347	AA216419		gb:nc16e03.s1 NCL_CGAP_Pr1 Homo sapiens cDNA	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
40	408633	AW963372	Hs.46677	PRO2000 protein	3.5
	427878	CD5766	Hs.181022	CGI-07 protein	3.5
	419945	AW290975	Hs.118923	ESTs	3.5
	448372	AW445166	Hs.170802	ESTs	3.5
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS	3.5
45	411274	NM_002776	Hs.69423	kallikrein 10	3.5
	400666			NM_002425:Homo sapiens matrix metalloproteinase	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
	402639			Target Exon	3.4
	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
50	412471	M53193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
	456296	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.4
	429274	AI379772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.335799	ESTs	3.4
55	419807	R77402		gb:yl75f11.s1 Soares placenta Nb2HP Homo sapi	3.4
	451778	AI826131	Hs.71243	ESTs, Weakly similar to zinc finger protein [3.4
	430397	AI924533	Hs.105607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23960	cyclin B1	3.4
60	455092	BE152428		gb:CMO-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
	418203	XS4942	Hs.83758	CDC28 protein kinase 2	3.4
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked molecu X	3.4
65	434206	AW136973	Hs.288518	ESTs, Weakly similar to S68890 mitogen induci	3.4
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	3.4
	438993	AA828995		gb:od77b08.s1 NCL_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target Exon	3.4
70	435360	AF105366	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to IS4374 gene NF2 prote	3.4
	443462	AI064690	Hs.171176	ESTs	3.3
	444910	AI201849		gb:qs76g04.x1 NCL_CGAP_Pr28 Homo sapiens cDNA	3.3
75	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from c	3.3
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	3.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	3.3
	419751	AW195581	Hs.93121	KIAA0751 protein	3.3
80	404782			C7001692::gij6724096[gb]AAF26844.1j (AF195021	3.3
	415613	R20233		gb:yg18h11.1r1 Soares infant brain 1N1B Homo s	3.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical p	3.3
	406599			Target Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3

	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
	421107	AA283822	Hs.55606	ESTs, Weakly similar to S47072 finger protein	3.3
	436985	AA740946	Hs.150895	ESTs	3.3
	443903	AI220547	Hs.135223	ESTs	3.3
5	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp58600724 (from c	3.3
	447153	AA805202	Hs.315562	ESTs	3.3
	450769	AA057418	Hs.33654	ESTs	3.3
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.3
	402481			NM_001821*:Homo sapiens choroideremia-like (R	3.3
10	459394	BE409894	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, complete	3.3
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
	417708	N74392	Hs.50495	ESTs	3.3
	414869	AA157291	Hs.21479	ublnuclein 1	3.3
	441690	R81733	Hs.33106	ESTs	3.3
15	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	zinc finger protein	3.3
	412903	BE007967	Hs.155795	ESTs	3.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placental)	3.3
	451177	AI969716	Hs.13034	ESTs	3.3
20	409990	AA079337		gb:zm95b09.r1 Stratagene colon HT29 (937221)	3.3
	418462	BE001596	Hs.85266	Integrin, beta 4	3.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	3.3
	405196			C2000662*:gi7512792[pir]T12482 hypothetical	3.3
25	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA libra	3.3
	432917	NM_014125	Hs.279812	PRO0327 protein	3.3
	448251	BE280486	Hs.84045	hypothetical protein FLJ20288	3.3
	415025	AW207091	Hs.72307	ESTs	3.3
	420218	AW958037	Hs.286	ribosomal protein L4	3.2
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB10	3.2
30	447762	AI939461	Hs.161370	ESTs	3.2
	414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
	445038	AI635444	Hs.143917	dJ467N11.1 protein	3.2
	448666	NM_014953	Hs.323346	KIAA1008 protein	3.2
	402800			Target Exon	3.2
35	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.2
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cere	3.2
	455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapi	3.2
	459666	W27362		gb:30g7 Human retina cDNA randomly primed sub	3.2
	401458			Target Exon	3.2
40	432361	AI378562	Hs.159585	ESTs	3.2
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLICING F	3.2
	405336			Target Exon	3.2
	446563	BE326588	Hs.141454	ESTs	3.2
	449276	AW241510	Hs.252713	ESTs	3.2
45	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
	420591	X53655	Hs.99171	neurotrophin 3	3.2
	401486			C4000647*:gi4758508[ref]NP_004253.1[] airway	3.2
	432979	AA573263	Hs.120860	ESTs	3.2
	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.2
50	438325	AA804258	Hs.123229	ESTs	3.2
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha-1C-a	3.2
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cysteine-r	3.2
	421777	BE562088	Hs.108196	HSPC037 protein	3.2
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone ADKA02	3.2
55	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone LNG004	3.2
	402337			Target Exon	3.2
	420930	AW888650		gb:CM4-NT0007-130500-551-406 NT0007 Homo sapi	3.2
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HEMBA10	3.2
60	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.1
	437641	AA811452	Hs.291911	ESTs	3.1
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
	434208	T92641	Hs.127648	hypothetical protein PRO2176	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.1
65	458923	Y12812	Hs.24422	regulatory factor X-associated protein	3.1
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, ep	3.1
	439750	AL359053	Hs.57684	Homo sapiens mRNA full length insert cDNA clo	3.1
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevisiae,	3.1
	445885	AI734009	Hs.127699	KIAA1603 protein	3.1
70	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.1
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine protein k	3.1
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription factor	3.1
75	455987	BE178323		gb:RC3-HT0600-240400-023-g05 HT0600 Homo sapi	3.1
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA, part	3.1
	423887	AL080207	Hs.134585	DKFZP434G232 protein	3.1
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.1
	447815	AI432199	Hs.247084	ESTs	3.1
	441974	AI683782	Hs.128245	ESTs	3.1
80	448474	AI301227	Hs.150186	hypothetical protein DKFZp566K1946	3.1
	452166	AI948607	Hs.264680	ESTs	3.1
	451659	BE379761	Hs.14248	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1

	447701	BE619526	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AI085377	Hs.143610	ESTs	3.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
5	449441	AI656040	Hs.195532	ESTs	3.1
	458145	AI239457	Hs.130794	ESTs	3.1
	444588	AI221321	Hs.167559	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195684	ESTs	3.1
10	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT2RP30	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB55Y Ho	3.1
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S. cere	3.1
	404107			Target Exon	3.1
15	419553	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (from c	3.1
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM040	3.1
	442824	BE178065	Hs.144081	ESTs	3.1
	435061	AI651474	Hs.163944	ESTs	3.1
20	420589	AA419360	Hs.192708	ESTs	3.0
	434569	AI311295	Hs.8294	KIAA0196 gene product	3.0
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
	406037			Target Exon	3.0
25	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
	459587	AA031958		gb:zkl5e04.s1 Soares_pregnanLuterus_NbHPU Ho	3.0
	435990	AI015862	Hs.131793	ESTs	3.0
	442577	AA292998	Hs.163900	ESTs	3.0
30	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
	458154	AW816379	Hs.335018	ESTs	3.0
	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950087		gb:wg05cd02.x1 NCL_CGAP_Kid12 Homo sapiens cDN	3.0
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.0
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810027O1	3.0
	445505	AI971156	Hs.148891	ESTs	3.0
	425005	AI558551		gb:tn07g03.x1 NCL_CGAP_Bm25 Homo sapiens cDN	3.0
	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
40	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens cDNA	3.0
	453509	AI040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
	455750	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA161071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
45	417734	Z42667	Hs.6724	ESTs	3.0
	449676	AW380579	Hs.209657	ESTs	3.0
	445425	AI223511	Hs.300722	ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:UI-H-BI2-atv-h-03-0-UI.s1 NCL_CGAP_Sub4 Ho	3.0
50	444477	AI150548	Hs.23155	ESTs	3.0
	446255	AI283257	Hs.257090	ESTs	3.0
	400612			C10001034:gij7513113 pir T13078 KIAA0992 pro	3.0
	450841	AI741466	Hs.270515	ESTs	3.0
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
55	433871	W02410	Hs.205555	ESTs	3.0
	401994			Target Exon	3.0
	449272	AW137658	Hs.197645	ESTs	3.0
	409703	NM_006187	Hs.56009	Z-5'-oligoadenylate synthetase 3 (100 kD)	3.0
	400250			Eos Control	3.0
60	408015	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
	436414	BE264633	Hs.143638	WD repeat domain 4	3.0
	432220	AI571306	Hs.232224	ESTs	3.0
	420831	AA280824	Hs.190035	ESTs	3.0
	433544	AW342028		gb:hb75d03.x1 NCL_CGAP_U12 Homo sapiens cDNA	3.0
65	447313	U92981	Hs.18081	Homo sapiens clone DT1P196 mRNA, CAG repeat r	3.0
	428262	AI651324	Hs.7298	bi-phenyl hydrolase-like (serine hydrolase; br	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.0
70	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2 (dihy	3.0
	423556	R72694	Hs.7720	dymein, cytoplasmic, heavy polypeptide 1	3.0
	426890	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.136672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.9
75	402556			C1001383:gij536595 pir A61183 hypothetical	2.9
	411098	AW817238		gb:QVO-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
	435399	AA679463		gb:ac50c03.s1 Stratagene hNT neuron (937233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
80	410658	AW105231	Hs.192035	ESTs	2.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TCBAP103235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621:Keratin, type II cytoskeletal	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

	455319	AW895387		gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118654	ESTs	2.9
5	432215	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.9
	434423	NM_006769	Hs.3844	LIM domain only 4	2.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	2.9
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapi	2.9
	436148	BE005252	Hs.321583	Homo sapiens cDNA FLJ20779 fis, clone COL0507	2.9
10	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.9
	404981			ENSP00000252242:Keratin, type II cytoskeletal	2.9
	448796	AA147829	Hs.301431	endothelial zinc finger protein induced by tu	2.9
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760			Target Exon	2.9
	443859	NM_013409	Hs.9914	folliculin	2.9
15	404253			NM_021058: Homo sapiens H2B histone family, m	2.9
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	2.9
	435867	AA954229	Hs.114052	ESTs	2.9
	429035	BE549781	Hs.270475	ESTs	2.9
20	446733	AA853360	Hs.26040	ESTs, Weakly similar to fatty acid omega-hydr	2.9
	446417	AI299050		gb:qn14d12.x1 NC1_CGAP_Lu5 Homo sapiens cDNA	2.9
	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.9
	452452	BE393822	Hs.29845	Homo sapiens mRNA; cDNA DKFZp761C029 (from cl	2.9
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	2.9
25	450698	W31489	Hs.95044	ESTs, Weakly similar to I38022 hypothetical p	2.9
	439430	AF124250	Hs.6564	cervical cancer anti-estrogen resistance 3	2.9
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502	ESTs	2.9
	401781			Target Exon	2.9
30	439625	AF086453	Hs.58611	ESTs	2.9
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical p	2.9
	410743	AA089474	Hs.272153	ESTs	2.9
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AJ668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
35	443479	AF027219	Hs.9443	zinc finger protein 202	2.9
	442601	AJ684969	Hs.46772	ESTs	2.9
	405932			C15000305:gi 3806122 gb AAC69198.1 (AF097887	2.9
	405454			C12000541:gi 5729884 ref NP_006539.1 IGF-II	2.9
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	2.9
40	408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, parti	2.9
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
	414581	AA256213	Hs.72010	ESTs	2.9
	411268	AK000512	Hs.69388	hypothetical protein FLJ20505	2.9
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_1NFLS	2.9
45	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugat	2.9
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.9
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical p	2.9
50	435711	AF226667	Hs.58553	CTP synthase II	2.9
	419088	AI538323	Hs.52620	integrin, beta 8	2.8
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clone IF	2.8
	429299	AI620463	Hs.293984	hypothetical protein MGC13102	2.8
	451702	AW665452	Hs.246503	ESTs	2.8
55	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.8
	405281			NM_002864: Homo sapiens pregnancy-zone protein	2.8
	438161	BE089028	Hs.20158	ESTs, Weakly similar to S34159 transcription	2.8
	409103	AF251237	Hs.112208	XAGE-1 protein	2.8
	425599	AW366745	Hs.214140	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
60	425274	BE281191	Hs.155462	minichromosome maintenance deficient (m1s5, S	2.8
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.8
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216	ESTs	2.8
	413083	BE064528		gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapi	2.8
65	437030	AA742577	Hs.303781	EST	2.8
	438113	AI467908	Hs.8882	ESTs	2.8
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone LNG096	2.8
	440994	AI160011	Hs.193341	ESTs	2.8
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HEMBA10	2.8
70	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin, tissu	2.8
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.8
	433788	AI810534	Hs.181275	ESTs	2.8
	403806			Target Exon	2.8
75	437182	AL080098		gb:Homo sapiens mRNA; cDNA DKFZp564C1072 (fro	2.8
	453955	AW579207	Hs.304666	ESTs, Weakly similar to I78885 serine/threonin	2.8
	420795	AA323037	Hs.128645	sorting nexin 16	2.8
	452696	AI826845	Hs.211534	ESTs	2.8
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.8
80	438052	AA776564	Hs.41891	zinc finger 1111	2.8
	441755	AW450826	Hs.127786	ESTs	2.8
	427981	AW293165	Hs.143134	ESTs	2.8
	449785	AI225235	Hs.288300	hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072	ESTs	2.8

	405831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.65666	Thyroid hormone receptor interactor 13	2.8
5	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
	448979	AI611378	Hs.192610	ESTs	2.8
	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410664	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250716	Hs.87614	ESTs	2.8
10	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
	445941	AI267371	Hs.172636	ESTs	2.8
	459719	AW749511	Hs.301554	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW284416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP20	2.8
15	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothetical p	2.8
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	438846	T63959	Hs.228320	hypothetical protein FLJ23537	2.8
20	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.8
	455091	BE079752		gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8
	452571	W31518	Hs.34665	ESTs	2.8
25	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8
	426343	NM_014642	Hs.169387	KIAA0036 gene product	2.8
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4	2.7
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.7
30	429128	AA446869	Hs.119316	ESTs	2.7
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	2.7
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.7
	403763			NM_001059*Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetical	2.7
35	406753	AA505665	Hs.217493	annexin A2	2.7
	415747	AA381209		gb:EST94257 Activated T-cells 1 Homo sapiens	2.7
	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
40	456181	L36463	Hs.1030	ras inhibitor	2.7
	416548	H62953		gb:yr4706.r1 Soares fetal liver spleen 1NFLS	2.7
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGE	2.7
45	417398	N78541	Hs.177366	ESTs	2.7
	408380	AF123050	Hs.44532	diubiquitin	2.7
	437724	AW444828	Hs.184323	ESTs	2.7
	408680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
	454202	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo sapi	2.7
50	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli RecA ho	2.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.7
	406092			Target Exon	2.7
	447748	AI422023	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
55	433743	AF075312	Hs.236760	Homo sapiens clone HQ0262	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
	405675			Target Exon	2.7
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-Rike)	2.7
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	2.7
60	448592	N69546	Hs.44563	hypothetical protein	2.7
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA10	2.7
	407287	AI678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA	2.7
	448276	BE514434	Hs.20830	kinasin-like 2	2.7
	412977	AA125910	Hs.191461	ESTs	2.7
65	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
	417357	AF260257	Hs.131917	retinitis pigmentosa GTPase regulator interac	2.7
	400298	AA032279	Hs.61635	slx transmembrane epithelial antigen of the p	2.7
	416294	D86980	Hs.79170	KIAA0227 protein	2.7
	458201	AI889961	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
70	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
	401230			NM_014191*Homo sapiens sodium channel, volta	2.7
	422058	AA862231	Hs.334443	ESTs	2.7
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.7
	430152	AB001325	Hs.234642	aquaporin 3	2.7
75	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.7
	443500	AV646388	Hs.93981	Homo sapiens mRNA; cDNA DKFZp667D095 (from cl	2.7
	418030	BE207573	Hs.83321	neuromedin B	2.7
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [Hsapiens]	2.7
	418869	AW516555		gb:bxq01d05.x1 Soares_NHCeC_cervical_tumor Hom	2.7
80	431688	AA513906		gb:mg67c08.s1 NCI_CGAP_Lip2 Homo sapiens cDNA	2.7
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	2.7
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	AI160386	Hs.125087	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

5	44659	AI35361	Hs.226376	ESTs	2.7
	419833	AA251131	Hs.220697	ESTs	2.7
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi	2.6
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothetical p	2.6
	446102	AW168067	Hs.252956	ESTs	2.6
	441408	AI733249	Hs.126897	ESTs	2.6
	436027	AJ864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transc	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
10	421470	R27496	Hs.1378	annexin A3	2.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnoid	2.6
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276866	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
15	433288	AI368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi	2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [Hs	2.6
	401260			C1001031*gi 7305041 ref NP_038876.1 erythro	2.6
20	435136	R27299	Hs.10172	ESTs	2.6
	412108	AA100293	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
25	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	2.6
	409594	AA076118		gb:zm18e06.s1 Stratagene pancreas (937208) Ho	2.6
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (937208) Ho	2.6
	423038	D26628	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
30	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth factor	2.6
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663		gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi	2.6
	408625	AW243323	Hs.266785	ESTs	2.6
35	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ectoe	2.6
	431890	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	centromere protein F (350/400kD, milosin)	2.6
40	401050			NM_014155*:Homo sapiens HSPC063 protein (HSPC	2.6
	405897			Target Exon	2.6
	451153	BE092900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC FINGE	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
45	404184			NM_030903*:Homo sapiens olfactory receptor, f	2.6
	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
50	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
	449432	AW451361	Hs.196529	ESTs	2.6
	425062	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U90304	Hs.25351	Iroquois homeobox protein 5	2.6
55	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.6
	408391	AW859276		gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapi	2.6
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mouse)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
60	453331	AI240665	Hs.8895	ESTs	2.6
	447175	AI365208	Hs.293608	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE288215	Hs.288968	RAB22A, member RAS oncogene family	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
65	434557	AW855466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435663	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
70	418067	AI27958	Hs.83393	cystatin E/M	2.6
	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
	407471	D55844		gb:Human spleen PABL (pseudautosomal boundar	2.6
75	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, complete	2.6
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from c	2.6
	425415	M13903	Hs.157091	Involucrin	2.6
	444826	AI674482	Hs.148441	ESTs	2.6
80	413331	BE083950		gb:PMO-BT0651-260200-001-b11 BT0651 Homo sapi	2.6
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001706*gi 1345652 sp P15989 CA38_CHICK COL	2.6
	413864	BE175582		gb:RCS-HT0580-100500-022-C01 HT0580 Homo sapi	2.6

	438746	AI885815	Hs.184727	ESTs	2.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
5	412723	AA648459	Hs.335951	hypothetical protein AF301222	2.5
	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.5
	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo sapi	2.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapi	2.5
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telencepha	2.5
10	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.5
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (from cl	2.5
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455549	AW994222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
	409676	AA077118	Hs.197298	NS1-binding protein	2.5
15	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201877	DESC1 protein	2.5
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	2.5
20	452834	AI638627	Hs.105685	KIAA1688 protein	2.5
	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455095	AW855598		gb:CM1-CT0278-031199-032-e08 CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kd (connexin	2.5
25	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.5
	458175	AW296024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
	453379	AA035261	Hs.61753	ESTs	2.5
30	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
	412313	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	2.5
	443767	H05479	Hs.62314	ESTs	2.5
	449300	AI656959	Hs.222165	ESTs	2.5
35	434913	AW872860	Hs.11056	RALBP1 protein	2.5
	448946	AI652856	Hs.23363	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp761L23121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10789	Hs.191990	ESTs	2.5
40	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	2.5
	449344	AI640355	Hs.312691	ESTs	2.5
	439436	BE140845	Hs.57868	ESTs	2.5
	449867	AI672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE158006	Hs.212296	ESTs	2.5
45	433675	AW977553	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo sapien	2.5
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	hypothetical protein MGC10520	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
50	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	AI014546	Hs.130912	ESTs	2.5
	411768	NM_013371	Hs.71979	Interleukin 19	2.5
55	436961	AW376974	Hs.156704	ESTs	2.5
	431124	AF284221	Hs.69506	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
60	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogene hom	2.5
	442966	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
65	440381	AA917808	Hs.190495	ESTs	2.5
	403983			Target Exon	2.5
	451340	AW936273		gb:QV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE620911	Hs.126889	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
70	424153	AA451737	Hs.141496	MAGE-like 2	2.5
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435647	AI653240	Hs.49823	ESTs	2.5
	428780	AI478578	Hs.50636	ESTs	2.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.5
75	422565	BE269035	Hs.118400	singed (Drosophila)-like (sea urchin fascin h	2.5
	428054	AI948688	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	2.5
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AI053464	Hs.165505	ESTs	2.5
80	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
	438214	H06076	Hs.26320	TRABID protein	2.5
	446745	AW118189	Hs.156400	ESTs	2.5
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 12B

Pkey: Unique Eos probaset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407642	1007175_1	AW178963 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845585 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW806969 AW845686 BE141054 BE141040 BE141044 BE141042 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178968 AW859276 AW859274 AW190959 T91463 AW864542 AA056567 AW882724 AA076118 AA976518 AA076220 AA296961 AA296889 AA076945 AA077528 AA077497 AA079337 AA079338 AW272100 AA079552 BE142525 BE142527 AW579475 AW939654 AW939655 AW803201 BE079700 BE062940 AW817238 AW993985 AW993998 AW820260 AW820332 R94406 AW847663 AW847861 AW861080 BE144081 BE144190 AW851155 AW947884 AW947918 AW947888 AW947897 AW947910 AW947905 AW864751 AW947878 AA099020 AW751275 AW751276 AW751289 BE245511 BE246133 AW935247 AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW936760 AW936819 AW937485 AW937589 AW937658 AW937654 AW937492 AW945964 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039 AW946045 AW946028 AW946036 BE092219 BE092361 BE060789 BE064528 BE064589 BE064561 BE083950 BE084017 BE084016 BE175582 BE175514 BE175505 BE175591 BE175530 BE091634 BE084049 AW292907 AA135984 Z43388 F05453 R19673 R20275 H06917 R20233 F12901 T74740 AA381209 AA381245 AA167683 H48739 H51513 H19779 H23687 H46460 H40239 H62953 N76608 N72413 R64719 Z44680 R12451 AA216419 F03238 AA229517 AW516565 AA229762 AA230035 R77402 AA262462 AA250988 R06794 AW958228 AA259146 W01465 AW976163 AA278945 AA747691 AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652 AW856665 AA315006 AW954733 AA330281 AA330232 AW962521 AA330259 AA661806 AA502431 AW974633 AA649496 AW753967 AA370795 AA331630 AW962550 A1565851 AA349656 R24788 AA884766 AW974271 AA52975 AA447312 AA492588 AA492498 AA492571 AW970622 AA503009 AA502998 AA502889 AA502806 T92188 AA513906 AA847734 A1357044 AW971125 AA527731 N52655 A1821608 AA532420 AA527941 A1810608 A1820190 AA635266 AW974094 AA569074 AA602574 AF005258 AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832 AW342028 AA641080 AA603282 AA629368 AW849574 AW849573 AA679463 AW813779 AW813709 AL080098 AL037472 AA432051 A1950087 N70208 R97040 N36809 A1308119 AW967677 N35320 A1251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 A1820501 A1820532 W87891 T85904 U71458 T82391 BE328571 T75102 R34725 AA884922 BE328517 A1219788 AA884444 N92578 F13493 AA927794 A1560251 AW874068 A134043 AW235363 AA663345 AW008282 AA488964 AA283144 A1890387 A1950344 A1741346 A1689062 AA282915 AW102898 A1872193 A1763273 AW173588 AW150329 A1533832 A1762688 AA988777 AA488892 A1356394 AW103813 A1539542 AA642789 AA856975 AW505512 A1961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 A1819225 AW205852 A1683338 A1858509 AW276905 A1633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 A1022056 AA780419 AA551005 W80701 AW613456 A1373032 A1564269 F00531 H83488 W37181 W78802 R66056 A1002839 R67840 AA300207 AW959581 T63226 F04005 AA22017 A1422945 A1383249 A1423113 A1925592 A1420795 A1208187 A1423279 A1423645 A1424090 A1359637 AL044732 D17003 AW979074 AA834841 AA828650 AA828995 AA834879 A1926361
408391	1055687_1	
408690	107490_1	
409594	114249_1	
409695	114876_1	
409990	116644_1	
410008	116812_1	
410049	1172307_1	
410784	1221005_1	
411098	1232093_1	
411171	1234393_1	
411465	1246768_1	
411559	1249417_1	
411819	1259748_1	
411958	126717_1	
412279	1287332_1	
412313	1288355_1	
412333	1289037_1	
412367	1291505_1	
412879	1334272_1	
413083	1348639_1	
413331	1361726_1	
413864	1395788_1	
414147	142127_1	
414148	142133_1	
415317	1533847_1	
415613	1540602_1	
415747	155189_1	
416120	1571266_1	
416168	1574545_1	
416548	1600181_1	
417742	1696282_1	
418347	174149_1	
418869	179863_1	
419807	188252_1	
420373	193194_1	
420637	195241_1	
420830	197736_1	
422889	219896_1	
423733	231476_1	
423735	231498_1	
423841	232507_1	
425005	245908_1	
429163	300543_1	
431120	328264_1	
431322	331543_1	
431688	336609_1	
432184	342677_1	
432189	342819_1	
432869	355475_1	
433289	36202_1	
433584	370400_1	
433644	371919_1	
434321	383473_1	
435399	405576_1	
437182	43421_1	
437938	44573_2	
438390	45662_1	
438966	467436_1	
438993	467651_1	

5	439579	47404_1	AF086400 W79232 W73990
	440320	491930_1	AA879294 N67538 A474541
	444910	624951_1	AI201849 BE069007 AW946544
	446417	676384_1	AI299050 BE256910
	447197	711623_1	R36075 AI366546 R36167
	448599	770766_1	AW860912 AI540866
	449034	794817_1	AI624049 AW117770 AI858360
	450024	82296_1	AA005129 AA679084 AA694399
10	450613	840016_1	AI702055 R89204 R86260
	451105	859083_1	AI761324 AW880941 AW880937
	451153	86054_1	BE092900 AA015877 AA018521
	451340	86640_1	AW936273 AW340350 AA017208
	454202	1050507_1	AW178353 AW846011 AW845964 AW845988 AW845977 AW846002
	454241	1067807_1	BE144668 BE184942 AW238414 BE184946
15	454707	1230250_1	AW814989 AW814852 AW814808
	454891	1239217_1	AW837349 AW837355 AW882717
	454988	1248607_1	AW850140 AW850195 AW850192
	455091	1252939_1	BE079752 BE079868 BE148989 AW855532 BE148818 BE148815 BE148796
	455092	1252971_1	BE152428 AW855572 AW855607
20	455095	1252987_1	AW855598 AW855608 BE148764 AW855845 AW855615 AW855596 AW855610 AW855601 AW855605
	455203	1259973_1	AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455319	1279172_1	AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538
	455365	1284681_1	AW948343 AW948341 AW902855 AW984737
25	455549	1324696_1	AW994222 AW994377
	455666	1349545_1	BE065813 BE065788 BE065889 BE065832
	455750	1355998_1	BE075114 BE075283 BE075118
	455838	1374605_1	BE145808 BE145807 BE181883
	455987	1397735_1	BE178323 BE177978
30	457405	333127_1	AA504860 AA504911
	458829	773443_1	AI557388 BE158936
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 12C

35	Pkey:	Unique number corresponding to an Eos probaset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
40	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
45	400612	9929646	Minus	151513-151662
	400668	8118496	Plus	17982-18115,20297-20456
	401050	8117628	Minus	78449-79425
	401137	2547238	Minus	598-1009
	401230	9929627	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
50	401260	8076883	Minus	86008-86355
	401367	9796198	Minus	145356-145807
	401458	9187886	Plus	76485-77597
	401486	7341763	Plus	32585-32766,36281-36540,40791-40933,44018-44179
	401575	7229804	Minus	76253-76364
55	401747	9789872	Minus	118598-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131865-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
60	402048	8072512	Plus	43936-44078
	402298	6598824	Plus	36758-37953
	402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
	402481	9797406	Plus	87891-88991
	402556	9863723	Plus	13579-14026
65	402639	9958129	Minus	20167-22383
	402800	6010175	Plus	43921-44049,46181-46273
	402892	8086844	Minus	194384-194645
	403274	8072441	Minus	104059-104179,105683-105859
	403471	9930659	Minus	85867-85983
70	403763	7229888	Minus	43575-43887
	403806	8140491	Plus	146390-146678
	403983	8576059	Minus	82441-82701
	404107	8099028	Minus	201699-202363
	404132	6981900	Plus	11307-12434
75	404184	4581418	Minus	12652-13548
	404253	9367202	Minus	55675-56055
	404440	7528051	Plus	80430-81581
	404782	9910094	Minus	15455-15589
	404959	7407984	Plus	45243-45368
80	404981	4432779	Minus	20626-20770,22513-22721
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405041	7547195	Plus	121230-121714
	405196	7230083	Minus	135716-135851

	405277	3980473	Plus	23471-23572
	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49780-49904,50231-50342,53583-53667,54111-54279
	405336	6094635	Plus	33267-33563
5	405454	7656675	Plus	133807-134053
	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
	405657	4827303	Minus	104132-104293
	405675	4557087	Plus	70304-70630
10	405708	4156182	Plus	55030-55604
	405897	6758795	Plus	59828-60535
	405932	7767812	Minus	123525-123713
	405943	6758796	Plus	20605-20812
	406087	9123919	Minus	7234-7626
	406092	9123919	Plus	251370-251797,252168-252682
15	406467	9795551	Plus	182212-182958
	406554	7711566	Plus	106956-107121
	406560	7711569	Minus	35162-35292
	406599	8248616	Plus	10933-11086

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TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 96th percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. Ig, fn3, egi, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigeneID	PPDomains	Unigene Title	R1
40	425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_term	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interstitial)	38.9
	439606	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
	452240	AI591147	Hs.61232	TM	ESTs	27.0
	424046	AF027866	Hs.138202	SS,TM,serpin	serine (or cysteine) proteinase inhibitor	24.5
45	400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stromelysin	20.5
	418345	AJ001698	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13(P113; se	20.1
	423017	AW178761	Hs.227948	SS,serpin	serine (or cysteine) proteinase inhibitor	19.2
	428227	AA321649	Hs.2248	SS,TM,IL8	small inducible cytokine subfamily B (Cys	15.9
	447164	AF026941	Hs.17518	TM,IBR	Homo sapiens cig5 mRNA, partial sequence	13.8
50	414764	AW013887	Hs.72047	TM	ESTs	12.9
	416661	AA634543	Hs.79440	TM	IGF-II mRNA-binding protein 3	12.7
	427585	D31152	Hs.178729	SS,C1q,Collagen	collagen, type X, alpha 1 (Schmid metaphy	12.6
	406467			TM,efhand	Target Exon	10.5
	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1	10.2
55	418882	NM_004996	Hs.89433	TM,ABC_membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	9.4
	419247	S65791	Hs.89764	TM,JH-domain	fragile X mental retardation 1	9.1
	446232	AI281848	Hs.194691	TM,7tm_3,Ribosomal_L13	retinoid acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,kinase	NIMA (never in mitosis gene a)-related ki	8.9
	422420	U03398	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamily	8.7
60	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
	444342	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
	422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
	447342	AI199268	Hs.19322	SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 20103	6.8
65	407839	AA045144	Hs.161566	TM,cadherin,Cadherin_C_term	ESTs	6.6
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
	414812	X72755	Hs.77367	SS,TM,IL8	monokine induced by gamma interferon	6.4
	421773	W69233	Hs.112457	SS	ESTs	6.2
	413385	M34455	Hs.840	TM,IDO	Indoleamine-pyrrole 2,3 dioxygenase	5.9
70	413753	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short	laminin, beta 3 (nuclein (125kD), kalinin	5.8
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
	418663	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
	407366	AF026942		TM,IBR	gb:Homo sapiens cig33 mRNA, partial seque	5.5
	433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
75	408536	AW381532	Hs.135188	SS,TME1-E2_ATPase,Cation_ATPase_C, N	ESTs	5.4
	420440	NM_002407	Hs.97644	SRORUteroglobin	mammaglobin 2	5.2
	437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ga	5.1
	405547			SS,TM,ABC_membrane,ABC_tran,Ig	NM_018833:Homo sapiens transporter 2, AT	5.1
	439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
80	426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
	423634	AW959908	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 3 (E polypeptide, protei	5.0
	409744	AW675258	Hs.56265	TM,metalho,Kelch	Homo sapiens mRNA; cDNA DKFZp586P2321 (fr	4.9

444461	R53734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon-I	4.8
423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrophage e	4.8
450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domai	4.8
401575	NA		TM	Target Exon	4.6
428484	AF104032	Hs.184601	TM	solute carrier family 7 (cationic amino a	4.5
425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, liothyronine, type II	4.4
431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
434699	AA643687	Hs.149425	TM,Nucleoside_tra2	Homo sapiens cDNA FLJ11980 fis, clone HEM	4.3
406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprotein 9	4.2
404440			TM,MAGE	NM_021048:Homo sapiens melanoma antigen,	4.2
449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
444105	AW189097	Hs.166597	TM,cdherin	ESTs	4.1
409632	W74001	Hs.55279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
423515	AA327017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
423553	AA405635	Hs.98854	TM	ESTs, Weakly similar to DYLL_HUMAN CYTOPL	4.1
445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
446989	AK001898	Hs.16740	TM	hypothetical protein FLJ11036	4.0
428536	AJ143139	Hs.2288	TM,elhand,Syndecan	visinin-like 1	3.9
413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
429441	AJ224172	Hs.204096	Uteroglobulin	lipophilin B (uteroglobulin family member),	3.9
409601	AF237621	Hs.80828	TM,filamentfilament,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
439238	N47305	Hs.46668	TM	ESTs	3.8
446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
405545			SS,TM,proteasome,Jg,ABC_memb,tranABC_tran,	(MDR/TAP) (TAP2)	3.8
422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
423217	NM_000094	Hs.1640	SS,TM,m3,ywa,Collagen,Kunitz_BPTI	collagen, type VII, alpha 1 (epidermolysi	3.7
430686	NM_001942	Hs.2633	SS,TM,cdherin,Cadherin_C_term	desmoglein 1	3.7
444707	AJ188613	Hs.41690	TM,cdherin	desmocollin 3	3.7
409582	R27430	Hs.271565	TM	ESTs	3.6
408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, delayed-	3.6
400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
413278	BE563085	Hs.833	TM,ubiquitinlinlaminin_G,laminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
424927	AW973668	Hs.153850	SS	hypothetical protein C321D2.4	3.6
408591	AF015224	Hs.46452	SS,TM,Uteroglobulin	mammaglobin 1	3.5
407756	AA116021	Hs.38260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
407137	T97307		TM,GDA1_CD39	gb:ye53h05.s1 Soares fetal liver spleen 1	3.5
411274	NM_002776	Hs.69423	trypsin	kalikrein 10	3.5
400668			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metalloprot	3.5
412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acyltransf	endothelial cell growth factor 1 (platelet	3.4
450650	T65617	Hs.101257	TM	hypothetical protein MGC3295	3.4
451778	AJ826131	Hs.71243	Ig	ESTs, Weakly similar to zinc finger prote	3.4
430397	AJ924533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
422487	AJ010901	Hs.198267	TM,ywd	mucin 4, tracheobronchial	3.4
449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
418994	AA296520	Hs.89546	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin	cadherin 3, type 1, P-cadherin (placental	3.3
418462	BE001596	Hs.85266	SS,TM,Integrin_B,fn3	Integrin, beta 4	3.3
424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
401486	NA		SS,TM,trypsin	C40006477:gi 4768508 ref NP_004253.1 air	3.2
408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, clone AD	3.2
427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	3.2
452934	AA581322	Hs.4213	SS,TM,Ig	hypothetical protein MGC16207	3.1
448988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectinrm	Homo sapiens mRNA full length insert cDNA	3.1
414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
435604	AA625279	Hs.26892	TM	uncharacterized bone marrow protein BM040	3.1
453883	AI638516	Hs.22630	TM,Ets,SAM_PNT	cofactor required for Sp1 transcriptional	3.0
448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,sodh,pkinase,DSPT,Ribosomal_L	solute carrier family 6 (neurotransmitter	3.0
444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
437938	AI950087		TM,histone,Ig,MHC_I	gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapiens	3.0
424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
409703	NM_006187	Hs.56009	SS	2'-5'-oligoadenylate synthetase 3 (100 kD	3.0
447313	U92981	Hs.18081	TGF-beta	Homo sapiens clone DT1P186 mRNA, CAG repe	3.0
431070	AW408164	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
421190	U95031	Hs.102482	TM,ywd	mucin 5, subtype B, tracheobronchial	2.9
452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
443859	NM_013409	Hs.9914	SS,kazal	folliculin	2.9
446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
449746	AI568594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
414581	AA258213	Hs.72010	TM,Cam_acyltransf,Choline_kinase,SCO1-SenC	ESTs	2.9
431629	AU077025	Hs.265827	SS,IRNA_antiSH2,SH3,pkinase	Interferon, alpha-inducible protein (clon	2.8
445873	AA250970	Hs.251946	SS,rm,PABPkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic 1-II	2.8
438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
410310	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, t	2.8

5	411558	AA102670	Hs.70725	SS,TM	gamma-aminobutyric acid (GABA) A receptor	2.8
	413273	U75679	Hs.75257	TM,Ig,pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
	433345	AI681545	Hs.152982	SS	hypothetical protein FLJ13117	2.7
	452234	AW084176	Hs.223296	TM	ESTs, Weakly similar to I38022 hypothetical	2.7
	456181	L36463	Hs.1030	TM,RA,VPS9	ras inhibitor	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor,sushi	diubiquitin	2.7
	422278	AF072873	Hs.114218	TM,Frtzzled,Fz	frtzzled (Drosophila) homolog 6	2.7
10	446839	BE091926	Hs.16244	TM	mitotic spindle coiled-coil related prote	2.7
	416250	AA581386	Hs.73452	TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Claudin	hypothetical protein MGC10791	2.7
	407287	AI678812		TM,rascadherin	gbtu59d08.x1 NCL CGAP_Gas4 Homo sapiens	2.7
	412977	AA125910	Hs.191461	TGF-beta	ESTs	2.7
	400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of t	2.7
15	425483	AF231022	Hs.158159	EGF,cadherin,laminin_G	FAT tumor suppressor (Drosophila) homolog	2.7
	430152	AB001325	Hs.234642	SS,TM,MIP	aquaporin 3	2.7
	444006	BE395085	Hs.10088	SS,TM	type I transmembrane protein Fn14	2.7
	418869	AW516565		TM,RasGAP,IQ,WW	gbxq01d05.x1 Soares_NHCeC_cervical_tumor	2.7
	416658	U03272	Hs.79432	SS,TM,EGF,TB	fibrillin 2 (congenital contractual arac	2.6
20	410290	AA402307	Hs.322844	SS,TM,Sema,TIG,Plaxdn_repeat	hypothetical protein DKFZp564A176	2.6
	419667	AU077005	Hs.92208	SS,TM,disintegrin,Repolysin,Pep_M12B_propep	a disintegrin and metalloproteinase domai	2.6
	406671	AA129547	Hs.285754	TM,pkinase,Plaxdn_repeat,Sema,TIG,LIM	mal proto-oncogene (hepatocyt growth fac	2.6
	434444	AI765276	Hs.101257	TM	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	TM,ABC_tran,ABC_membrane,Rhomboid	ATP-binding cassette, sub-family C (CFTR/	2.6
25	431890	X17033	Hs.271986	vwa,FG-GAP,Integrin_A	Integrin, alpha 2 (CD49B, alpha 2 subunit	2.6
	452281	T93500	Hs.28792	TGF-beta,TGFb_propeptide	Homo sapiens cDNA FLJ11041 fis, clone PLA	2.6
	421508	BE302796	Hs.105097	TM,TK	thymidine kinase 1, soluble	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep,Repolysin	ESTs	2.6
	447197	R36075		TM,SDF	gbxh88b01.s1 Soares placenta Nb2HP Homo	2.5
30	459688	U72671	Hs.151250	SS,TM,Ig	intercellular adhesion molecule 5, telenc	2.5
	437412	BE069288	Hs.34744	TM,ABC_tran,ABC_membrane,Rhomboid	Homo sapiens mRNA; cDNA DKFZp547C136 (fro	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	424420	BE614743	Hs.146688	TM,MAPEG	prostaglandin E synthase	2.5
	427239	BE270447	Hs.174070	TM,UQ_con	ubiquitin carrier protein	2.5
35	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	431130	NM_006103	Hs.2719	SS,TM,wap	epididymis-specific, whey-acidic protein	2.5
	453379	AA035261	Hs.61753	PAN,krtigle,trypsin	ESTs	2.5
	421733	AL119671	Hs.1420	SS,TM,Ig,pkinase	fibroblast growth factor receptor 3 (acho	2.5
	452220	BE158006	Hs.212296	TM,Integrin_A,FG-GAP	ESTs	2.5
40	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	440381	AA917808	Hs.190495	TM	ESTs	2.5
	441794	AW197794	Hs.253338	TM	ESTs	2.5
	439108	AW163034	Hs.6467	SS,TM	synaptogyrin 3	2.5
	401103	NA		TM,vwd	C12001233.g 7305361 ref NP_038652.1 oto	2.4
45	430630	AW269920	Hs.2621	TM,cystatin	cystatin A (stefin A)	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	415621	AI648602	Hs.55468	TM,histone,Sec1sugar_lr	ESTs	2.4
	402745			SS,TM,EGF,ldl_recept_b,thyroglobulin_1	ESTs	2.4
	407758	D50915	Hs.38365	SS,TM	NM_002608:Homo sapiens nidogen (enactin)	2.4
50	457570	AA579428		TM	KIAA0125 gene product	2.4
	429574	BE266321	Hs.208912	SS,TM	gbnf37cd9.s1 NCL CGAP_Py2 Homo sapiens c	2.4
	431211	M86849	Hs.323733	SS,TM,connexin	hypothetical protein MGC861	2.4
	425865	AI924046	Hs.119587	SS,TM,PMP22_Claudin	gap junction protein, beta 2, 26kD (conne	2.4
	420511	AF052692	Hs.98485	SS,TM,connexin	ESTs, Weakly similar to A47582 B-cell gro	2.4
55	437897	AA770561	Hs.146170	SS,pro_isomerase	gap junction protein, beta 3, 31kD (conne	2.4
	437846	AA773868	Hs.244569	TM	hypothetical protein FLJ22969	2.4
	418432	M14156	Hs.85112	Insulin	esophagus cancer-related gene-2	2.4
	438108	AI471795	Hs.287776	TM	Insulin-like growth factor 1 (somatomedin	2.3
60	453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_domain	vanilloid receptor-related osmotically ac	2.3
	435542	AA687376	Hs.269533	pkinase,RhoGEF,Ig,PH,SH3	hypothetical protein FLJ14451	2.3
	434517	AA635690	Hs.337251	TM	ESTs	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,Integrin_A	hypothetical protein MGC2487	2.3
	422310	AA316622	Hs.98370	SS,TM,fn3,Ig,pkinase,Ribosomal_L36e,p450	Integrin, alpha 3 (antigen CD49C, alpha 3	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	cytochrome P450, subfamily IIS, polypepti	2.3
65	416091	AF295370	Hs.283082	SS,TM,Defensin_beta	Fanconi anemia, complementation group G	2.3
	429359	W00482	Hs.2399	SS,TM,Peplidase_M10,hemopexin	defensin, beta 3	2.3
	409402	AF208234	Hs.695	TM,cystatin	matrix metalloproteinase 14 (membrane-ins	2.3
	432284	AA532807	Hs.105822	TM,pkinase	cystatin B (stefin B)	2.3
	408243	Y00787	Hs.624	SS,TM,IIL8	ESTs	2.3
70	423229	AC003965	Hs.125532	SS,trypsin	Interleukin 8	2.3
	408713	NM_001248	Hs.47042	GDA1_CD39	protease, serine, 26	2.3
	440502	AI824113	Hs.78281	RGS,GoLoco,RBD	ectonucleoside triphosphate diphosphohydr	2.3
	429929	AB014583	Hs.226275	TM	regulator of G-protein signalling 12	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	KIAA0683 gene product	2.3
75	428953	AA306610	Hs.194876	SS,TM,TNFR_c6,arf,Stathmin,DEAD	platelet-activating factor acetylhydrolas	2.3
	439398	AA284267	Hs.221504	SS	tumor necrosis factor receptor superfamil	2.3
	440371	BE268550	Hs.80449	TM	ESTs	2.2
	452203	X57522	Hs.158164	SS,TM,ABC_tran,ABC_membrane	Homo sapiens, clone IMAGE:3535294, mRNA,	2.2
80	407811	AW190902	Hs.40098	SS	transporter 1, ATP-binding cassette, sub-	2.2
	432078	BE314877	Hs.24553	TM	cysteine knot superfamily 1, BMP antagoni	2.2
	429113	D28235	Hs.196384	SS,TM,EGF	hypothetical protein FLJ12541 similar to	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	prostaglandin-endoperoxide synthase 2 (pr	2.2
	428434	AW363590	Hs.65551	SS	ESTs, Weakly similar to A34087 hypothetical	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	Homo sapiens, Similar to DNA segment, Chr	2.2
					H1 histone family, member 0	2.2

5	417903	NM_002342	Hs.1116	SS,TM,ASC,TNFR_c6	lymphotoxin beta receptor (TNFR superfam	2.2
	422012	AW403423	Hs.110746	SS,homeobox,pou	HCR (a-helix coiled-coil rod homologue)	2.2
	433090	A1720050	Hs.145362	SS,TM	immortalization-upregulated protein	2.2
	417576	AA339449	Hs.82285	TM,AIIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltransfera	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	417433	BE270266	Hs.82128	SS,TM,LRRCT,LRRNT,LRR	ST4 oncotelal trophoblast glycoprotein	2.2
	416763	A1908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators of di	2.2
10	425999	AW513051	Hs.332981	TM,FAD_binding_2,P53PA,Ribosomal_S2,FAD_bindi	ESTs, Weakly similar to I38022 hypothetical	2.2
	452799	A1948829	Hs.213786	TM	ESTs	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficient (S.	2.2
	448153	Y10805	Hs.20521	SS,TM,Na_Ca_Ex	HMT1 (hnRNP methyltransferase, S. cerevis	2.2
	426969	AF120274	Hs.194689	SS	artemin	2.2
	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
15	409533	AW969543	Hs.21291	TM	mitogen-activated protein kinase k	2.2
	408201	AK000568	Hs.43654	TM	hypothetical protein FLJ20561	2.1
	408996	A1979168	Hs.82226	TM	glycoprotein (transmembrane) nmb	2.1
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. cerevis	2.1
20	437191	NM_006846	Hs.331555	SS,TM,kazal	serine protease inhibitor, Kazal type, 5	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	2.1
	431117	AF003522	Hs.250500	SS,TM,DSL,EGF	dellai (Drosophila)-like 1	2.1
	447674	BE270640	Hs.19192	TM,pkinaseras,arf	cyclin-dependent kinase 2	2.1
	409651	H96643	Hs.283565	bZIPoolin_ADF,EGF	FOS-like antigen-1	2.1
25	440495	AA887212	Hs.14161	TM,NSFN,Ca_Ex	hypothetical protein DKFZp43411930	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TILa,vwd,EPO_TPO	procollagen C-endopeptidase enhancer	2.1
	421013	M62397	Hs.1345	TM	mutated in colorectal cancers	2.1
	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,lg,MAM	protein tyrosine phosphatase, receptor ty	2.1
	449224	AW995911	Hs.299883	fn3	hypothetical protein FLJ23399	2.1
30	452679	Z42387	Hs.83883	TM	transmembrane, prostate androgen induced	2.1
	409956	AW103364	Hs.727	SS,TGF-beta,TGFb_propeptide	inhibin, beta A (activin A, activin AB al	2.1
	436580	AA811262	Hs.299202	TM,pkinasasugar_tr	ESTs	2.1
	406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8 (neur	2.1
	424955	AW956282	Hs.144609	TM	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
35	412270	AC005262	Hs.73797	TM,G-alpha	guanine nucleotide binding protein (G pro	2.1
	426471	X57348	Hs.184510	TM,14-3-3	stradlin	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpepl,hormone5Reprolysin	metallocarboxypeptidase CPX-1	2.1
	416498	U33632	Hs.79351	TM	potassium channel, subfamily K, member 1	2.1
	423453	AW450737	Hs.128791	SS,GranIn,CDP-OH_P_transf	CGI-09 protein	2.1
40	417944	AU077196	Hs.82985	SS,COLFI,Collagen,vwc	collagen, type V, alpha 2	2.1
	424197	AF096834	Hs.142989	SS,TM,CSD	germ cell specific Y-box binding protein	2.1
	446163	AA026880	Hs.25252	TM,fn3	prolactin receptor	2.1
	417331	AW411297	Hs.81972	TM,SH2,PID	SHC (Src homology 2 domain-containing) tr	2.1
	430413	AW842182	Hs.241392	IL8,PX	small inducible cytokine A5 (RANTES)	2.1
45	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	ATPase, Ca transporting, type 2C, member	2.1
	407305	AA715284		TM,pkinase,Sema,Plexin_repeat,TIG,LIM	gb:mv3503.r1 NCL_CGAP_Br5 Homo sapiens c	2.1
	407792	AJ077715	Hs.39384	SS	putative secreted ligand homologous to f	2.0
	418695	AA447014	Hs.193261	SS	hypothetical protein MGC2991	2.0
	439738	BE246502	Hs.9598	TM,RasGAP,IQ,WW	sema domain, immunoglobulin domain (lg),	2.0
50	433398	AW843150	Hs.112412	TM,PMP22_Claudin	ESTs	2.0
	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	446872	X97058	Hs.16362	TM	pyrimidinergic receptor P2Y, G-protein co	2.0
	419726	U50330	Hs.1274	SS,TM,Astachn,CUB,EGF	bone morphogenetic protein 1	2.0
	410116	AW630671	Hs.58636	SS,TM	squamous cell carcinoma antigen recognize	2.0
55	426500	NM_014638	Hs.170156	TM	KIAA0450 gene product	2.0
	452194	AJ694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily 1	2.0
	418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
	425855	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
	434346	AA630445	Hs.116773	TM,Ferro_reduct	ESTs	2.0
60	426274	D38122	Hs.2007	TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
	440008	AW051683	Hs.277686	TM,RhoGEF,FYVE,PH	ESTs	2.0
	424634	NM_003613	Hs.151407	lg,isp_1	cartilage intermediate layer protein, nuc	2.0
	446641	AL049229	Hs.15787	TM,pkinase,rm	Homo sapiens mRNA; cDNA DKFZp564O1016 (tr	2.0
	418851	AJ417828	Hs.192435	TM	ESTs	2.0
65	440351	AF030933	Hs.7179	TM,Rad1,Cadherin_C_term	RAD1 (S. pombe) homolog	2.0
	439496	BE616501	Hs.32343	SS	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
	454197	BE140966		TM,Ammonium_transpkinasin,Ammonium_transp	gb:MR0-HT0065-081199-002-b08 HT0065 Homo	2.0
	433573	AF234887	Hs.57652	TM,7tm_2,GPSIRNA-synt_2b,Seryl_LRNA_N	cadherin, EGF LAG seven-pass G-type recep	2.0
	429211	AF052693	Hs.198249	TM,connexin	gap junction protein, beta 5 (connexin 31	2.0
70	420737	L08096	Hs.99899	SS,TM,TNF	tumor necrosis factor (ligand) superfamil	2.0
	455333	AW897851		TM,Glyco_hydro_2	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
	414784	NM_000344	Hs.288986	SS,TM,BIR	survival of motor neuron 1, telomeric	2.0
	435836	AW292532	Hs.250175	TM,GNS1_SUR4	homolog of yeast long chain polyunsaturat	2.0
	411789	AF245505	Hs.72157	TM,jg,LRRCT	DKFZP564I1922 protein	2.0
75	441455	AJ271671	Hs.7854	TM,ras,DENN	zinc/iron regulated transporter-like	2.0
	426068	AF029778	Hs.166154	SS,TM,DSL,EGF,NUDIX	jagged 2	2.0
	439733	AL365412	Hs.107203	TM,Sm	hypothetical protein from EUROMAGE 17593	2.0
	435014	BE660898	Hs.10026	TM,Ribosomal_L17	mitochondrial ribosomal protein L17	1.9
	457819	AA057484	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	1.9
80	422737	M26939	Hs.119571	SS,Collagen,COLFI	collagen, type III, alpha 1 (Ehlers-Danlo	1.9
	431104	AW970859	Hs.313503	Sema,jg	ESTs	1.9
	432210	AJ567421	Hs.273330	TM,laminin_G,laminin_EGF,kazatubiquitin	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
	436511	AA721252	Hs.291502	TM,disintegrin,Reprolysin,Pep_M12B_propep,pkinase,	ESTs	1.9
	419216	AU076718	Hs.164021	SS,IL8	small inducible cytokine subfamily B (Cys	1.9

432169	Y00971	Hs.2910	TM,Phibosyltran	phosphoribosyl pyrophosphate synthetase 2	1.9
441128	AA570256	Hs.54628	TM,ras	ESTs, Weakly similar to T23273 hypothetical	1.9
447160	AA330310	Hs.24181	TM	ESTs	1.9
419138	U48508	Hs.89631	TM,RVDR,ITPR,RyR,SPRY	ryanodine receptor 1 (skeletal)	1.9
457817	AA247751	Hs.79572	TM,hemopexin,Peptidase_M10	cathepsin D (lysosomal aspartyl protease)	1.9
431009	BE149762	Hs.48956	SS,TM,connexin	gap junction protein, beta 6 (connexin 30)	1.9
428957	NM_003881	Hs.194679	SS,TM,vwc,IGFBP,isp_1	WNT1 inducible signaling pathway protein	1.9
418546	AA224827		TM,vwa,FG-GAP,Integrin_A	gbnc32g04.s1 NCL_CGAP_P12 Homo sapiens c	1.9
400749			SS,TM,idi_recept_a,h3,idi_recept_b	NM_003105*Homo sapiens sorf1in-related	1.9
408369	R38438	Hs.182575	F-protein	solute carrier family 15 (H777) transporter	1.9
422765	AW409701	Hs.1578	TM,BIR	baculoviral IAP repeat-containing 5 (surv	1.9
417409	BE272508	Hs.82109	TM,Syndecan	syndecan 1	1.9
407720	AB037776	Hs.38002	TM,catponin,CH	KIAA1355 protein	1.9
418830	BE513731	Hs.88959	TM,CDP-OH_P_transf,MCM	hypothetical protein MGC4816	1.9
434769	AA648884	Hs.134278	TM,CDP-OH_P_transf,MCM	Homo sapiens cDNA FLJ12676 fis, clone NT2	1.9
421593	NM_017436	Hs.105956	SS,TM	globotriaosylceramide/CD77 synthase; Gb3/	1.9
426064	BE387014	Hs.166146	TM,WH1	Homer, neuronal immediate early gene, 3	1.9
404504	NA		TM	Target Exon	1.9
422753	AJ928995	Hs.1575	SS,TM,Sm	small nuclear ribonucleoprotein D3 polype	1.9
422739	H20106	Hs.119591	SS,ClaL_adaptor_s	adaptor-related protein complex 2, sigma	1.9
433068	NM_006456	Hs.288215	SS,Phibosyltran	siatyltransferase	1.9
419694	AA013051	Hs.91417	TM	topoisomerase (DNA) II binding protein	1.9
428188	M98447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 1 (K polypeptide epiderm	1.9
428343	AL043021	Hs.12705	TM,Rhomboid,HMG_boxTPR	ESTs	1.9
429592	AB029041	Hs.209646	Troponin	KIAA1118 protein	1.9
431620	AA126109	Hs.264981	C2,PH,RasGAP,NTP_transf_2	2'-5'-oligoadenylate synthetase 2 (69-71	1.9
424670	W61215	Hs.116651	Ig	epithelial V-like antigen 1	1.9
428373	A1751656	Hs.183986	SS,TM,Ig	poxvirus receptor-related 2 (herpesviri	1.9
453449	W16752	Hs.32981	SS,Ig,Sema	sema domain, immunoglobulin domain (Ig),	1.9
432304	AA932186	Hs.69297	TM,7tm_1	ESTs	1.9
432673	AB028859	Hs.278605	TM,DnaJ,DnaJ_C,DnaJ	DnaJ (Hsp40) homolog, subfamily B, member	1.9
416207	NM_014745	Hs.336433	SS,TM,zf-DHHC	Homo sapiens, clone MGC:2908, mRNA, compl	1.9
408988	AL119844	Hs.49476	TM,Plexin_repeat,Sema,isp_1	Homo sapiens clone TUA8 C1-du-chat regio	1.9
417426	NM_002291	Hs.82124	SS,laminin_EGF,laminin_Nterm	laminin, beta 1	1.9
443883	AA114212	Hs.9930	SS,TM,serpin,Marek_A	serine (or cysteine) proteinase inhibitor	1.9
433328	AW298159	Hs.23644	SS,TM	ESTs, Weakly similar to S65824 reverse tr	1.9
419981	AA897581	Hs.128773	TM,SkI_Sno	ESTs	1.8
420931	AF044197	Hs.100431	SS,TM,IL8	small inducible cytokine B subfamily (Cys	1.8
415023	AA932146	Hs.133494	TM,Ribosomal_L17,Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.8
413644	BE154910	Hs.278793	TM,Glyco_hydro_2	ESTs, Weakly similar to Z195_HUMAN ZINC F	1.8
449987	AW079749	Hs.184719	TM,ABC_tran,ABC_membrane,trans	ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8
421340	F07783	Hs.1369	SS,sushi	decay accelerating factor for complement	1.8
417866	AW067903	Hs.82772	SS,TM,Collagen,COL1,TPSN	collagen, type XI, alpha 1	1.8
430259	BE550182	Hs.127826	TM,transmembrane4RasGEF,RA	RaGEF-like protein 3, mouse homolog	1.8
432998	AA835948	Hs.153307	TM,SDF	ESTs	1.8
431671	NM_016937	Hs.267289	TM,NA	polymerase (DNA directed), alpha	1.8
411773	NM_006799	Hs.72026	trypsin	protease, serine, 21 (testisin)	1.8
425247	NM_005940	Hs.155324	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 11 (stromelysin	1.8
422976	AU076657	Hs.1600	TM,cpn60_TCP1,Sema	chaperonin containing TCP1, subunit 5 (ep	1.8
425159	NM_004341	Hs.154868	SS,TM,GATase,OTCace,CPSase_L_chain,Dihydrooro	carbamoyl-phosphate synthetase 2, asparta	1.8
447776	A1525625	Hs.130181	Ricin_B_inactin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.8
426908	AW815163	Hs.172851	SS,TM,fusion_gly,Myosin_tail,adh_short	arginase, type II	1.8
408116	AA251393	Hs.289052	TM,Na_Ca_ExCam_acyltransf	Homo sapiens, Similar to RIKEN cDNA 54304	1.8
417847	A1521558	Hs.7331	Uteroglobulin	hypothetical protein FLJ22316	1.8
415791	H09366	Hs.78853	SS,TM,UNG	uracil-DNA glycosylase	1.8
407903	A1287341	Hs.154029	TM,ubiquitin,laminin_G,laminin_EGF,kazal	bHLH factor Hes4	1.8
422511	AU076442	Hs.117938	TM,p450	collagen, type XVII, alpha 1	1.8
414117	W88559	Hs.1787	TM,lon_trans,K_tetra	proteolipid protein 1 (Pelizaeus-Merzbach	1.8
426841	A1052358	Hs.193726	TM,esp	ESTs	1.8
415272	AA164215	Hs.203188	TM,TPR,pkinase,Ig,B56	ESTs	1.8
426440	BE382756	Hs.169902	TM,sugar_tr,Fork_head	solute carrier family 2 (facilitated gluc	1.8
419488	AA316241	Hs.90691	FGF	nucleophosmin/nucleoplasm 3	1.8
418452	BE379749	Hs.85201	SS,TM,lectin_c	C-type (calcium dependent, carbohydrate-r	1.8
431363	M86528	Hs.266902	SS,NGF	neurotrophin 5 (neurotrophin 4/5)	1.8
440975	AW499914	Hs.7579	SS,TM	hypothetical protein FLJ10402	1.8
438962	BE046594		TGF-beta,bZIP	gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	1.8
414602	AW630088	Hs.76550	SS	Homo sapiens mRNA; cDNA DKFZp564B1264 (tr	1.8
418054	NM_002318	Hs.83354	TM,mito_carr,Lysyl_oxidase	lysyl oxidase-like 2	1.8
440501	AA887391	Hs.202229	TM,GalactosylT	ESTs	1.8
449309	AW589823	Hs.224189	TM	ESTs	1.8
421461	AW291023	Hs.97255	TM,Lysyl_oxidase,SCP2,Band_7	ESTs, Weakly similar to A46010 X-linked r	1.8
412584	X54870	Hs.74085	TM,lectin_c	DNA segment on chromosome 12 (unique) 248	1.8
441565	AW953575	Hs.303125	TM	p53-induced protein PIGPC1	1.8
431837	T79326	Hs.326553	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	1.8
438251	BE515065	Hs.296585	SS,Y_phosphatase,TIG	nucleolar protein (KKE/D repeat)	1.8
448633	AA311426	Hs.21635	TM,EGF,laminin_G,fibrinogen_C,F5_F8_type_C,tubulin	tubulin, gamma 1	1.8
424291	AL120051	Hs.144700	TM,Ephrin,Hist_deacetyl	ephrin-B1	1.8
415388	AF016081	Hs.78409	SS,TM,TPSN,Collagen	collagen, type XVIII, alpha 1	1.8
435550	A1224458	Hs.4934	TM,LRR,LRRCT	Hsapiens polyA site DNA	1.8
448568	AA149121	Hs.71947	TM,LRRCT	ESTs	1.8
439246	AA498072	Hs.77783	SS,TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla	membrane-associated tyrosine- and threoni	1.8
410001	AB041038	Hs.57771	SS,TM,trypsin	kallikrein 11	1.8
417312	AW888411	Hs.81915	SS,Stathmin	leukemia-associated phosphoprotein p18 (s	1.8

	444152	AI125694	Hs.149305	TM	hypothetical protein MGC2603	1.8
	453454	AW052006	Hs.8551	TM	PRP4/STK/WD splicing factor	1.8
	449320	AB030835	Hs.23476	SS,adenylatekinase	Cip1-interacting zinc finger protein	1.8
5	428329	AA426091	Hs.98453	TM,Gal-bind,Jectin	ESTs, Moderately similar to R27328 2 (Hs	1.8
	452875	BE275760	Hs.30928	TM,Apopoptotnig	DNA segment on chromosome 19 (unique) 117	1.8
	444031	BE271513	Hs.25303	TM,Pepidase_M10,hemopexin	hypothetical protein FLJ13154	1.8
	443534	AI078123		TM	gbcy92e04.x1 Soares_fetal_liver_spleen_1	1.8
	413313	NM_002047	Hs.75280	TM,WHEP-TRS,7tm_2	glycyl-tRNA synthetase	1.8
10	452874	AK001061	Hs.30925	SS	hypothetical protein FLJ10199	1.8
	453140	AA032238	Hs.170531	TM	ESTs	1.8
	418641	BE243136	Hs.86947	SS,TM,disintegrin,Pep_M12B_propep,Repolysin	a disintegrin and metalloproteinase domain	1.8
	432925	AA878324	Hs.192734	SS	ESTs	1.8
	453857	AL080235	Hs.35861	TM	DKFZP586E1621 protein	1.8
15	457663	AW371946	Hs.337459	TM	ESTs	1.8
	452873	AK001247	Hs.30922	TM	hypothetical protein FLJ10385	1.8
	436396	AI683487	Hs.152213	SS,wnt	wingless-type MMTV integration site fami	1.8
	452835	AK001269	Hs.30738	TM	hypothetical protein FLJ10407	1.7
	459847	R34107	Hs.198287	lg	pregnancy specific beta-1-glycoprotein 11	1.7
20	418245	AA088757	Hs.83883	TM,PEPCK	transmembrane, prostate androgen induced	1.7
	448484	BE813340	Hs.334725	TM	Homo sapiens, Similar to RIKEN cDNA 94300	1.7
	431369	BE184455	Hs.251754	SS,wap	secretory leukocyte protease inhibitor (a	1.7
	434877	AW974792	Hs.292171	TM	ESTs	1.7
	428923	BE047698	Hs.188785	TM	ESTs	1.7
25	402815	NA		TM,HCO3_cotransp	ENSP00000202587~Bicarbonate transporter-	1.7
	420185	AL044056	Hs.158047	TM	ESTs	1.7
	445739	AW136354	Hs.145303	TM	ESTs	1.7
	409435	AI810721	Hs.95424	TM,p450	ESTs	1.7
	408688	AI634522	Hs.152925	TM	KIAA1268 protein	1.7
30	420085	AI741909	Hs.44680	TM	hypothetical protein FLJ20979	1.7
	433933	AI754389	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.7
	430965	AA489732	Hs.154918	homone_rec,Prog_receptor,zf-C4	ESTs	1.7
	414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_TDP	ATPase, Na? transporting, beta 3 polypept	1.7
	423464	NM_016240	Hs.128856	TM,Collagen	CSR1 protein	1.7
35	416737	AF154335	Hs.79691	SS,TM,LIM,PDZsugar_tr,PDZ,LIM	LIM domain protein	1.7
	409012	AL117435	Hs.49725	TM,RhoGEFzf-DHHC,adh_short	DKFZP434I216 protein	1.7
	423804	AW403448	Hs.1705	TM,IRF	Interferon-stimulated transcription facto	1.7
	410418	D31382	Hs.63325	SS,TM,trypsin,ldl_recept_La	transmembrane protease, serine 4	1.7
	440028	AW473875	Hs.125843	TM	ESTs, Weakly similar to T17227 hypothetic	1.7
40	457646	AA725650	Hs.112948	TM,SPRY	ESTs	1.7
	445439	BE243084	Hs.12719	SS,TGF-beta	regulator of nonsense transcripts 1	1.7
	420426	AA262045	Hs.36567	TM,Galactosyl_T_2ATP-syn_LC	Homo sapiens cDNA FLJ14227 fs, clone NT2	1.7
	431341	AA307211	Hs.251531	TM,proteasome	proteasome (prosome, macropain) subunit,	1.7
	412338	AA151527	Hs.69485	TM,Sema,Plxn_repeat,TIG,Plxn_repeat	hypothetical protein FLJ12436	1.7
45	414799	AI752416	Hs.77326	SS,thyroglobulin_1,JGFBP	Insulin-like growth factor binding protel	1.7
	452700	AI859390	Hs.288940	TM,DIX,RGS,thioded	five-span transmembrane protein M83	1.7
	430877	NM_005269	Hs.2693	GST_C,IRNA-syn_L1,WHEP-TRS,TGF-beta	glioma-associated oncogene homolog (zinc	1.7
	428824	AI125222	Hs.98712	TM,thioded,Y_phosphatase,MAM,lg,fn3MSP_domain	hypothetical protein DKFZP434H0311	1.7
	444085	AW449415	Hs.10260	TM,ion_trans	Homo sapiens cDNA FLJ11341 fs, clone PLA	1.7
50	416319	AI815601	Hs.79197	SS,TM,lg	CD83 antigen (activated B lymphocytes, Im	1.7
	429367	AB007867	Hs.278311	Sema,Plxn_repeat,TIG	plexin B1	1.7
	430425	AA531428	Hs.241412	TM	apolipoprotein L, 2	1.7
	441668	AI611973	Hs.127525	TM,Ammonium_transp	ESTs	1.7
	418469	U34879	Hs.85279	SS,TM,adh_short	hydroxysteroid (17-beta) dehydrogenase 1	1.7
55	450835	BE262773	Hs.25584	TM,AriGap	hypothetical protein FLJ10767	1.7
	418859	AA229558		TM	gbnc15d10.s1 NCL_CGAP_Pr1 Homo sapiens c	1.7
	425304	AA463844	Hs.31339	TM,lg,ITAM	fibroblast growth factor 11	1.7
	423635	X85019	Hs.130181	TM,Ricin_B_Jectin	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.7
	414820	AA371931	Hs.77422	TM,ion_trans,LIM,Synaptophysin	proteolipid protein 2 (colonic epithelium	1.7
60	440654	AW014242	Hs.159998	TM,connexin	ESTs	1.7
	412276	BE262621	Hs.73798	SS,MIF	macrophage migration inhibitory factor (g	1.7
	422087	X58968	Hs.111301	SS,Pepidase_M10,fn2,hemopexin	matrix metalloproteinase 2 (gelatinase A,	1.7
	407151	H25836	Hs.301527	SS,TNF	ESTs, Moderately similar to unknown (Hsa	1.7
	410726	AI623859	Hs.15936	TM,PX	ESTs	1.7
65	452012	AA307703	Hs.279766	TM,kinesin	kinesin family member 4A	1.7
	433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADlipocalin	Homo sapiens cDNA: FLJ22993 fs, clone KA	1.7
	409220	BE243323	Hs.51233	TM,death,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
	427082	AB037858	Hs.173484	TM,mito_carr	hypothetical protein FLJ10337	1.7
	426410	BE298446	Hs.205890	TM,Bcl-2,BH4	BCL2-like 1	1.7
70	433598	AI762836	Hs.271433	TM,Cytidylyltransf,SIR27tm_2	ESTs, Moderately similar to ALU2_HUMAN AL	1.7
	436495	BE258948	Hs.290874	TM,Armadio_seg	ESTs, Weakly similar to ALU8_HUMAN ALU SU	1.7
	422032	AA476956	Hs.110857	TM,TFIIS,RNA_POL_M_15KDsarpin,homone_rec,zf-C4	polymerase (RNA) III (DNA directed) polyp	1.7
	429738	AF125304	Hs.212680	SS,TNFR_c6	tumor necrosis factor receptor superfamil	1.7
	427600	AW630918	Hs.179774	TM,Transglutamin_C,Transglutamin_N,Transglut_core	proteasome (prosome, macropain) activator	1.7
75	431981	AA684069	Hs.115779	laminin_B,laminin_EGF	ESTs	1.7
	407738	N41744	Hs.19978	TM,Sulfatase	CGI-30 protein	1.7
	420187	AK001714	Hs.95744	TM	hypothetical protein similar to ankyrin r	1.7
	424620	AA101043	Hs.151254	SS,TM,trypsin	kallikrein 7 (chymotryptic, stratum come	1.7
	430488	D19589	Hs.13453	TM	hypothetical protein FLJ14753	1.7
80	423393	R37772	Hs.21420	TM,thiodedphkinase	p21-activated protein kinase 6	1.7
	444051	N48373	Hs.10247	SS,lg		

TABLE 13B

5	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
10	Accession:	Genbank accession numbers	
	Pkey	CAT Number	Accessions
15	408344	105240_1	AA053843 BE162213
	418546	176677_1	AA224827 T59708 T59843 BE156903
20	418859	179717_1	AA229558 AA345492 AA228582
	418869	179863_1	AW516565 AA229762 AA230035
25	437938	44573_2	AJ950087 N70208 R97040 N36809 AJ308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
			AJ820501 AJ820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AJ219788 AA884444 N92578 F13493
30			AA927794 AJ560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AJ890387 AJ950344 AI741346 AJ689062
			AA282915 AW102898 AJ872193 AJ763273 AW173586 AW150329 AJ653832 AJ762688 AA988777 AA488892 AJ356394 AW103813 AJ539642
35			AA642769 AA856975 AW505512 AJ961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499
			AW961101 AA251669 AA251874 AJ819225 AW205862 AJ683338 AJ858509 AW276905 AJ633006 AA972584 AA908741 AW072629 AW513996
40			AA293273 AA969759 N75628 N23288 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AK373032 AJ564269 F00531
			H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
45	438962	467390_1	BE046594 BE046667 AA828585 AJ207343
	443534	572957_1	AJ076123 AJ244834 AJ695239
50	447197	711623_1	R36075 AJ366546 R36167
	454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969
55			BE141673 BE141650 BE141674 BE141650 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975
			BE141667 BE141675 BE141657 BE141681 BE141658 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013
60			BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646
			BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671
65			AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
	455333	1281044_1	AW897851 AW897852
70	457570	357443_1	AA579426 AA579436 AA573736

TABLE 13C

40	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
45	Strand:	Indicates DNA strand from which exons were predicted.	
	NT_position:	Indicates nucleotide positions of predicted exons.	
50	Pkey	Ref	Strand NT_position
	400666	8118496	Plus 17982-18115,20297-20456
55	400749	7331445	Minus 9162-9293
	401103	8568122	Minus 98330-98449
60	401486	7341763	Plus 32585-32756,36281-36540,40791-40933,44018-44179
	401575	7229804	Minus 76253-76364
65	402745	9212200	Minus 76516-76690
	402915	7406502	Minus 140-276
70	404440	7528051	Plus 80430-81581
	404604	9212537	Minus 72019-72509
75	405545	1054740	Plus 118677-118807,119091-119296,121626-121823
	405547	1054740	Plus 124361-124520,124914-125050
80	406400	9256298	Plus 1553-1712,1878-2140,4252-4385,5922-6077
	406467	9795551	Plus 182212-182958

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 96th percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulatable by small molecules (e.g. kinase, peptidase, phosphatase, ATPase, or ion transporter domains). The predicted protein domains are noted.

70	Pkey:	Unique Eos probeset identifier number	
	ExAccn:	Exemplar Accession number, Genbank accession number	
75	UnigeneID:	Unigene number	
	PPDomains:	Predicted Protein Domains	
80	Unigene Title:	Unigene gene title	
	R1:	Ratio of tumor to normal adult tissues	
85	Pkey	ExAccn	UnigeneID PPDomains Unigene Title R1
	418007	M13509	Hs.83169 SS,hemopexin,Peptidase_M10 matrix metalloproteinase 1 (interl 38.9
90	439608	W79123	Hs.58561 TM,7tm_1 G protein-coupled receptor 87 28.8
	400289	X07820	Hs.2258 hemopexin,Peptidase_M10 matrix metalloproteinase 10 (stroma 20.5
95	415817	U88967	Hs.78857 SS,TM,Y_phosphatase,carb_anhyd protein tyrosine phosphatase, recep 16.4
	416209	AA236776	Hs.79078 TM,HORMA MAD2 (mitotic arrest deficient, yea 15.4
100	404996	NM_001333	Hs.87417 Peptidase_C1 CTSL2 Cathepsin L2 13.1

5	428618	AA885360	Hs.160199	pklnase	Target CAT	12.7
	429486	AF155827	Hs.203953	helicase_C,SNF2_Nhelicase_C	hypothetical protein FLJ10339	12.6
	419183	U06069	Hs.89563	p450	cytochrome P450, subfamily XXIV (vi	12.3
	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromal	10.2
	420759	T11832	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	10.2
	458194	AW383618	Hs.265459	p450	ESTs, Moderately similar to ALU2_HU	9.4
	446232	AJ281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,PKlnase	NIMA (never in mitosis gene a)-rela	8.9
10	452291	AF015592	Hs.28853	TM,PKlnase	CDC7 (cell division cycle 7, S. cer	8.7
	424086	AJ351010	Hs.102267	Lysyl_oxidase	lysyl oxidase	8.3
	425710	AF030880	Hs.159275	TM,Sulfate_transp,STAS	solute carrier family, member 4	7.8
	433133	AB027249	Hs.104741	TM,Collagen,PKlnase	PDZ-binding kinase; T-cell originat	7.4
	447254	NM_004153	Hs.17908	SS,AAA,BAH	origin recognition complex, subunit	7.1
15	431941	AK000106	Hs.272227	PKlnase,Furin-like,Recep_L_dom	Homo sapiens cDNA FLJ20099 fis, clo	6.9
	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	438211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA	6.9
	403471	NA		SS,TM,trypsin	Target Exon	6.7
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
20	457405	AA504880		TM,7tm_2	gb:ab03a10.s1 Stratagene fetal reti	6.4
	421948	L42583	Hs.334309	filament,HCO3_cotranspfilament	keratin 6A	6.3
	439292	AA090421	Hs.5555	TM,AAA,Ferrie_reduct	hypothetical protein MGC5347	5.8
	413525	AW451103	Hs.71371	TM,E1-E2_ATPase,Hydrolase	ESTs	5.8
	425695	NM_005401	Hs.159238	TM,Band_41,V_phosphatase	protein tyrosine phosphatase, non-r	5.7
25	438394	BE379623	Hs.27693	SS,pro_Isomerase	peptidylprolyl isomerase (cyclophil	5.6
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collag	5.5
	408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPA	ESTs	5.4
	432226	AW182766	Hs.273558	Cydidyltransf	phosphate cytidyltransferase 1, c	5.2
	419520	AB009303	Hs.90800	TM,hemopexin,Peptidase_M10	matrix metalloproteinase 16 (membra	5.1
30	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutam	transglutaminase 3 (E polypeptide,	5.0
	421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,E	lysyl oxidase	4.9
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrop	4.8
	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep	a disintegrin and metalloproteinase	4.8
	418379	AA218940	Hs.137516	AAA	fidgetin-like 1	4.7
35	457465	AW301344	Hs.122908	Pribosyltran,Sulfatase	DNA replication factor	4.6
	412333	AW937485		TM,7tm_1	gb:QV3-DT0044-221299-045-b09 DT0044	4.6
	450510	AA010058	Hs.242998	DNA_topoisom,DNA_topoisomIGF	ESTs	4.6
	436291	BE568452	Hs.5101	abhydrolase	protein regulator of cytokinesis 1	4.6
	446353	AJ290919	Hs.153661	HECTPKlnase	ESTs	4.5
40	435435	T89473	Hs.192328	lipase,PLAT	ESTs	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_delodlnase	delodlnase, Iodothyronine, type II	4.4
	433322	H50621	Hs.134156	TM,Ion_transNB-ARC,CARD_milb_c	ESTs, Weakly similar to I38022 hypo	4.4
	408908	BE296227	Hs.250822	TM,PKlnase	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	PH,lactamase_B	GPI-anchored metastasis-associated	4.4
45	428479	Y00272	Hs.184572	PKlnase	cell division cycle 2, G1 to S and	4.2
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprot	4.2
	423035	AW449679	Hs.156739	TM,Glyco_transf_8	H.sapiens XG mRNA (clone PEP11)	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
50	457030	AJ301740	Hs.173381	TM,Dihydroorolase	dihydropyrimidinase-like 2	4.1
	448995	A1613276	Hs.5652	adenylatekinase	guanine nucleotide binding protein	4.0
	415857	AA866115	Hs.127797	helicase_C	Homo sapiens cDNA FLJ11381 fis, clo	4.0
	438390	AJ422017		TM,DSL,7tm_17tm_1	gb:af45f12x1 NCL_CGAP_Bm23 Homo s	4.0
55	429900	AA460421	Hs.30875	PKlnase	ESTs	4.0
	446292	AF081497	Hs.275682	Ammonium_transp	Rh type C glycoprotein	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
	408771	AW732573	Hs.47584	TM,K_tetra,Ion_trans	potassium voltage-gated channel, de	3.6
	424296	A1631874	Hs.155140	PKlnase	casein kinase 2, alpha 1 polypeptid	3.6
	436246	AW450963	Hs.119991	connexinhormone_rec,zf-C4	ESTs	3.5
60	411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
	400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metal	3.5
	426920	AA393351	Hs.132121	PDEase	ESTs	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acy	endothelial cell growth factor 1 (p	3.4
65	430704	AW813091	Hs.335799	Epimerase	ESTs	3.4
	455092	BE152428		Sulfatase	gb:CM0-HT0323-151299-126-b04 HT0323	3.4
	453775	NM_002916	Hs.35120	AAA,PI3_P14_klnase,PI3Ka,PI3K_	replication factor C (activator 1)	3.4
	438993	AA828995		Integrin_B	gb:od77b08.s1 NCL_CGAP_Ov2 Homo sap	3.4
	426572	AB037783	Hs.170623	hormone_rec,zf-C4	hypothetical protein FLJ11183	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
70	427660	AT741320	Hs.114121	hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23228 fis, cl	3.3
	402481			TM,GDI,7tm_1	NM_001821:Homo sapiens choroiderem	3.3
	414774	X02419	Hs.77274	SS,Irtingla,trypsin	plasminogen activator, urokinase	3.3
	412246	A1160873	Hs.69233	SulfotransferACOX	zinc finger protein	3.3
	418462	BE001596	Hs.85266	SS,TM,Integrin_B,fn3	Integrin, beta 4	3.3
75	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatin	3.3
	401486	NA		SS,TM,trypsin	C4000647:gil4758508[ret]NP_004253.	3.2
	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, cl	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	3.2
80	402337			SS,p450	Target Exon	3.2
	420930	AW886650		ribonuclease_T2	gb:CM4-NT0007-130500-551-f08 NT0007	3.2
	443426	AF098158	Hs.9329	PKlnase	chromosome 20 open reading frame 1	3.1
	439750	AL359053	Hs.57664	TM,Integrin_B,Ricln_B,lectinrr	Homo sapiens mRNA full length inser	3.1
	420039	NM_004605	Hs.94581	CARD,SulfotransferDAGKc	sulfotransferase family, cytosolic,	3.0
	448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,Isodh,PKlna	solute carrier family 6 (neurotrans	3.0

5	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
	450841	AJ741466	Hs.270515	pro_isomerase	ESTs	3.0
	428262	AJ651324	Hs.7298	death_pkinase	biphenyl hydrolase-like (serine hyd	3.0
	435399	AA679463		pkinese	gbac50c03.s1 Stratagene hNT neuron	2.9
	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid	2.9
10	449746	AJ668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kin	ESTs	2.9
	431629	AJ077025	Hs.265827	SS,IRNA_antISH2,SH3,pkinese	interferon, alpha-inducible protein	2.8
	445873	AA250570	Hs.251945	SS,rm,PABPpkinese,14-3-3,rm	poly(A)-binding protein, cytoplasmic	2.8
15	438113	AJ487908	Hs.8882	TM,7tm_1	ESTs	2.8
	422689	AW856665		helicase_C,SNF2_Nhelicase_C	gb:RC3-CT0297-290100-013-d03 CT0297	2.8
	439453	BE264974	Hs.6566	SS,AAA	thyroid hormone receptor interactor	2.8
	413582	AW295847	Hs.71331	carb_anhydrase	hypothetical protein MGC5350	2.8
	410664	NM_006033	Hs.65370	TM,lipase,PLAT	lipase, endothelial	2.8
20	456456	AA477609	Hs.89563	FBPase	nuclear cap binding protein subunit	2.8
	413273	U75679	Hs.75257	TM,lg,pkinese	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0035 gene product	2.8
	403763			TM,7tm_1	NM_001059*:Homo sapiens tachykinin	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor	diubiquitin	2.7
25	401230			SS,TM,ion_trans,IQ	NM_014191*:Homo sapiens sodium chan	2.7
	418030	BE207573	Hs.83321	SS,TM,Peptidase_S26,Bombesin	neuromedin B	2.7
	445640	AW969626	Hs.31704	TM,alpha-amylase	ESTs, Weakly similar to KIAA0227 [H	2.7
	432865	AJ753709	Hs.152484	TM,ion_transNB-ARC,CARD,WD40,m	ESTs, Weakly similar to I38022 hypo	2.6
	419667	AJ077005	Hs.92208	SS,TM,disintegrin,Reprolysin_P	a disintegrin and metalloproteinase	2.6
30	406671	AA129547	Hs.285754	TM,pkinese,Plexin_repeat,Sema,	met proto-oncogene (hepatocyte grow	2.6
	412530	AA766268	Hs.266273	abhydrolase	hypothetical protein FLJ13346	2.6
	431890	X17033	Hs.271986	vwa,FG-GAP,Integrin_A	Integrin, alpha 2 (CD49B, alpha 2 s	2.6
	404184	NA		SS,TM,7tm_1	NM_030903*:Homo sapiens olfactory r	2.6
	428450	NM_014791	Hs.184339	pkinese,KA1	KIAA0175 gene product	2.6
35	425698	NM_016112	Hs.159241	TM,pkinese,ion_trans	polycystic kidney disease 2-like 1	2.6
	453331	AJ240665	Hs.8895	TM,disintegrin,Pep_M12B_propep	ESTs	2.6
	444826	AJ674482	Hs.148441	pkinese,SAM	ESTs	2.6
	414987	AA524394	Hs.294022	connexin,hormone_rec,zf-C4,conn	hypothetical protein FLJ14950	2.6
	438746	AJ885816	Hs.184727	Ribosomal_S2,transferrin	ESTs	2.5
40	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	453379	AA035261	Hs.61753	PAN,Integlin,trypsin	ESTs	2.5
	421733	AL119671	Hs.1420	SS,TM,lg,pkinese	fibroblast growth factor receptor 3	2.5
	452220	BE158006	Hs.212296	TM,Integrin_A,FG-GAP	ESTs	2.5
45	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	400301	X03635	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	estrogen receptor 1	2.5
	408938	AA059013	Hs.22607	Y_phosphatase	ESTs	2.4
	411643	AJ924519	Hs.192570	DEAD_helicase_C	hypothetical protein FLJ22028	2.4
	446638	AL133063	Hs.15783	TM,pkinese	Homo sapiens mRNA; cDNA DKFZp434P11	2.4
50	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	417655	AA780791	Hs.14014	Peptidase_M41,AAApkinese	hypothetical protein FLJ14813	2.4
	448005	AW207437	Hs.170378	pkinese	ESTs	2.4
	423973	AF038461	Hs.136574	TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase, 12R1	2.4
	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
55	426397	J04088	Hs.156346	DNA_topoisomII,DNA_topoisomVIGF	topoisomerase (DNA) II alpha (170kD	2.4
	432777	AA564891	Hs.269477	alpha-aryase	ESTs	2.4
	421247	BE391727	Hs.102910	TM,IRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIH, p	2.4
	425465	L18964	Hs.1904	TM,pkinese,DAG_PE-bind,OPR,pld	protein kinase C, tota	2.4
	419281	H96452	Hs.42189	TM,E1-E2_ATPase,HMA,Hydrolase	ESTs	2.4
60	434205	AF119861	Hs.283032	SH3,efhand,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
	453406	AJ192987	Hs.61784	pkinese,Furin-like,Recep_L_dom	hypothetical protein FLJ14451	2.3
	435542	AA687376	Hs.269533	pkinese,RhoGEF,lg,PH,SH3	ESTs	2.3
	443151	AJ827193	Hs.132714	DNA_mis_repair,HATPase_cAcyph	ESTs	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,Integrin_A	integrin, alpha 3 (antigen CD49C, a	2.3
65	422310	AA316622	Hs.98370	SS,TM,fn3,lg,pkinese,Ribosomal	cytochrome P450, subfamily IIS, pol	2.3
	441954	AJ744935	Hs.8047	TM,band_7,AAA,cdc48_N	Fanconi anemia, complementation gro	2.3
	414907	X90725	Hs.77597	SS,TM,pkinese,POLO_box	pelo (Drosophila)-like kinase	2.3
	439810	AL109710	Hs.85668	aconitase,Aconitase_C	EST	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membra	2.3
70	432284	AA532807	Hs.105822	TM,pkinese	ESTs	2.3
	452947	AW130413		alpha-amylase	gb:cd50f04.x1 NCL_CGAP_Gas4 Homo sa	2.3
	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
	453941	U39817	Hs.36820	DEAD,HRDC,helicase_C	Bloom syndrome	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylth	2.3
75	424439	AA579635	Hs.1770	DNA_ligase	ligase I, DNA, ATP-dependent	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypo	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2
	434149	Z43829	Hs.19574	TM,EPH_lbd,fn3,pkinese,SAM	hypothetical protein MGC5469	2.2
	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltra	2.2
80	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor, SREC	2.2
	416763	AJ908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficien	2.2
	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONU	2.2
	430637	BE160081	Hs.256290	S_100Peptidase_M16	S100 calcium-binding protein A11 (c	2.2
	452367	U71207	Hs.29279	SS,Hydrolase	eyes absent (Drosophila) homolog 2	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. c	2.1

5	424490	AJ278016	Hs.55565	TM,ptkase,ank	ankyrin repeat domain 3	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
	410855	X97795	Hs.66718	SNF2_N,helicase_C	RAD54 (S.cerevisiae)-like	2.1
	418804	AA809632		HATPase_c,HSP90,PHD,zf-C2H2	gb:nz17h04.s1 NCL_CGAP_GC81 Homo sa	2.1
	447674	BE270640	Hs.19192	TM,ptkinaseras,ari	cyclin-dependent kinase 2	2.1
	450663	H43540	Hs.25292	SS,TM,RNase_HII	ribonuclease H1, large subunit	2.1
	408805	H69912	Hs.48269	TM,ptkase	vaccinia related kinase 1	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TILa,vwd,EP	procollagen C-endopeptidase enhance	2.1
10	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,Ig,MAM	protein tyrosine phosphatase, recep	2.1
	428273	AI867228	Hs.303211	Glycos_transf_2	ESTs	2.1
	404274			SS,TM,ptkase,fn3	NM_002944*:Homo sapiens v-ros avian	2.1
	403133			ptkase,K_tetra,Band_41,RhoGEF	Target Exon	2.1
	440249	AI246590	Hs.337275	VHL,TatD_DNase	ESTs	2.1
15	438580	AA811262	Hs.299202	TM,ptkinasesugar_tr	ESTs	2.1
	406400			SS,TM,trypsin	NM_007196:Homo sapiens kallikrein 8	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprol	metallocarboxypeptidase CPX-1	2.1
	423453	AW450737	Hs.128791	SS,Grnln,CDP-OH_P_transf	CGI-09 protein	2.1
	433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
20	420757	X78592	Hs.89915	TM,hormone_rec,Androgen_recep,	androgen receptor (dihydrotestoster	2.1
	425018	BE245277	Hs.154196	DNase_I,K_tetra	E4F transcription factor 1	2.1
	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
	457288	AA521458	Hs.192738	pro_Isomerase	ESTs	2.1
	407305	AA715284		TM,ptkase,Sema,Plexin_repeat,	gb:nv35f03.r1 NCL_CGAP_Br5 Homo sap	2.1
25	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	422429	AA310527		ptkase,RGS,PHkinase,PH,RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
	402974	NM_001501	Hs.129715	GnRHhormone5,hormone4	gonadotropin-releasing hormone 2	2.0
	458016	AW188099	Hs.131813	ptkase	ESTs	2.0
	452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfa	2.0
30	428028	U52112	Hs.182018	TM,ptkase,MBD	Interleukin-1 receptor-associated k	2.0
	427747	AW411425	Hs.180655	ptkase,lipoxygenase,PLATilpox	serine/threonine kinase 12	2.0
	452841	T17431	Hs.65412	TM,DEAD,helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
	449539	W80363	Hs.58446	ptkase,Furin-like,Recep_L_dom	ESTs	2.0
	418140	BE613838	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
35	430076	AA465115	Hs.318773	AAA,BAH	KIAA1836 protein	2.0
	425749	AW328587	Hs.159448	Ribosomal_L7Ae,LRR,LRRCT,ptkase	surfeit 2	2.0
	425855	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
	400135	L40027	Hs.118890	ptkase	glycogen synthase kinase 3 alpha	2.0
40	TABLE 14B					
	Pkey:	Unique Eos probaset Identifier number				
	CAT number:	Gene cluster number				
45	Accession:	Genbank accession numbers				
	Pkey	CAT number	Accessions			
50	412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492			
	418804	179138_1	AA809632 AI917245 AI701732 AA228406			
	420930	197733_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652			
	422429	218469_1	AA310527 AW962295 Z44865 H06641			
	422689	218986_1	AW856665 AA315006 AW954733			
	435399	405576_1	AA679463 AW813779 AW813709			
55	438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003			
	438993	467651_1	AA828995 AA834879 AI926361			
	452947	939810_1	AW130413 AI932362			
	455092	1252971_1	BE152428 AW855572 AW855607			
	457405	333127_1	AA504860 AA504911			
60	TABLE 14C					
	Pkey:	Unique number corresponding to an Eos probaset				
65	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.				
	Strand:	Indicates DNA strand from which exons were predicted.				
	Nt_position:	Indicates nucleotide positions of predicted exons.				
	Pkey	Ref	Strand	Nt_position		
70						
	400666	8118496	Plus	17982-18115,20297-20456		
	401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758		
	401488	7341763	Plus	32685-32756,36281-36540,40791-40933,44018-44179		
75	402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205		
	402481	9797406	Plus	87891-88991		
	403133	7331427	Plus	38314-38634		
	403471	9930659	Minus	85867-85983		
	403763	7229888	Minus	43576-43887		
	404184	4581418	Minus	12652-13548		
80	404274	9885189	Plus	104127-104318		
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077		

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

5 Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 95th percentile value amongst cervical cancers was greater than or equal 80 units.

10	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of cervical cancer to normal cervix			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMBA1004341	36.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), mem	35.6
20	421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
	443639	BE269042	Hs.9661	proteasoma (prosome, macropain) subunit, beta type, 1	32.0
	454390	AB020713	Hs.56966	KIAA0906 protein	30.5
	416665	BE267931	Hs.76998	proliferating cell nuclear antigen	30.4
	433226	AW503733	Hs.9414	KIAA1488 protein	30.0
25	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
	414132	AI801235	Hs.48480	ESTs	28.3
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
	448569	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	27.2
30	418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldehyde red	26.9
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
	449722	BE280074	Hs.23960	cyclin B1	26.2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	25.3
35	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
	432917	NM_014125	Hs.279812	PRO327 protein	24.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	23.6
	457465	AW301344	Hs.122908	DNA replication factor	23.1
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
40	429083	Y09397	Hs.227817	BCL2-related protein A1	22.9
	401405			Target Exon	22.8
	426272	AW450671	Hs.189284	ESTs	22.7
	424878	H57111	Hs.221132	ESTs	22.6
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakkinin 6)	22.5
45	444371	BE540274	Hs.239	forkhead box M1	22.2
	418030	BE207573	Hs.83321	neuromedin B	22.0
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-	21.6
	400195			Eos Control	21.3
50	416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
	424865	AF011333	Hs.153563	lymphocyte antigen 75	21.0
	438011	BE466173	Hs.145696	splicing factor (CC1.3)	20.7
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
	436923	AW293704	Hs.122658	ESTs	20.2
	415791	H09366	Hs.78853	uracil-DNA glycosylase	20.0
55	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moiety X)-type m	19.6
	435647	AI653240	Hs.49823	ESTs	19.6
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.5
	428433	AA521410	Hs.41371	ESTs	19.4
60	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
	417308	H50720	Hs.81892	KIAA0101 gene product	19.2
	429574	BE268321	Hs.208912	hypothetical protein MGC861	19.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	19.0
65	438899	AF085833	Hs.135624	ESTs	19.0
	456362	AW973003	Hs.179909	hypothetical protein FLJ22955	18.9
	438598	AI805943	Hs.326067	hypothetical protein MGC5178	18.8
	408908	BE296227	Hs.250822	serine/threonine kinase 15	18.8
	427488	M91401	Hs.176658	RAD23 (S. cerevisiae) homolog B	18.6
70	400195			NM_007057*:Homo sapiens ZW10 interactor (ZWINT), tran	18.5
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	18.4
	410324	AW292539	Hs.30177	ESTs	18.3
	453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
	410608	AI538438	Hs.159087	ESTs	18.1
75	432503	AA551196	Hs.188952	ESTs	17.9
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	17.7
	430709	R34356		gbyh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
	449962	AA004879	Hs.187820	ESTs	17.3
	425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
80	440774	AI420611	Hs.127832	ESTs	16.8
	408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
	435110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [16.7
	426897	AW976570	Hs.97387	ESTs	16.5
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

5	433159	AB035898	Hs.150587	kinesin-like protein 2	16.3
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	16.3
	453883	AF638516	Hs.22630	cofactor required for Sp1 transcriptional activation,	16.3
	453941	U39817	Hs.36820	Bloom syndrome	16.1
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	16.0
10	407999	AJ126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTE	16.0
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP2006454	15.7
	407720	AB037776	Hs.38002	KIAA1355 protein	15.6
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1 protein - mou	15.6
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elastase)	15.5
15	419777	D60134	Hs.270975	ESTs	15.3
	453886	R66282	Hs.20247	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	15.2
	443715	AI583187	Hs.9700	cyclin E1	15.2
	407786	AA687538	Hs.38972	tetraspan 1	16.2
	431910	AK000142	Hs.101774	hypothetical protein FLJ23045	15.2
20	417634	W27202	Hs.82327	glutathione synthetase	15.1
	432692	AW974944	Hs.200577	ESTs	15.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), membe	15.1
	427999	AJ435128	Hs.181369	ubiquitin fusion degradation 1-like	15.0
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	15.0
25	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clone IFI-6-16)	14.9
	435354	AA678267	Hs.117115	ESTs	14.8
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	14.8
	416109	AJ420311	Hs.126550	suppressor of K transport defect 1	14.8
	417933	X02308	Hs.82962	thymidylate synthetase	14.7
30	438970	AA837782	Hs.321058	ESTs	14.7
	409680	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.7
	432401	NM_013330	Hs.274479	NME7	14.6
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
	420734	AW972872	Hs.293736	ESTs	14.5
35	434256	AJ378817	Hs.191847	ESTs	14.5
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960673	Hs.177530	ATP synthase, H transporting, mitochondrial F1 comple	14.3
	427081	AJ474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN III ALU CLASS	14.2
	420309	AW043637	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	14.2
40	429966	BE081342	Hs.283037	HSPC039 protein	14.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-inducible, 67	14.1
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
	418803	U50079	Hs.88556	histone deacetylase 1	14.0
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	14.0
45	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding pr	13.9
	433255	AI274270	Hs.96840	KIAA1527 protein	13.9
	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	13.8
	449801	AA477355	Hs.288300	hypothetical protein FLJ23231	13.8
50	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.8
	439398	AA284267	Hs.221504	ESTs	13.6
	404630			Target Exon	13.6
	408321	AW405882	Hs.44205	cortistatin	13.6
55	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219-gil12737280refXP_006682.2 keratin 18 [Ho	13.5
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	13.5
	425261	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
60	439926	AW014875	Hs.137007	ESTs	13.3
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	13.2
	419828	T81422	Hs.14922	ESTs	13.2
65	428147	AW628965	Hs.234983	ESTs, Weakly similar to 2109260A B cell growth factor	13.2
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	13.1
	407595	BE350012	Hs.248365	ESTs	13.1
	432721	AL121478	Hs.180532	glucose phosphate isomerase	13.1
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associ	13.0
70	413314	BE081585		gb:QV2-BT0635-210400-156-b07 BT0635 Homo sapiens cDNA	13.0
	430929	AA489166	Hs.156933	ESTs	12.9
	449571	AW016812	Hs.200266	ESTs	12.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the prostate	12.8
	417105	X60992	Hs.81226	CD6 antigen	12.6
75	434263	N34895	Hs.44648	ESTs	12.6
	412059	AA317862	Hs.249721	ESTs, Moderately similar to PC4259 fertilin associate	12.6
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	12.5
	437056	AI147081		gb:ok33a11.s1 Soares_NSIF_F8_9W_OT_PA_P_S1 Homo sapien	12.5
	438768	AI307416	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
80	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.5
	450738	AA010907	Hs.184456	hypothetical protein	12.4
	418205	L21715	Hs.83760	tropotin 1, skeletal, fast	12.4
	442994	AI026718	Hs.16954	ESTs	12.4
	433301	AW298280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	12.4
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycoprotein beta-1,4-N-acetylgl	12.3
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973668	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
5	432325	AW973209	Hs.261782	ESTs	12.3
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.3
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LNG00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
10	427295	AW291212	Hs.293943	hypothetical protein MGC11266	12.2
	415443	T07353	Hs.7948	ESTs	12.1
	429770	AI766047	Hs.89736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
	432810	AA863400	Hs.23054	ESTs	12.1
15	434423	NM_006769	Hs.3844	LIM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	459273	AW608906	Hs.334767	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
20	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566	11.9
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
	434408	AJ031771	Hs.132586	ESTs	11.8
25	406747	AJ925153	Hs.217493	annexin A2	11.8
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	445655	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
30	427527	AI809057	Hs.302083	immunoglobulin heavy constant mu	11.7
	432287	AK001057	Hs.274268	Homo sapiens cDNA FLJ10195 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
35	409931	BE293233	Hs.129771	ESTs	11.4
	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE408813	Hs.152337	protein arginine N-methyltransferase 3(hnRNP methyltr	11.4
	456880	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
	433849	BE465884	Hs.280728	ESTs	11.4
40	430519	AF128534	Hs.49210	F-box only protein 4	11.4
	434442	AA737415	Hs.152826	ESTs	11.3
	457205	AI905780	Hs.198272	Target CAT	11.3
	422713	AA902780	Hs.119325	Huntingtin-interacting protein A	11.3
	443491	AW499665	Hs.9456	SW/SNF related, matrix associated, actin dependent r	11.3
45	424339	BE257148	Hs.145416	endoglycan	11.3
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	AI686945	Hs.272062	ESTs	11.2
	446849	AU076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, similar to RIKEN cDNA 5730578N08 gene,	11.2
50	442737	AB002319	Hs.8653	KIAA0321 protein	11.2
	409113	AA074897		gb:zm85a05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA169345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402539	AW502761	Hs.30909	KIAA0430 gene product	11.0
55	413677	AW503116	Hs.301819	zinc finger protein 146	11.0
	414706	AW340125	Hs.76989	KIAA0097 gene product	11.0
	421632	AA825426	Hs.238832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	11.0
	436995	AI277986	Hs.164875	ESTs	11.0
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	10.9
60	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
	451655	H85689	Hs.225560	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AI393122	Hs.134726	ESTs	10.9
	444655	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
	410093	AW589558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
65	400080			Eos Control	10.8
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675:Homo sapiens promyelocytic leukemia (PML),	10.8
	446099	T93096	Hs.17126	hypothetical protein MGC15912	10.7
70	451066	AI758660	Hs.206132	ESTs	10.7
	409235	AA188827	Hs.7988	ESTs, Weakly similar to 138022 hypothetical protein [10.7
	451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AI948688	Hs.266619	ESTs	10.6
	441836	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (from clone DKFZ	10.6
75	438654	AI005270	Hs.123543	ESTs	10.6
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AI815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AI056769	Hs.133512	ESTs	10.6
	417883	AB000450	Hs.82771	vaccinia related kinase 2	10.6
	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside triphosphate pyrop	10.6
80	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812535		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687376	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110067	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	10.5

	416564	AW795793	Hs.179827	Homo sapiens cDNA FLJ12257 fis, clone MAMMA1001501, h	10.5
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT2RM4002390	10.5
	408329	AF155510	Hs.44227	heparanase	10.5
5	410146	AW592655		gb:hi45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.5
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (10.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	10.4
	407241	M34516		gb:human omega light chain protein 14.1 (lg lambda ch	10.4
	435061	AI651474	Hs.163944	ESTs	10.4
10	409653	AW451693	Hs.220826	ESTs	10.4
	428294	AA425488		gb:zw46d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	10.4
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sensitivity prote	10.4
	408809	AW274673	Hs.279706	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4
15	424792	U92538	Hs.153138	origin recognition complex, subunit 5 (yeast homolog)	10.3
	422406	AF025441	Hs.116208	Opa-interacting protein 5	10.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelati	10.3
	413809	L25851	Hs.851	Integrin, alpha E (antigen CD103, human mucosal lymph	10.3
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypothetical protein [10.3
20	448119	H38587	Hs.82295	dedicator of cyto-kinesis 1	10.2
	457288	AA521458	Hs.192738	ESTs	10.2
	402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2
	440572	AW183778	Hs.249584	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside transporters), m	10.2
25	443780	NM_012068	Hs.9754	activating transcription factor 5	10.1
	422429	AF310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1
	430848	AW021726		gb:df27e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1
30	422470	AB017919	Hs.117232	peptidyl arginine deiminase, type V	10.1
	449501	AI652924	Hs.231942	ESTs	10.1
	420731	AI042052	Hs.104432	ESTs	10.1
	404345	AA730407	Hs.159155	protocadherin 11	10.1
	400438	AF185611		Target	10.1
35	438170	AI916685	Hs.194601	ESTs	10.1
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	10.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1
	427766	AA412258	Hs.188817	ESTs	10.1
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0
40	403038			Target Exon	10.0
	434674	AA831879	Hs.136985	ESTs	10.0
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0
	439428	AA835825	Hs.190490	ESTs	10.0
	403310			Target Exon	9.9
45	408392	U28831	Hs.44566	KIAA1641 protein	9.9
	421849	AW410872	Hs.108894	hypothetical protein FLJ20411	9.9
	433384	AI021992	Hs.124244	ESTs	9.9
	443343	BE409809	Hs.301005	purine-rich element binding protein B	9.9
	437267	AW511443	Hs.258110	ESTs	9.9
50	455978	AI310151	Hs.173524	ESTs	9.9
	435851	AA700946	Hs.191933	ESTs	9.9
	452243	AL355715	Hs.28555	programmed cell death 9	9.9
	441703	AW390054	Hs.192843	isoleucine zipper protein FKSG14	9.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.9
55	436669	AA535975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), member 2	9.8
	417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fis, clone HEMBA1001835	9.8
	455855	BE147440		gb:RC1-HT0229-080100-015-09 HT0229 Homo sapiens cDNA	9.8
	410390	AA876905	Hs.125286	ESTs	9.8
60	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid transpo	9.8
	442660	AW138174	Hs.130651	ESTs	9.8
	436186	BE390717	Hs.5074	similar to S. pombe dim1	9.8
	426773	NM_015556	Hs.172180	KIAA0440 protein	9.8
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	9.7
65	418347	AA216419		gb:mc16e03.s1 NCL_CGAP_Pr1 Homo sapiens cDNA clone si	9.7
	448752	AA593887	Hs.300842	KIAA1608 protein	9.7
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone THYRO1001322	9.7
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7
	430752	AA485330	Hs.303278	ESTs	9.7
70	436523	BE612990	Hs.5212	single-strand selective monofunctional uracil DNA gly	9.7
	415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00089 protein, partial cds	9.7
	411930	F06485	Hs.7740	oxysterol binding protein-like 1	9.7
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H	9.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical protein [9.6
75	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA1011 protein	9.6
	434957	AF283775	Hs.35380	x 001 protein	9.6
	407292	AA876638		gb:nz45e06.s1 NCL_CGAP_Pr12 Homo sapiens cDNA clone s	9.6
	459109	AW292447	Hs.140821	ESTs	9.6
	457892	AA744389		gb:ny51e10.s1 NCL_CGAP_Pr18 Homo sapiens cDNA clone s	9.6
80	432074	AA525248	Hs.149723	ESTs	9.6
	440463	AI733087	Hs.129994	ESTs	9.6
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	9.6
	445326	AI220072	Hs.165893	ESTs	9.6
	434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALIN [Hsap	9.6

5	420361	N92054	Hs.194718	zinc finger protein 265	9.8
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA806106	Hs.123664	ESTs	9.6
	417037	BE083936	Hs.80976	antigen identified by monoclonal antibody KJ-67	9.6
	449317	AW293413	Hs.132906	19A24 protein	9.6
10	436588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374:gi10764778 gb AA622817.1 AF302150.1 (AF30	9.5
	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PLACE1006851	9.5
	409902	AI337658	Hs.156351	ESTs	9.5
15	432258	AW973078	Hs.293039	ESTs	9.5
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serine/threonine-s	9.5
	405536			NM_005805:Homo sapiens 26S proteasome-associated pad1	9.5
	418216	AA652240	Hs.283099	AF15q14 protein	9.5
	434573	AW372340	Hs.159717	ESTs	9.5
20	439354	AF086174		gb:Homo sapiens full length insert cDNA clone ZB94A08	9.5
	455410	AW936678		gb:PM2-DT0023-080300-004-e04 DT0023 Homo sapiens cDNA	9.5
	400738			Target Exon	9.5
	419474	AW968619	Hs.155849	ESTs	9.4
	406464			C17000168:gi7294725 gb AAF50062.1 (AE003544) CG7547	9.4
25	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400091	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
	433840	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDNA clone EURO1	9.4
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	9.4
30	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapiens]	9.4
	435099	AC004770	Hs.4758	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
	419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, complete cds	9.4
	402967			Target Exon	9.3
35	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441075	AA915991	Hs.179214	ets variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
	420897	AW139261	Hs.232280	ESTs	9.3
40	418867	D31771	Hs.69404	msh (Drosophila) homeo box homolog 2	9.3
	420288	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothetical protein [9.3
	420101	AW500529	Hs.95180	KIAA0767 protein	9.3
	428166	AA423849	Hs.79530	M5-14 protein	9.3
45	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92962	Hs.35052	ESTs	9.3
	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE:363894, mRNA, partial cds	9.3
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
50	415009	C75253	Hs.220950	ESTs	9.3
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877998	Hs.125376	ESTs, Weakly similar to J1C5314 CDC28/cdc2-like kinase	9.2
	417881	AI879117		gb:cau54g09.y1 Schneider fetal brain 00004 Homo sapien	9.2
	446354	AW449850	Hs.202249	ESTs	9.2
55	427018	AA397538	Hs.136280	Homo sapiens cDNA: FLJ22288 fis, clone HRC04157	9.2
	434410	AA632644		gb:np87b07.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI459308	Hs.24908	ESTs	9.2
	457322	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	9.2
	424317	AI865032	Hs.26017	ESTs	9.2
60	433001	AF217513	Hs.278905	clone HQ0310 PRO0310p1	9.2
	404112	BE302729	Hs.173162	neighbor of COX4	9.2
	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
	434960	AW374941	Hs.72545	ESTs	9.1
	431658	BE409917	Hs.266935	tRNA selenocysteine associated protein	9.1
65	439158	R60323	Hs.193888	ESTs	9.1
	443081	H86858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFEIT LOCUS	9.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	9.1
70	430780	N95102	Hs.334858	hypothetical protein MGC12250	9.1
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	AA218940	Hs.137516	fidgetin-like 1	9.1
	431405	AI470895	Hs.252574	ribosomal protein L10a	9.0
	405454			C12000541:gi5729884 ref NP_006539.1 IGF-II mRNA-bin	9.0
75	438362	AA805678	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.0
	424232	BE093589	Hs.38178	hypothetical protein FLJ23468	9.0
	459086	AA021163	Hs.22287	ESTs	9.0
80	418653	AI734064	Hs.136212	ESTs	9.0
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	9.0
	437534	AA814471	Hs.291800	ESTs	9.0
	435074	AI760944	Hs.116937	ESTs	9.0
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW263123	Hs.127554	ESTs	9.0
	431675	AA699565	Hs.202375	ESTs	9.0
	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AA814971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
5	441370	A1242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
	437966	AW891130	Hs.38173	ESTs	8.9
	426360	AW290981	Hs.211296	ESTs, Weakly similar to 2109260A B cell growth factor	8.8
	448111	AA053486	Hs.20315	Interferon-induced protein with tetratricopeptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
10	429228	AI553633	Hs.337139	ESTs	8.8
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partial	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDNA clone EURO1	8.8
15	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
	450881	W80462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	AJ146771	Hs.158008	ESTs	8.8
	453204	R10799	Hs.191990	ESTs	8.7
	412719	AW016510	Hs.129911	ESTs	8.7
20	408805	H69912	Hs.48269	vaccinia related kinase 1	8.7
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410506	Hs.27973	KIAA0874 protein	8.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
25	454132	AW131759	Hs.248286	ESTs	8.7
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236778	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441525	AW241867	Hs.127728	ESTs	8.7
30	459539	AJ279186		gb:qm24a04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone 3'	8.7
	443148	AJ034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
	424255	AI192657	Hs.143897	dysferlin, limb girdle muscular dystrophy 2B (autosom	8.7
	459435	AA320038		gb:EST22383 Adipose tissue, white II Homo sapiens cDN	8.7
	443117	AJ248826	Hs.42029	ESTs	8.6
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	8.6
35	442505	AW003775	Hs.198248	UDP-Gal4betaGlcNAc beta 1,4- galactosyltransferase, p	8.6
	439091	AA488833	Hs.126711	ESTs, Weakly similar to I38588 reverse transcriptase	8.6
	439223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995		gb:HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
	415961	H10983	Hs.155919	ESTs	8.6
40	424042	Y10601	Hs.137674	ankyrin-like with transmembrane domains 1	8.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	8.6
	447155	AA100805	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412668	AA456195	Hs.10056	hypothetical protein FLJ14621	8.6
	458042	AW058464	Hs.6430	protein with polyglutamine repeat; calcium (ca2) home	8.6
45	456530	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKF	8.6
	433345	AJ681545	Hs.152982	hypothetical protein FLJ13117	8.6
	445006	W91903	Hs.124814	ESTs	8.6
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
	455161	BE145900		gb:MR0-HT0208-221299-204-b12 HT0208 Homo sapiens cDNA	8.5
50	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cerevisiae)	8.5
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interacting protein	8.5
	416018	U9395	Hs.77807	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534			C1001768*.g112621132ref[NP_075243.1] MEGF1 [Rattus	8.5
55	438451	AJ081972	Hs.220261	ESTs	8.5
	435176	AA744875	Hs.189413	ESTs	8.5
	443245	AJ040955	Hs.151973	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	8.5
	457478	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), catalytic subuni	8.5
60	403839			Target Exon	8.5
	434932	BE613162	Hs.284135	hypothetical protein MGC3036	8.5
	420991	AW504814	Hs.121004	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	8.4
	455994	BE179190		gb:RCO-HT0613-210300-032-07 HT0613 Homo sapiens cDNA	8.4
65	402786			Target Exon	8.4
	423426	AW389579	Hs.128434	Homo sapiens ELISC-1 mRNA, partial cds	8.4
	429568	AJ088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (from clone DKF	8.4
	404110			NM_020245*-Homo sapiens tubby super-family protein (T	8.4
	424441	X14850	Hs.147097	H2A histone family, member X	8.4
70	433155	AL037035	Hs.100426	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
	414839	X63692	Hs.77462	DNA (cytosine-5)-methyltransferase 1	8.4
	406867	AA157857	Hs.182265	keratin 19	8.4
	418278	AJ088489	Hs.83937	hypothetical protein	8.4
	458696	AW375333	Hs.199890	ESTs	8.4
75	456248	AL035786	Hs.82425	actin related protein 2/3 complex, subunit 5 (18 kD)	8.4
	403152	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene homolog-like	8.4
	407649	BE066724	Hs.37427	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	446387	AJ874402	Hs.170810	ESTs	8.4
	433671	AW138797	Hs.132906	19A24 protein	8.4
80	425891	AJ041717	Hs.132141	ESTs	8.4
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 protein [H.sapie	8.4
	439079	AF085937	Hs.38348	ESTs	8.4
	458115	BE091587		gb:JL2-BT0731-240400-069-H04 BT0731 Homo sapiens cDNA	8.4
	428144	BE269243	Hs.182625	VAMP (vesicle-associated membrane protein)-associated	8.4

	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	8.3
	443056	AA57996	Hs.132578	ESTs	8.3
	410391	H17881	Hs.15043	Homo sapiens clone FLB5227 PRO1367 mRNA, complete cds	8.3
5	407989	AW135208	Hs.256092	ESTs	8.3
	410536	N39533		gb:yy27d04.s1 Soares fetal liver spleen 1NFLS Homo sa	8.3
	452273	AI870685	Hs.231022	ESTs	8.3
	454297	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	8.3
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	8.3
10	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/Hs) b	8.3
	432891	AF161483	Hs.279761	HSPC134 protein	8.3
	419923	AW081455	Hs.120219	ESTs	8.2
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914	8.2
	435452	AA831004	Hs.124874	ESTs	8.2
15	418583	U80908	Hs.87241	hypothetical protein from clones 23549 and 23762	8.2
	440065	W03476	Hs.266331	hypothetical protein MGC4595	8.2
	439762	T78968	Hs.14411	ESTs	8.2
	447983	AW612726	Hs.282113	ESTs, Weakly similar to I38022 hypothetical protein [8.2
	441966	AA568689	Hs.16131	hypothetical protein FLJ12876	8.2
20	408182	AA047854		gb:zf49g04.r1 Soares retina N2b4HR Homo sapiens cDNA	8.2
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	8.2
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143	8.2
	414962	AF273304	Hs.235376	XPMC2 protein	8.2
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), soluble	8.2
	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	8.2
25	413940	AI633205	Hs.159914	ESTs, Weakly similar to I78885 serine/threonine-speci	8.2
	437277	AA748016	Hs.123370	ESTs	8.2
	431445	AA505135	Hs.44037	ESTs	8.1
	418927	BE349635	Hs.190284	ESTs	8.1
	452446	AA086123	Hs.297856	ESTs	8.1
30	445380	AI222019	Hs.144838	ESTs	8.1
	421174	AW969058	Hs.291974	ESTs, Moderately similar to A46010 X-linked retinopat	8.1
	444374	AA009841	Hs.11039	hypothetical protein MGC2722	8.1
	417247	N58024		gb:yy63c01.s1 Soares fetal liver spleen 1NFLS Homo sa	8.1
35	438335	AI498421	Hs.243168	ESTs	8.1
	445235	AI564022	Hs.138207	ESTs	8.1
	422585	NM_016186	Hs.118620	protein Z-dependent protease inhibitor precursor	8.1
	442522	AI087038	Hs.146592	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	8.1
	430684	AI808979	Hs.293193	ESTs	8.1
40	446442	BE221533	Hs.257858	ESTs	8.1
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothetical protein [8.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein product [H.sa	8.0
	449539	W80363	Hs.58446	ESTs	8.0
	406663	U24683	Hs.302063	immunoglobulin heavy constant mu	8.0
45	423767	H18283	Hs.132753	F-box only protein 2	8.0
	450937	RA9131	Hs.26267	ATP-dependant interferon response protein 1	8.0
	430977	AA490069	Hs.308676	Homo sapiens cDNA FLJ14302 fis, clone PLACE2000003	8.0
	455677	BE066061	Hs.8867	cysteine-rich, angiogenic inducer, 61	8.0
	436706	AA725808	Hs.194609	ESTs	8.0
50	459407	N92114		gb:za22h11.r1 Soares fetal liver spleen 1NFLS Homo sa	8.0
	444132	AK000452	Hs.10340	hypothetical protein FLJ20445	8.0
	437149	AI686651	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2	8.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	8.0
	411298	AW835859		gb:PMO-LT0017-031299-001-h07 LT0017 Homo sapiens cDNA	8.0
55	432571	AF151054	Hs.278429	hepatocellular carcinoma-associated antigen 59	8.0
	416295	AI064824	Hs.193385	ESTs	8.0
	427485	AF039652	Hs.178655	ribonuclease H1	8.0
	409857	AW501908		gb:UL-HF-BR0p-ajp-c-12-0-UL.r1 NIH_MGC_52 Homo sapien	7.9
	433854	AA610649	Hs.333239	ESTs	7.9
60	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo sapiens cDNA	7.9
	423573	AA328504		gb:EST31993 Embryo, 12 week I Homo sapiens cDNA 5' en	7.9
	404495			C8001441*:g[18923061]ref[1NP_060114.1] hypothetical pr	7.9
	443135	AI376331	Hs.156103	ESTs	7.9
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	7.9
65	413283	R78669	Hs.23756	hypothetical protein similar to swine acyneuraminata	7.9
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	7.9
	434197	AA627223		gb:nq63b04.s1 NCL_CGAP_Ov6 Homo sapiens cDNA clone si	7.9
	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor protein 1	7.9
	434502	AW974915	Hs.116550	ESTs	7.9
70	435507	AI143579	Hs.26510	vacuolar protein sorting 33B (yeast homolog)	7.9
	444896	AI201480	Hs.144856	ESTs	7.9
	419320	H96666	Hs.6137	ESTs	7.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	7.9
	425569	AA359597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HEMBB1002387	7.9
	445209	AW294230	Hs.80988	collagen, type VI, alpha 3	7.9
75	449193	AI637997	Hs.195653	ESTs	7.9
	447397	BE247676	Hs.18442	E-1 enzyme	7.9
	455037	BE144549		gb:MR0-HT0167-081199-001-a02 HT0167 Homo sapiens cDNA	7.9
	453367	AW732847	Hs.70573	PKC-1-related HIT protein	7.8
80	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothetical protein D	7.8
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	7.8
	406562			NM_004520*:Homo sapiens kinesin heavy chain member 2	7.8
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor 3, subunit 8	7.8
	413500	BE144914		gb:CM3-HT0183-181099-023-b05 HT0183 Homo sapiens cDNA	7.8

	436216	AA380887	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1,	7.8
	418623	AW194757	Hs.265804	ESTs	7.8
	447197	R26075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapiens cDNA	7.8
5	430146	AW815330		gb:QV0-ST0215-060100-083-a09 ST0215 Homo sapiens cDNA	7.8
	441841	AA971819	Hs.176083	ESTs	7.8
	457677	AA626890	Hs.158701	ESTs	7.8
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),	7.8
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	7.8
10	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo sapiens cDNA	7.8
	406410			CS000010*:g 10440464 dbj BAB15765.1 (AK024475) FLJ0	7.8
	453579	AI204463	Hs.61857	ESTs	7.8
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogene homolog-lik	7.7
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone COL05135	7.7
	405510			ENSP00000233779: hypothetical 68.0 kDa protein.	7.7
15	440777	AA994020	Hs.128553	ESTs	7.7
	446424	AW134529	Hs.244647	ESTs	7.7
	448004	AW451477	Hs.257456	ESTs	7.7
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	7.7
20	427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate 2 (rho famil	7.7
	451693	BE220445	Hs.279635	ESTs	7.7
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	7.7
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	7.7
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (polypyrimidin	7.7
25	425423	NM_005897	Hs.157180	Intracisternal A particle-promoted polypeptide	7.7
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	7.7
	432585	AA705591	Hs.180209	ESTs	7.7
	402682			Target Exon	7.7
	400247			Eos Control	7.7
30	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	7.7
	426761	AI015709	Hs.172089	Homo sapiens mRNA: cDNA DKFZp58612022 (from clone DKF	7.7
	405514			ENSP00000241075:TRRAP PROTEIN.	7.7
	412406	AW948172		gb:RC0-MT0013-280300-021-b08 MT0013 Homo sapiens cDNA	7.7
	440226	AA873387	Hs.207330	ESTs	7.7
35	435625	H50654	Hs.113999	ESTs	7.7
	418529	AW005695	Hs.250897	TRK-fused gene	7.6
	407758	D50915	Hs.38365	KIAA0125 gene product	7.6
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	7.6
	449938	AW970612	Hs.172635	Homo sapiens cDNA: FLJ21367 fis, clone COL03051	7.6
40	422893	X98411	Hs.121555	myosin II	7.6
	451593	AF151879	Hs.26706	CGI-121 protein	7.6
	424148	BE242274	Hs.1741	integrin, beta 7	7.6
	447519	U46258	Hs.339665	ESTs	7.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	7.6
45	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	7.6
	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	7.6
	456926	AB018284	Hs.158688	KIAA0741 gene product	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	409208	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo sapiens cDNA	7.6
50	417085	AA194446	Hs.73451	ESTs, Weakly similar to S55024 nebulin, skeletal musc	7.6
	418181	U37012	Hs.83727	cleavage and polyadenylation specific factor 1, 160kD	7.5
	436910	AA926944		gb:cm68g01.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3'	7.5
	401008			Target Exon	7.5
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacting protein	7.5
55	446820	AW295037	Hs.254986	ESTs	7.5
	439279	AI039473	Hs.130636	ESTs	7.5
	426116	AA868729	Hs.144694	ESTs	7.5
	410098	BE326839	Hs.17433	hypothetical protein FLJ20967	7.5
	422326	AI114875	Hs.78592	eukaryotic translation initiation factor 2B, subunit	7.5
60	435513	AW404075	Hs.42785	DC11 protein	7.5
	421629	N80121	Hs.4983	ESTs	7.4
	434663	AA641972	Hs.130058	ESTs	7.4
	452461	N78223	Hs.108106	transcription factor	7.4
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	7.4
65	405417			CX001144*:g 7242973 dbj BAA92547.1 (AB037730) KIAA1	7.4
	414076	AA467738		gb:nc74e05.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone, m	7.4
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	7.4
	449610	AI242042	Hs.14044	ESTs	7.4
	403397			Target Exon	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
70	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant; spastin)	7.4
	404914			NM_004046*:Homo sapiens ATP synthase, H+-transporting	7.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activating fact	7.4
	432820	AI554057	Hs.152477	ESTs	7.4
	418978	T85295	Hs.268606	ESTs	7.4
75	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonine kinase 21)	7.4
	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo sapiens cDNA	7.4
	434522	AF189259	Hs.283081	gamma-aminobutyric acid (GABA) receptor, theta	7.4
	458236	AW297043	Hs.255604	ESTs, Weakly similar to A47234 homeobox protein H6 [H	7.4
	441043	AA913422	Hs.182104	ESTs	7.4
80	422838	AA524065	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone HS108202	7.3
	455096	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens cDNA	7.3
	442307	AW027690	Hs.90037	ESTs	7.3
	425453	AW374284	Hs.297215	Homo sapiens chromosome 19, cosmid R26894	7.3

5	455327	AW896238	Hs.334805	Homo sapiens cDNA FLJ14504 fis, clone NT2RP1000363, m	7.3
	420982	AW576160	Hs.100729	KIAA0692 protein	7.3
	424563	AA446332	Hs.151428	ret finger protein 2	7.3
	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein 1	7.3
	453902	BE502341	Hs.3402	ESTs	7.3
10	446842	AI343510	Hs.176992	ESTs	7.3
	454128	AL031259	Hs.41639	programmed cell death 2	7.3
	427011	BE302729	Hs.173162	neighbor of COX4	7.3
	450872	AI742594		gb:wg55h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	7.3
	451512	AI800236	Hs.207080	ESTs	7.3
15	405708	AI282759		gb:qt184a01.x1 NCL_CGAP_Co14 Homo sapiens cDNA clone I	7.3
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I36022 hypothetical protein I	7.3
	459304	AW005809	Hs.281076	ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELIC	7.3
	401375			NM_020999: Homo sapiens neurogenin 3 (NEUROG3), mRNA	7.3
	413258	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapiens cDNA	7.3
20	406016			Target Exon	7.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	7.3
	422742	AA316117	Hs.337128	ESTs	7.3
	440031	BE045970	Hs.244746	ESTs	7.3
	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PLACE1005111	7.3
25	449656	AA002008	Hs.188633	ESTs	7.3
	444310	AI140432	Hs.175936	ESTs	7.3
	459274	AA382590	Hs.170980	KIAA0948 protein	7.3
	425404	BE048060	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.3
	431150	T63857		gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens c	7.3
30	443217	NM_001545	Hs.9078	immature colon carcinoma transcript 1	7.2
	413405	AW022253	Hs.215976	ESTs	7.2
	447653	BE327277	Hs.161145	ESTs	7.2
	414704	NM_014757	Hs.76986	mastermind (Drosophila), homolog of	7.2
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, clade B (o	7.2
35	409188	AW363284	Hs.32553	ESTs	7.2
	453493	AL039478	Hs.304447	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	456111	AK000150	Hs.78185	MAX-like bHLHZIP protein	7.2
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	7.2
	446364	AB005624	Hs.14912	KIAA0286 protein	7.2
40	432216	AU076609	Hs.2934	ribonucleotide reductase M1 polypeptide	7.2
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine protease	7.2
	446336	AW816036	Hs.151251	ESTs	7.2
	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	7.2
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	7.2
45	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP3002304	7.2
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polypeptide 1	7.2
	416450	AA180467		gb:zp14g08.s1 Stratagene fetal retina 937202 Homo sap	7.2
	449714	AB033015	Hs.23941	KIAA1189 protein	7.2
	455447	AW947507		gb:RCO-MT0002-140300-011-a12 MT0002 Homo sapiens cDNA	7.2
50	437154	AI023133	Hs.10739	ESTs	7.2
	423059	AW378445	Hs.123080	Homo sapiens unknown protein mRNA, partial cds	7.2
	419092	J05581	Hs.89603	mucin 1, transmembrane	7.2
	426736	AA431615	Hs.130722	ESTs	7.2
	417748	Z43011	Hs.21169	ESTs	7.2
55	434748	AI862604	Hs.211884	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	438929	AW195515	Hs.253177	ESTs	7.2
	452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	7.1
	446416	AV658299	Hs.163959	ESTs	7.1
	415023	AA932146	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.1
60	434766	AA742222	Hs.120634	ESTs	7.1
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell growth factor	7.1
	420252	AW270404	Hs.193161	ESTs	7.1
	435403	AA779987	Hs.269658	ESTs	7.1
	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo sapiens cDNA	7.1
65	427908	AA417272	Hs.24122	ESTs	7.1
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter transporter	7.1
	400098			Eos Control	7.1
	412647	AW975090		gb:EST387196 MAGE resequences, MAGN Homo sapiens cDNA	7.1
	437234	AI472213	Hs.247711	hypothetical protein FLJ20557	7.1
70	453368	AW958751	Hs.28921	zinc finger protein	7.1
	425803	AI825204	Hs.211408	ESTs	7.1
	447383	N24231		gb:yn22a11.r1 Soares melanocyte 2NbHM Homo sapiens cD	7.1
	423864	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	7.1
	450799	AW407504		gb:UI-HF-BMO-ask-g-12-0-UI.r1 NIH_MGC_38 Homo sapiens	7.1
75	409592	BE280951	Hs.55058	EH-domain containing 4	7.1
	453945	NM_005171	Hs.36908	activating transcription factor 1	7.0
	425196	AL037915	Hs.155097	carbonic anhydrase II	7.0
	439778	AL109729	Hs.99364	putative transmembrane protein	7.0
	417662	R07478	Hs.268845	ESTs	7.0
80	438087	AI883770	Hs.190422	ESTs	7.0
	452724	R84810	Hs.30484	cyclin E2	7.0
	448633	AA311426	Hs.21635	tubulin, gamma 1	7.0
	433154	AA578526	Hs.160994	ESTs	7.0
	440094	AI651558	Hs.270372	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.0
	409253	H91200	Hs.52002	CD5 antigen-like (scavenger receptor cysteine rich fa	7.0
	431270	BE046609		gb:hn41e11.x1 NCL_CGAP_RDF2 Homo sapiens cDNA clone 3	7.0
	407629	AA649242	Hs.62632	ESTs	7.0

5	408296	AL117452	Hs.44155	DKFZP586G1517 protein	7.0
	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	7.0
	427106	AA398193	Hs.97584	ESTs	7.0
	408623	AW811978	Hs.254037	ESTs	7.0
	426561	AA381437		gb:EST94514 Activated T-cells I Homo sapiens cDNA 5'	7.0
	408492	AA555217	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2	7.0
	428894	AA437086	Hs.271736	ESTs	7.0
	419102	AA234098	Hs.42424	ESTs, Weakly similar to 2004399A chromosomal protein	7.0
10	429067	AA445019	Hs.104967	ESTs	7.0
	422684	BE561617	Hs.119192	H2A histone family, member Z	7.0
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase kinase 5	7.0
	412513	AA322589	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H.	7.0
	443599	AI079559	Hs.134125	ESTs	7.0
15	400715			ENSP00000237081:KJAA1217 PROTEIN (FRAGMENT).	7.0
	446514	AW449233	Hs.150847	ESTs	7.0
	413992	W26276	Hs.136075	RNA, U2 small nuclear	7.0
	402442			Target Exon	7.0
	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	7.0
20	439575	W79259		gb:zcd75c06.r1 Soares_fetal_heart_NbHH19W Homo sapiens	7.0
	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gene, exons 1B a	7.0

Table 158

25	Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers		
30	Pkey	CAT Number	Accessions
	408182	104479_1	AA047854 AAD57506 AA053841
	409113	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204
35			AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070
			AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209
			AA070928 AA068994 AA069817 AA076187 AA069063 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053
			AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070827 AA078802 AA076622 AA065051 AA079143 AA071110
			AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200
			AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
40	409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
	409857	1156298_1	AW501908 AW502959 AW502540
	410146	1178974_1	AW592655 R05927 R06918
	410536	1207322_1	N39533 AW753094 AW753093
	411298	1237955_1	AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835
45	412406	1293055_1	AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838
			AW948172 AW948178 AW948169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181
			AW948177 AW948171 AW948183 AW948173
	412647	1317604_1	AW975090 N44182
	413258	1355998_1	BE075114 BE075283 BE075118
	413314	1360034_1	BE081585 BE081717 BE081863 BE081794 BE081659
50	413500	1373933_1	BE144914 BE394989
	414076	141490_1	AA467736 AA135210 AW968166 AA467804
	416450	159551_1	AA180467 AA449184 AA464831 AA505048
	417247	1660859_1	N56024 T58194 T11693 N64222 T05848
	417739	1695198_1	Z43995 R12357 R34740
55	417881	170544_1	AW879117 AW161351 Z45755 BE003661 AA206949 AA476541
	418347	174149_1	AA216419 F03238 AA229517
	422429	216469_1	AA310527 AW962285 Z44865 H06641
	423573	229714_1	AA328504 AA327783 AW962370
60	425561	269158_1	AA381437 AA628833 AW407275
	428294	289365_1	AA425488 AA496895 F23221
	430146	313562_1	AW815330 AW968170 A1732687 A1732725 AA468343 AA467817 AW063961
	430151	313568_1	AW968203 A1732767 AA470353 AA468025 AA468479 A1734151
	430709	322338_1	R34356 AW969880 AA484613
	430848	324621_1	AW021726 AA487752 AA488085
65	431150	328626_1	T63857 AW971220 AA493469 T63699
	431270	330676_1	BE046609 BE046118 AA501504
	432363	345469_1	AA534489 AW970240 AW970323
	434197	381655_1	AA627223 AA643443 AA650619 AA643463 AA643453 AA643439 AA643438 AW802964 AW821595 AW821594 AA643431 AA643432
70	434407	385744_1	AW827513
	434410	385798_1	AW815333 AW815409 AA632563
	436910	429182_1	AA632644 AA635376 AA664188
	437056	432262_1	AA926944 AA767974 AA737237
	439354	47146_1	A1147061 AA743380 AA765223 AW976398 A1803927
75	439575	47400_1	AF086174 W31798 W04694
	444314	606667_1	W79259 AF086396 W73927
	447197	711623_1	A1140497 AW749625 AW749626 AW749644
	447383	71990_1	R36075 A1366548 R36167
	450799	847242_1	N24231 BE617964 N36313
80	450872	849959_1	AW407504 W31274 A1738877
	454355	1130264_1	A1742594 A1761397 R31198 A1819332 R31257
	454639	1227728_1	AW812535 AW812536 AW390307
	454765	1233905_1	AW811633 AW811652 AW811698
			AW819629 AW854320

455037	1249783_1	BE144549 AW851677 AW851643 AW851711 AW851719
455096	1253078_1	AW855718 AW855740 AW855748
455161	1256167_1	BE145900 AW859906 BE145895 BE145831 BE145914 BE145820 BE145817 BE145890 BE145908
5	1288380_1	AW936678 AW936637 AW936682 AW936685 AW936687 AW936811 AW936762 AW936653 AW936815 AW936812 AW936683 AW936822
		AW936823 AW936821 AW936732 AW936730 AW936781
	1292444_1	AW947507 AW947509 AW947791 BE008335
	1375834_1	BE147440 BE147708 BE147563 BE147456
	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
10	432926_1	AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA845905 AA847698
	458080	BE142728 AA834047 AW937124
	458115	BE091587 BE091730 BE091577 BE091655 BE091728 BE091640 BE091578 BE091727 BE091803 BE091660 BE091721 BE088255 BE076582
		AW992312 BE008791 BE082385 BE083504 BE083466 AW997967 AW997991 BE166595 AW843686 AW844334 BE078091 AW603391 BE081427
		AW79514 BE184580 BE009962 BE008722 AW579912 AW860561 AW890184 AW795276 AW860410 AW860411 AW610330 AW860564 AW860578
15		AW862519 BE073924 BE008687 BE073857 BE073921 AW274106 BE011050 AW268120 AJ335067 AW793748 AW997736 BE080117 AW867987
		AJ547161 AW844767 AW393596 AW579444 BE083334 AJ547158 AW799863 AA585179 AW992792 AW882215 BE011913 AW997694 AJ547159
		AW992772 AW581178 AA092247 AW843916 BE079190 AW878478 BE083648 BE066454 AJ69937 AW393594 AW579899 AW939276 BE173265
		AW878631 AW878638 AW992802 BE079913 AA633638 AW369008 BE076590 AW843456 AW992791 BE173247 AW843921 AW843333 AW878334
		BE090235 BE078240 BE066325 AW603276 BE169310 AW817299 BE091641 BE000160 AW898164 AW994624 AW999391 AW862797 AW899438
20		AW750667 AW939585 AW940017 AI200402 BE167391 AW393918 AW799837 AW939953 AW939681 BE078188 AA490595 BE076595 AW297451
		BE076544 AW803372 BE081223 AW939237 BE084239 AI174202 BE077804 BE078028 AA512912 AI124808 AI147524 AI884882 AW939962
		AW939254 BE171687 AW998400 AW998348 AW998353 AW998288 AW998303 AW998302 AW998299 AA502748 BE077882 AW998295 BE090238
		AW604665 AI423051 BE093093 AW579913 AW606384 BE006143 BE170415 AW980564 BE084608 AW992779 BE088111 AW610555 AW844153
		AW939423 BE085404 AW579905 BE080994 AW468482 AW876865 BE091581 BE080940 AI811189 AW868088 AW893127 BE080064 BE184254
25		AW998350 AW884228 AW992315 AW992364 BE091569 AW750680 BE066388 AA578227 BE091735 AW939830 BE078710 BE087253 BE084182
		AW800859 AW801017 AW581371 BE088300 AW995341 BE090233 AW663786 BE091739 BE080113 AW578162 AW799799 AW992366 AW994673
		BE185170 AW792778 AW663225 BE075590 BE080111 AA682934 BE090227 AI475441 BE085684 BE090223 AW581366 BE010705 AW898740
		BE088170 AW992375 BE077833 BE083557 BE010688 AW998450 AW803434 BE083280 AW892655 AA506666 BE088288 BE005859 BE173856
		BE001319 AA610814 BE011965 BE005855 BE005869 AA973929 BE185729 AW884298 BE185743 BE001342 BE005876 AI002988 AW799058
30		BE085411 AW841264 AW603110 BE006134 BE006139 BE006148 BE006147 BE006155 AA578273 BE008706 BE185440 AW8446428 AA501940
		AW603114 BE085757 AI460195 AA491145 AA772914 AA632730 AA508388 BE080196 BE185442 BE093446 AW844643 BE080113 BE001352
		AW393003 BE006145 BE085405 BE008680 BE081428 AW581373 AW607246 BE094328 BE001336 AW868170 BE074119 AW884149 BE091734
		BE087444 AI540867 BE185808 BE080193 BE185858 AA476398 BE081040 BE074724 BE085426 BE074725 AW998297 AW867606 BE185798
		AW898734 BE076369 BE081672 BE088178 AA610264 BE088118 AA284217 AW578085 BE074518 BE001359 BE001328 AW820227 AW668196
35		AW968180 AW904548 BE008526 BE012037 BE079061 BE005870 AW867804 AW878433 BE008751 BE005875 BE008748 BE093440 BE183050
		AA506676 BE001329 BE008803 BE080123 BE008041 AW994688 AW994675 AW994760 AW994691 AW994681 BE000189 BE080112 AW868173
		AJ768000 AW883094 AW868179 BE080201 AW665449 BE067473 BE008746 BE184053 BE076437 BE076376 BE076402 AA480395 BE082436
		BE184134 BE185224 BE085428 BE008682 AW868181 AW998358 AW866102 BE083507 BE077974 BE008835 BE093439 BE076108 AI416987
		BE008788 BE089909 BE093441 BE185502 BE183053 AW750689 BE011812 BE008672 BE081684 BE093445 AW868184 BE081839 BE008797
40		AW842067 BE008678 BE008670 BE551820 AW38974 BE081637 BE046696 BE008673 BE010328 BE083250 BE089614 BE082052 BE081424
		BE001678 AW581368 AA503194 AW883721 AW883522 BE085564 AW868717 BE171078 BE078249 BE078194 AA565255 BE083486 AW842081
		AW842080 AW868204 BE008717 AA484369 AJ831719 AW997365 BE079327 AA503956 BE091999 AW793852 BE080251 BE078086 BE092515
		BE170384 AW866193 AW679558 BE008042 BE008761 BE081681 BE081671 AW867400 BE082003 BE082253 BE081439 BE081486 BE081692
		AW606020 AA501778 AW996417 BE045756 BE088394 AA491068 AW893099 AW578895 BE150440 BE006150 BE084684 AW992796 BE086891
45		AW866792 AW753605 BE082045 BE081106 BE008373 BE075399 AW996528 AW578707 BE084309 AW753604 BE185916 AW842220 BE185222
		BE006152 BE008795 AW578706 BE080256 BE183984 AJ934532 AA449648 AW578699 BE150514 AW883580 AA493568 BE085748 AW753601
		BE150562 AW882677 BE091787 AW899123 BE081679 BE080121 AW606787 AW603410 BE001317 AW905799 BE150513 BE092206 AW996343
		BE086922 BE008806 AW844759 AW606009 BE150487 AW750728 BE150491 BE150515 AW606010 BE150508 BE008718 AW578702 BE150509
		AA436751 AW883918 BE183883 AW763607 BE008669 BE150446 AA533458 BE079219 AW838884 AW606380 AW063837 AW878479 BE078815
50		BE008802 AW992789 BE007925 AW802204 BE011825 BE092130 BE184059 BE079087 BE150568 BE185497 BE078808 AW883761 AW842295
		BE161523 AA484798 AA480390 AW994667 BE073205 AW607316 BE083201 AW802265 AW578700 BE078715 AW860403 AW897455 AW996558
		AW890602 AW860413 AA425412 BE008364 BE150438 AW602606 AI435236 AA574285 AI823745 AA501773 AI002987 AW832749 BE185491
		AW995489 BE001442 AW948425 BE001586 AI524864 BE085556 AW867549 AW604038 BE079832 AI752160 AW999398 AW883904 AW882376
		AW67098 BE080116 AW883984 AW883995 AA424095 BE074091 AW996348 AW860625 AW860633 AW860631 BE083485 AW860412 AW602207
55		BE075407 AW838972 AW607023 AW602201 AW789772 AW862452 AW862451 BE506041 BE161537 AW602206 AW860404 AW860555 BE007843
		AW860632 AW862457 AW998019 AW860405 BE092062 AW603921 BE183388 AW888194 BE075664 BE078184 AJ541202 AI204949 BE092451
		AW603111 AA484587 AA484402 AW998675 AW896064 BE069923 AW867965 BE059919 BE092069 AA807842 AW605500 AW605501 BE085409
		AA506738 BE080080 AW749523 AA493134 AW370137 AA491844 AA504425 AW605473 BE092456 BE010682 AW602608 BE079093 AA484911
		BE010942 AI205087 AW794933 BE081848 BE011792 AW799897 BE174618 AW838848 AW821741 AW842724 BE080764 BE183962 AA501765
60		BE092513 BE183342 AW799806 AA442935 BE092268 AA580022 AW843219 BE093308 BE092275 BE087111 BE183392 AW842678 BE185597
		BE183895 BE185278 BE082343 AW946219 BE079189 BE092272 AA586687 AW946109 AW946175 AW946184 BE008365 BE078172 BE085673
		BE076240 BE083194 BE010604 BE079196 AW878636 AW799803 BE001348 BE077883 BE081835 AW992309 BE080102 BE078106 AW881899
		BE008407 BE008410 AW842670 AW603738 BE088661 AA484571 AI799184 BE174545 BE001405 AA436957 AW995884 AW995785 AW869598
		AW883999 BE075967 AA503938 BE092281 BE092279 BE087460 BE087669 BE081542 AI375386 AW843886 BE080115 BE171517 BE079898
65		AW882382 BE001450 BE076430 AW579377 BE008412 BE008790 BE182299 BE182297 BE078805 AW899132 BE078810 BE185867 BE087790
		AA484928 AW578985 BE008400 BE074080 AW605101 BE076110 AW799904 AI205094 BE008370 BE182345 BE182373 BE008401 AA884441
		BE182362 BE182372 BE008414 BE078186 BE009185 BE010266 BE009162 BE009167 BE011008 BE073335 BE182370 AW760556 BE182347
		BE011000 AA484576 BE092982 BE183897 BE092973 AA573037 AW882317 BE081832 AA478471 AA551613 BE182366 AW838888 AW026827
		BE008413 AW896605 AA503558 AA776622 BE084825 AA502971 BE081842 BE010528 AW802218 AW889924 AW867996 AW881775 BE079220
70		AI241060 AW802041 AW802005 BE011244 BE087051 AA984758 AA452997 AW992786 AW797500 BE077829 BE008402 AW881760 BE093516
		AW802084 AW369007 BE185123 BE087775 AW801018 BE093443 AW867978 AW843271 BE173850 AW997859 BE010620 AW992516 AW843908
		BE083200 BE164675 BE074340 AW880289 BE075433 BE008456 AW846438 BE066570 BE093547 AA508107 AW867992 BE076239 BE183881
		AW817422 BE087717 AW899147 BE010608 AW992295 AA436737 BE075412 BE093011 AW581656 BE089529 BE008756 BE150494 AW903020
		AW883102 BE076370 BE000625 BE166095 AW867978 BE182159 AW577601 AW577488 AW577491 BE010637 BE069910 BE093295 BE005243
75		AJ620783 AW992550 AW909590 AW577496 AW577450 AW842725 AW842666 AW846931 AW997722 AW842662 BE009233 AW867809 BE083196
		AA287768 AW939591 AW815631 BE001453 AW841903 BE077613 AW577500 BE081479 AW992558 BE011065 AW843187 AW867990 AW898295
		BE074339 AA501697 AW749997 BE076249 AW867991 BE085718 AW994607 BE010578 BE076436 AW368625 AA484467 BE081144 AW577492
		AW997932 AW899089 AW842706 AW890727 AW843175 BE075428 AW843155 AW842679 AW842708 BE059915 AW842721 AW438792 AI251478
		BE069911 BE087054 BE079889 BE075453 BE069927 AA491920 BE170606 BE182305 BE080052 AW843406 BE011075 BE075959 AA525261
80		AW391518 BE079202 AA658195 BE076138 AW799901 AA493859 AW992510 BE011810 AA508724 BE075488 BE005661 AA258982 BE078726
		BE069914 AA213598 BE075376 AA846600 AW580999 BE077872 AA503571 AW884724 AW880124 AW868454 AW577502 AW577489 AW799829
		AW992545 BE075806 AW994606 BE350368 AA557838 BE077682 AW844660 AW883431 BE085872 AW838888 AW868404 AA578417
		BE074115 AW842680 AW277193 AW890728 AW605111 BE093940 AW890710 BE085560 AW868180 AW896778 BE069925 BE011054 BE075965
		AW842668 AW868310 BE011071 BE075429 AW843152 AW905848 BE075397 AW842762 BE075402 BE077950 AW837810 BE079998 BE183965

BE075431 AW815917 AW998359 AW799883 AW603782 AA557480 AW841444 BE075915 AA548034 AW843393 AW391559 BE083265 AW939721
 AW800857 AW079109 AW364901 AJ435993 AA985526 AW799848 BE182463 AA776111 AW799915 BE008399 BE075377 AW577809 BE010272
 BE182443 BE010295 AW577806 BE008415 BE184036 BE076597 AJ817413 AW795053 AW896761 AW841433 BE182458 AW603796 AW842676
 BE085455 AW884879 BE075414 AW838836 AW878273 AW998088 AW799778 AW899125 BE082247 AA774670 BE001401 BE001485 AW817297
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 AW603765 AW843919 AW578235 BE184139 AW997742 BE183923 BE084210 AW802033 AW748724 AW939018 AW997459 AW842742 AA213697
 BE182308 BE011078 AW607702 AW882623 BE080016 AW580994 BE076531 AA443462 AW607407 AW883382 AW939399 AW605627 AW844615
 AW939724 AW815931 AW883765 AA287421 BE075626 AW946171 AW841445 AW797994 AW815957 AA683300 AW369004 BE075368 BE081560
 AW605626 AW939398 AA507280 AA506317 AW841230 AW992519 AA465332 AA425246 BE090234 BE090236 AA483259 AA451961 AA535566
 AA506406 AA888571 AA503568 AA507130 AA532944 AA501672 BE168634 AA492022 AA507662 AW842286 AA494226 AA776038 AA442419
 AW579900 BE171816 AA863065 AA491916 AA447490 AA461423 AA434543 AA243279 AW997466 AW603740 BE000295 AA658571

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400715	8118885	Minus	80151-80297
400738	8118985	Plus	143447-143851
401008	8117391	Minus	81421-81551,82364-82512,82862-82938
401069	3927852	Minus	45682-45831
401375	7417809	Minus	6121-6766
401405	7768126	Minus	69276-69452,69548-69958
401539	8072433	Minus	62028-62608
401557	8099866	Minus	112785-112924
401654	9097132	Minus	64695-64797
401940	3738108	Plus	153460-153592
402025	7547159	Plus	173835-173998
402442	9798503	Plus	141714-141842,142010-142122
402682	8138477	Minus	147522-147795
402796	3646083	Minus	6126-6265,6416-6689
402967	5360987	Minus	33518-34546
403038	7717439	Minus	290021-290284
403055	8748904	Minus	109532-110225
403310	8139936	Minus	183883-184026
403397	9438368	Minus	84481-84655
403839	4176355	Plus	21201-22223
404110	9212839	Minus	18344-18510
404495	8151634	Minus	59449-60477
404534	8247909	Minus	147853-148086
404630	9796665	Plus	74495-74715
404649	9796926	Minus	100027-100399
404680	9797204	Minus	159810-159979,160213-160321,161023-161304,162862-163140,164490-164644,166404-166530,166936-167083,167392-167522
404914	7341760	Plus	92603-92827
405417	4753290	Minus	50704-51499
405454	7656675	Plus	133807-134053
405510	7630909	Minus	101028-101174
405514	9454624	Plus	35953-36151
405538	9795661	Plus	164091-164162,164397-164516,166720-166790,167785-167935
406016	8272661	Plus	41341-41940
406410	9256394	Minus	115806-116104
406464	9789674	Plus	72161-72562
406562	7711584	Plus	37316-37426

TABLE 16A: 200 GENES DOWN-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 16A shows 200 genes down-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 15A, except that the numerator and denominator were switched, the median value amongst normal cervixes was greater than or equal 40 units, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal cervix).

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigeneID	Unigene Title	R1
453596	AA441838	Hs.62905	hypothetical protein FLJ14834	18.1
443912	R37257	Hs.184780	ESTs	16.8
420923	AF097021	Hs.273321	differentially expressed in hematopoietic lineages	13.6
414422	AA147224	Hs.337232	Homeo box A13	13.1
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672	12.9
412639	AW961284	Hs.296235	ESTs	12.4

	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	12.4
	407938	AA905097	Hs.85050	phospholamban	11.3
	410544	AI446543	Hs.95511	ESTs	11.3
5	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65557 alpha-1C-adrenergic rece	11.1
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]	11.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	10.9
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	10.6
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia inducib	10.5
10	452106	AI141031	Hs.21342	ESTs	9.5
	428780	AI478578	Hs.50636	ESTs	9.5
	431706	AI816086	Hs.295341	adenylyl cyclase-associated protein 2	9.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PLACE1002968	9.0
	430468	NM_004673	Hs.241519	angiotensin-like 1	9.0
15	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	8.7
	448944	AB014605	Hs.22599	atrophin-1 Interacting protein 1; activin receptor inte	8.6
	401486	NA		C40006477:gi4758508 ref NP_004253.1 airway trypsin-II	8.4
	417511	AL049176	Hs.82223	chordin-like	8.3
	429900	AA460421	Hs.30875	ESTs	8.2
20	411908	L27943	Hs.72924	cytidine deaminase	8.0
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	8.0
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp	8.0
	437846	AA773868	Hs.244569	esophagus cancer-related gene-2	8.0
	421666	AL035250	Hs.1408	endothelin 3	7.9
25	450164	AI239923	Hs.30098	ESTs	7.9
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatoietin A; scatter factor	7.7
	425608	AA360486	Hs.82448	ESTs	7.6
	442748	AI016713	Hs.135787	ESTs	7.3
	415672	N53097	Hs.193579	ESTs	7.2
30	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	7.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	7.0
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nucleotide pyroph	6.7
	414214	D49958	Hs.75819	glycoprotein M5A	6.5
	436637	AI783629	Hs.26766	ESTs	6.5
35	408921	AI970572	Hs.46638	chromosome 11 open reading frame 8	6.5
	432101	AI918950	Hs.123642	EphA3	6.3
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA, complete cds	6.3
	424153	AA451737	Hs.141496	MAGE-like 2	6.3
	420228	R25023	Hs.12369	ESTs	6.2
40	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myotilin)	6.1
	444931	AV652066	Hs.75113	general transcription factor IIA	6.1
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HEMBA1002970	6.1
	425849	AJ000512	Hs.295323	serum/glucocorticoid regulated kinase	6.1
	410425	BE276367	Hs.63510	KIAA0141 gene product	6.0
45	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	6.0
	424973	X92521	Hs.154057	matrix metalloproteinase 19	6.0
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like 1	5.9
	429414	AI783656	Hs.202095	empty spiracles (Drosophila) homolog 2	5.9
	440594	AW445167	Hs.126036	ESTs	5.9
50	452768	AW069459	Hs.61539	ESTs	5.9
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 protein [H.sapiens]	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
	425010	T16837	Hs.4241	ESTs	5.9
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.8
55	437980	R50393	Hs.278436	KIAA1474 protein	5.8
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.7
	404097	NA		C50002427:gi9369379 gb AA67128.1 AC006434_24 (AC00643	5.7
	422546	AB007969	Hs.301478	KIAA0500 protein	5.7
	445872	AI581573	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458	5.7
60	429999	AI761902	Hs.99597	ESTs	5.6
	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492	5.6
	442082	R41823	Hs.7413	ESTs	5.5
	452073	AA625150	Hs.82098	ESTs	5.4
	430032	AW936136	Hs.99610	ESTs	5.4
65	408767	AA057279	Hs.211928	ESTs	5.4
	433234	AB040928	Hs.65366	KIAA1495 protein	5.3
	431708	AI698136	Hs.108873	ESTs	5.3
	421200	AA284811	Hs.264433	ESTs	5.2
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HEMBA1001008	5.2
70	409643	AW450866	Hs.257359	ESTs	5.1
	416676	AW392022	Hs.79507	KIAA0582 protein	5.1
	420357	U94333	Hs.97199	complement component C1q receptor	5.0
	417355	D13168	Hs.82002	endothelin receptor type B	5.0
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL06674	5.0
75	430965	AA489732	Hs.154918	ESTs	4.9
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.9
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	4.8
	404485	NA		Target Exon	4.8
	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB1001024	4.8
80	417692	R09338	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC1000540	4.8
	432304	AA932186	Hs.69297	ESTs	4.7
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.7
	448851	AI582207	Hs.177166	ESTs	4.7
	405523			C80014097:gi7441226 pir S31212 collagen alpha 1(XIV)	4.7

	450656	AA010539	Hs.18912	ESTs	4.6
	422942	AF054839	Hs.122540	tetraspan 2	4.6
	401479	T49304	Hs.110950	Rag C protein	4.6
	444192	AW469413	Hs.151145	ESTs	4.6
5	439648	AW780192	Hs.267596	ESTs	4.5
	410378	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4	4.5
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	4.5
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX	4.5
10	452249	BE394412	Hs.202095	empty spiracles (Drosophila) homolog 2	4.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	4.5
	411037	BE145915	Hs.99472	ESTs	4.4
	442803	AI675298	Hs.199917	ESTs	4.4
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, beta	4.4
15	400628	NA		C100018711:gil1705533[sp]P32018[CA1E_CHICK COLLAGEN ALP	4.3
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage serine esterase	4.3
	437110	AL049240	Hs.144995	ESTs	4.2
	410646	W79408	Hs.50745	ESTs	4.2
	456304	AI820973		gb:nc21c02.y5 NCL CGAP_Pr1 Homo sapiens cDNA clone, mRN	4.2
20	401270			Target Exon	4.2
	419447	BE092696	Hs.75928	ESTs	4.2
	414807	AI738618	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	4.2
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.2
	434469	AA634806		gb:ab28c02.r1 Stratagene lung (937210) Homo sapiens cDN	4.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR	4.1
25	418947	W52990	Hs.22860	ESTs	4.1
	416434	AW163045	Hs.79334	nuclear factor, Interleukin 3 regulated	4.0
	454736	BE184348		gb:CM0-HT0676-010500-355-e11 HT0676 Homo sapiens cDNA,	4.0
	407945	X69208	Hs.606	ATPase, Cu transporting, alpha polypeptide (Menkes synd	4.0
30	447499	AW262580	Hs.147674	prolactin beta 16	4.0
	430686	NM_001942	Hs.2633	dasmogelin 1	4.0
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (cardiovascula	3.9
	419047	AW952771	Hs.90043	ESTs	3.9
	414272	AI651603	Hs.46988	ESTs	3.9
	443808	AW377736	Hs.12420	ESTs	3.9
35	426883	H21520	Hs.35088	ESTs	3.9
	410659	AI080175	Hs.68826	ESTs	3.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.9
	432181	AA527650	Hs.156037	ESTs	3.9
40	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.8
	453296	AA034413	Hs.62560	ESTs	3.8
	400878	NA		Target Exon	3.8
	401103	NA		C12001233:gil7305351[ref]NP_038652.1] otogelin [Mus mus	3.8
	436670	AI690021	Hs.201536	ESTs	3.7
45	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface receptor	3.7
	408793	BE258371	Hs.254660	ESTs	3.7
	419093	AI804054	Hs.112885	spinal cord-derived growth factor-B	3.7
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.7
	450776	NM_007250	Hs.320861	Kruppel-like factor 8	3.7
50	437140	AA312799	Hs.283689	activator of CREM in testis	3.6
	418421	R58620	Hs.85050	phospholamban	3.6
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN	3.6
	417194	N53793		gb:yz07a01.r1 Soares_multiple_sclerosis_2NbHMSP Homo sa	3.6
	443567	AI077540	Hs.134090	ESTs	3.6
55	451879	AI821030		gb:yz52f11.y5 Stratagene ovary (937217) Homo sapiens cD	3.6
	421013	M52397	Hs.1345	mutated in colorectal cancers	3.5
	451896	AF196304	Hs.27197	SUMO-1-specific protease	3.5
	413237	AI468574	Hs.171965	ESTs	3.5
	424636	AA453734	Hs.10198	ESTs	3.5
60	432660	AI288430	Hs.64004	ESTs	3.5
	414681	AL079440	Hs.74002	nuclear receptor coactivator 1	3.5
	400802	NA		Target Exon	3.5
	430015	AW768399	Hs.112157	ESTs	3.5
	451978	AW813747	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (from clone DKFZp5	3.5
65	449088	AI654048	Hs.198556	ESTs	3.5
	425113	AI936992	Hs.154658	pleckstrin and Sec7 domain protein	3.5
	458459	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone COL09609	3.5
	420249	BE262895	Hs.276916	nuclear receptor subfamily 1, group D, member 1	3.5
	401159	NA		Target Exon	3.5
70	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQ	3.5
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5 [Hsapiens]	3.4
	407118	AA156790	Hs.262036	ESTs, Weakly similar to ZZZ3_HUMAN ZINC FINGER PROTEIN	3.4
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induc	3.4
	443178	AI631241	Hs.47312	ESTs	3.4
75	430694	AA810624	Hs.30938	ESTs, Weakly similar to H2BH_HUMAN HISTONE H2B H [Hsapi	3.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) homol	3.4
	437950	U79244	Hs.112642	ESTs	3.3
	419368	AI753518	Hs.209464	KIAA1604 protein	3.3
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	3.3
80	451398	AI793124	Hs.144479	ESTs	3.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	3.3
	407570	Z19002	Hs.37098	zinc finger protein 145 (Kruppel-like, expressed in pro	3.3
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	3.3
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	3.3

5	444216	D25303	Hs.222	Integrin, alpha 9	3.3
	418771	AA807881	Hs.25329	ESTs	3.3
	433036	AA574091	Hs.105964	ESTs	3.2
	404584			Target Exon	3.2
	404195			NM_015718: Homo sapiens NADPH oxidase 3 (NOX3), mRNA. V	3.2
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	420833	R47948	Hs.188732	ESTs	3.1
10	413156	AA127133		gbz187e03.r1 Stralagene colon (937204) Homo sapiens cD	3.1
	413607	T64741		gbz048f11.r1 Stralagene liver (937224) Homo sapiens cD	3.1
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.1
	428790	AF023456	Hs.193558	protein phosphatase, EF hand calcium-binding domain 2	3.1
	434520	AA205273	Hs.177011	hypothetical protein	3.1
15	432247	AA531287	Hs.105805	ESTs	3.1
	428303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	3.1
	439734	AC005013	Hs.149	cAMP response element-binding protein CRE-BPa	3.1
	433546	AO75877	Hs.125461	hypothetical protein FLJ11539	3.0
	430317	AB020645	Hs.239189	glutaminase	3.0
20	425130	AA448208	Hs.99163	ESTs	3.0
	444195	AB002351	Hs.10587	KIAA0353 protein	3.0
	409007	AL122107	Hs.49599	Homo sapiens mRNA: cDNA DKFZp434G0827 (from clone DKFZp	3.0
	453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2) Homo sapiens c	3.0
	442974	AI025670	Hs.109308	ESTs, Weakly similar to leucine-rich glioma-inactivated	3.0
25	446936	H10207	Hs.47314	ESTs	3.0
	454086	AW885909	Hs.6975	PRO1073 protein	3.0
	420271	AI954365	Hs.42892	ESTs	3.0
	435545	AA687415	Hs.28107	ESTs	3.0
	445175	AV652851	Hs.20255	ESTs	3.0

30 TABLE 16B

35 Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
413156	135116_1	AA127133 AA384396 AW958912 T72119
413607	1379911_1	T64741 BE158393 BE152805
417194	1657323_1	N53793 N53716 N53739
434469	387447_1	AA634806 C18732 AA729161 AA729860
451879	888642_1	AI821030 T47126 AI821318
453773	980699_1	AL133761 AL133767
454738	1232235_1	BE184348 AW817453 BE011068
456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101

45 TABLE 16C

50 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position
400628	3818355	Plus	41851-41984
400802	8567867	Minus	174571-174856
400878	9864757	Plus	31493-32842
401103	8568122	Minus	98330-98449
401159	6067118	Minus	3180-3953
401270	9797168	Minus	141659-141813
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
404097	7770701	Plus	55512-55781
404195	3805917	Minus	39186-39332
404485	8096921	Plus	75166-75264,124036-124232
404584	9857511	Plus	138651-139153
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

70

75 TABLE 17A: 605 genes upregulated in testicular cancer relative to normal body tissues

Table 17A lists about 605 genes upregulated in cervical cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Arraymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

80

Pkey: Unique Eos probeset Identifier number
 ExAccon: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M,

UniGene Title: UniGene gene title
 R1 95th percentile of cervical cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenelD; Unigenel Title; Pred.Prod.Domains; R1

- 408522; A1541214; Hs.46320; Small proline-rich protein SPRK [human, ; none, Cornifin; 33.942
 422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; ehand, S_100; TM=M; SS=N; 33.05
 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin; TM=M; SS=N; 32.856
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; was; TM=M; SS=Y; 29.604
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt; TM=M; SS=Y; 27.95064945
 421948; L42583; Hs.334309; keratin 6A; filament, RhoGAP, DUF266, bZIP, Tropomyosin, tubulin, DUF164, TBCA, Collagen; TM=M; SS=N; 26.778
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp, FecCD; TM=Y; SS=M; 26.1133829
 407242; M18728; ; gb:Human nonspecific crossreacting antig; lg; TM=M; SS=M; 23.382
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 22.522
 412719; AW016810; Hs.816; ESTs; none, none; 21.198
 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; lg; TM=M; SS=M; 20.028
 402075; ; ENSP00000251056; Plasma membrane calcium; none; 19.038
 431958; X63628; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin, Cadherin_C_term; TM=Y; SS=M; 17.92061281
 412471; M63193; Hs.73946; endothelial cell growth factor 1 (plate; Glycos_transf_3, Glycos_trans_3N; TM=M; SS=M; 17.8978979
 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M; SS=N; 17.08333333
 429259; AA420450; Hs.380088; Plakophilin; none, none; 17.08235294
 417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1; 16.91558628
 439926; AW014875; Hs.137007; ESTs; none, none; 16.69
 419693; AA133749; Hs.301350; FXFD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 16.365
 413763; Y17760; Hs.75517; laminin, beta 3 (nicotin (125kD), kalinin; laminin_EGF, laminin_Nterm; 15.75294118
 413278; BE563085; Hs.833; Interferon-stimulated protein, 15 kDa; ubiquitin; 15.48600509
 401781; ; Target Exon; filament; TM=M; SS=N; 15.43668831
 420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobulin; 15.394
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M; SS=M; 15.12264151
 452240; AJ691147; Hs.61232; ESTs; none, none; 14.63
 428957; NM_003881; Hs.194679; WNT1 Inducible signaling pathway protein; tsp_1, wvc, IGFBP; TM=M; SS=M; 14.49772727
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; SS=N; 14.4389313
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none, none; 14.00909091
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin, Peptidase_M10, Astacin; 13.824
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 13.7754396
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 13.74595843
 400284; ; NM_000125; Homo sapiens estrogen receptor; hormone_rec, zf-C4, Oest_recpt; TM=M; SS=M; 13.31578947
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 13.05294118
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 13.038
 406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 13.00311527
 427666; A791495; Hs.180142; calmodulin-like skin protein (CLSP); ehand; TM=M; SS=N; 12.79
 400301; AK03835; Hs.1657; estrogen receptor 1; F-box, hormone_rec, zf-C4, Oest_recpt, adh_zinc, ketoacyl-synt, pp-binding, Acyl_transf, Thioesterase, ketoacyl-synt, CAAA, E7, RFX_DNA_binding; TM=M; SS=N; 12.472
 410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M; SS=M; 12.47
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none, pkinase, fn3, lg; 12.28597122
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; SS=N; 12.13379205
 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M; SS=M; 12.04945055
 418462; BE001596; Hs.85266; integrin, beta 4; fn3, integrin_B, Cdx-beta, EGF; TM=M; SS=M; 11.95538462
 443859; NM_013409; Hs.8914; follistatin; kazat; 11.95467422
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypeptide, prote; Transglutamin_N, Transglutamin_C, Transglut_core; TM=M; SS=N; 11.61
 408243; Y00787; Hs.624; interleukin 8; IL8, PAS, IL8; TM=M; SS=N; 11.564
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6, lactamase_B; 11.55285714
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ;
 aa permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DOT, PI3_P4_kinase, FAT, FATC, BclA, RUN; TM=M; SS=N; 11.47956989
 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin_C_term; none; 11.456
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; 11.45352113
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz, BPTI, fn3, vwa, Collagen, beta-lactamase; TM=M; SS=M; 11.32234432
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3; TM=Y; SS=M; 11.28666327
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none, none; 11.076
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 11.0381579
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (mo; ank; 11
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin, Peptidase_M10; TM=M; SS=M; 11
 425071; NM_013989; Hs.154424; delodrinase, iodothyronine, type II; T4_delodrinase; TM=M; SS=Y; 10.93859649
 437938; AJ950087; Hs.369628; gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapiens; none, none; 10.78064516
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none; TM=M; SS=Y; 10.74825176
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAPI_HUMAN DEATH; none, none; 10.542
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC; none; 10.49538462
 431629; AJ077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 10.48210736
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_membr; TM=Y; SS=M; 10.26714286
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M, SMC_N, SMC_C, DUF164, none; 10.142
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN, HIN; TM=M; SS=N; 10.1
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin, Reprolysin, Pep_M12B_propept, EGF; TM=Y; SS=M; 10.072
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolv, HATPase_c; 9.996363636
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; 9.896825397
 421506; BE302798; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 9.888888889
 407788; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 9.876056338
 424441; X14850; Hs.147097; H2A histone family, member X; histone, C8FD_NFYB_HMF; 9.851635514
 438091; AW373082; Hs.351546; nuclear receptor subfamily 1, group 1, m; hormone_rec, zf-C4, none; 9.840720222
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT, none; 9.823170732
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (Z30/240kD); ehand, spectrin, GAS2, SH3, Plectin, RA_Xylose_isom, F1D, bZIP, Tropomyosin, Myc-LZ, Mdh_C, CHAIP3; TM=M; SS=N; 9.812

- 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S.; MCM,aldo_kat_red;TM=M;SS=N; 9.787878788
442599; AF078037; Hs.324051; RetA-associated inhibitor; SH3,ank;TM=M;SS=N; 9.637037037
425505; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin;TM=M;SS=M; 9.596
417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevis; WD40;TM=M;SS=N; 9.558
444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 9.55
421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 9.529085873
408591; AF015224; Hs.46452; mammaglobin 1; Uteroglobulin;TM=M;SS=M; 9.506
444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 9.477961433
444008; BE395085; Hs.334762; type I transmembrane protein Fn14; tlr_recept_a_PKD,MHC_I;TM=M;SS=Y; 9.415151515
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 9.408
424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin; ras;TM=M;SS=N; 9.36
429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;SS=N; 9.315693431
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 9.31
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.29
454034; NM_000693; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 9.264
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 9.241561181
445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 9.207272727
443426; AF098158; Hs.8329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 9.195167286
439223; AW238299; Hs.250618; UL16 binding protein 2; tlr_recept_a_PKD,MHC_I;TM=M;SS=Y; 9.108
428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;SS=N; 9.028
421777; BE562088; Hs.108196; HSPC037 protein; none;TM=M;SS=N; 9.004
448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 9.001096491
418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 8.942
455601; A1368680; Hs.816; SRY (sex determining region Y)-box 2; HMG_box; 8.87
429211; AF050693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 8.77131783
456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zfc3HC4,Cbl_N2,Cbl_N3;TM=M;SS=N; 8.738
430397; A1924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 8.738
417034; NM_006183; Hs.80962; neurotensin; none; 8.592
429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 8.536
408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3;none; 8.49
438285; A133916; Hs.47860; hypothetical protein FLJ20093; ig_pkinase,LRR,LRRNT,LRRCT;none; 8.460655738
409420; Z16008; Hs.54451; laminin, gamma 2 (nuclein (100kD), kallin; laminin_B,laminin_EGF; 8.414
438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferin,Guanylate_kin,PDZ,SH3; 8.376205788
439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.37
430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 8.364
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 8.266
417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none,none; 8.248314607
431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetase 2 (69-71; NTP_transf_2;TM=M;SS=N; 8.156
412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,art;TM=M;SS=N; 8.142857143
448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter; SNF;TM=Y;SS=N; 8.137559809
427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh; 8.043478261
424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase; 8.038194444
418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 8.024752475
453857; AL080235; Hs.35861; Ras-Induced senescence 1 (RIS1); none;TM=Y;SS=M; 8
424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 7.982
418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.973684211
413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.892
422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 7.824
452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 7.823874755
431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhbd_glycop,Integrin_A;TM=Y;SS=M; 7.758985201
432874; W94322; Hs.279551; melanoma inhibitory activity; SH3;TM=M;SS=Y; 7.75887574
439453; BE264974; Hs.6566; thyroid hormone receptor Interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 7.757751938
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig_Rhbd_glycop;TM=Y;SS=M; 7.624
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4;none; 7.605660377
427747; AW411425; Hs.180556; serine/threonine kinase 12; pkinase;TM=M;SS=N; 7.578
430280; AA361258; Hs.237868; Interleukin 7 receptor; fn3;none; 7.476
429299; A1620463; Hs.347408; hypothetical protein MGC13102; none;TM=Y;SS=N; 7.442528736
441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3;none; 7.442495127
446163; AA026880; Hs.25252; prolactin receptor; none;NA;NA; 7.436781609
414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,lypsin,plant_thionins; 7.435897436
439237; AW408158; Hs.318893; ESTs, Weakly similar to A47682 B-cell gr; Furin-like,pkinase,Recep_L_domain,YLP;none; 7.398360656
432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 7.394039735
431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 7.383419689
416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none,none; 7.382
436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 7.327180494
409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 7.316
448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 7.315412188
428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.2984375
422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45;TM=M;SS=N; 7.28
451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_jetra;TM=Y;SS=M; 7.256802721
416819; U77735; Hs.80205; p1m-2 oncogene; pkinase; 7.234455959
421817; AF148074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 7.162534435
451035; AU076785; Hs.430; plasmin 1 (I isoform); eifhand,CH,Adaplin_N; 7.145454546
424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 7.126
414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 7.122413793
425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX ; Troponin_Exo_endo_phos,IQ;TM=M;SS=N; 7.106719368
430890; X54232; Hs.2689; glypican 1; Glypican;TM=M;SS=M; 7.088937093
407792; A1077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 7.052
426514; BE616633; Hs.170195; bone morphogenetic protein 7 (osteogenic; TGF-beta,TGFb_propeptide; 7.042
431241; AA486799; Hs.36958; ESTs, SH2,RasGEF;none; 7.03
437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 7.03
420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 7.026
439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 7.008

- 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3, PX; TM=M; SS=N; 6.991626794
 416250; AA581386; Hs.73452; Kremen 2; kringle, CUB, WSC; 6.972
 430770; AA765694; Hs.123296; ESTs; none, none; 6.95
 5 418869; AW516565; ; gb|x01d05.x1 Soares_NHCEc_cervical_tumor; none, RasGAP, WW, IQ; 6.948
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily, 60s, ribosomal, Ribosomal_L10, TNFR_c6, DEAD; 6.914
 418283; S79895; Hs.83942; cathepsin K (pseudosarcosis); Peptidase_C1; 6.876190476
 419667; AU077005; Hs.92208; a disintegrin and metalloproteinase domain disintegrin, Reprolysin, Pep_M12B_propep; TM=M; SS=M; 6.862970711
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing Ig; Ig_LRR, LRRNT, LRRCT; TM=M; SS=M; 6.849056604
 10 456181; L38463; Hs.1030; ras inhibitor; RA, SH2, VPS9; TM=M; SS=N; 6.762
 436856; A1469355; Hs.127310; ESTs; pkinase, rmc; TM=M; SS=N; 6.721428571
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y; SS=M; 6.720348837
 439750; AL359053; Hs.57654; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, integrin_B, Rfcin_B, Jectin; 6.717307692
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y; SS=M; 6.715240642
 15 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 6.688194444
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, Integrin_B; TM=Y; SS=N; 6.670553936
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2, SH3; 6.682821348
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 6.653713299
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN, HIN; 6.652671756
 20 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; SS=N; 6.639655172
 438113; A1467908; Hs.8882; ESTs; 7tm_1, none; 6.6
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog); act; PH, none; 6.6
 408482; NM_000876; Hs.45743; adenosine A2b receptor; 7tm_1; TM=Y; SS=M; 6.548148148
 410290; AA402307; Hs.322844; hypothetical protein DKFp554A176; Sema, PSI, TIG, Integrin_B; TM=Y; SS=M; 6.532763533
 25 414809; A1434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 6.526961673
 426440; BE382758; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 6.512704174
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B; ; Sulfotransfer; 6.496
 423031; A1278995; Hs.374579; ESTs; none, none; 6.447658402
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; Ion_trans, K_letra, asp; 6.426666667
 30 433933; A1754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none; NA; NA; 6.4
 435094; A1560129; Hs.289008; EST; none, none; 6.312
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin, none; 6.276556777
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8, SHMT, MIF, GST_C, EF1G_domain, GST_N, S1, Fz, Frizzled, catreticulon, 7tm_2, rmc, PAP_assoc; TM=Y; SS=M; 6.272727273
 35 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank; TM=M; SS=N; 6.269720102
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 6.219081272
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin; TM=M; SS=N; 6.19
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; SS=N; 6.188888889
 449230; BE613348; Hs.355392; melanoma cell adhesion molecule; Ig, Isohd, Ribosomal_L6, F-box; TM=Y; SS=M; 6.188046647
 400060; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; AAA, NB-ARC, PAAD_DAPIN; NA; NA; 6.15503876
 40 450581; AF081613; Hs.25195; TGF-beta 4; TGF-beta, TGFb_propeptide; 6.152
 432314; AA533447; Hs.285173; ESTs; Xlink, none; 6.123040762
 418844; M52982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.12
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (sch; Ig, pkinase; TM=Y; SS=M; 6.095758355
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr; TM=M; SS=N; 6.089164786
 45 452683; A1089575; Hs.374574; progesterone membrane binding protein; homeobox, none; 6.08284153
 445537; A1245671; Hs.12844; EGF-like domain, multiple 6; EGF, MAM; 6.05513308
 444309; X83236; Hs.10803; calcium and integrin binding protein (DN; etiamd; 6.04015544
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD, helicase_C, rmc, Ndr, Cys_knot, TIL, vwa, vwc, vwd, I, Q, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPC, lrp_1, Ribosomal_S21, rvp; TM=M; SS=N; 6.009562842
 50 438108; A1471795; Hs.287776; vanilloid receptor-related osmotically a; ank, ion_trans; TM=Y; SS=N; 6.004
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none; TM=Y; SS=M; 5.984536083
 405484; ; C3002124; gi12737280ref|XP_006682.2|; none; 5.878964401
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae, pkinase, POLO_box, tRNA-sym_1b, dynamin, dynamin_2, GED, bZIP, M; 5.978431373
 55 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8; 5.976
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese, DSPC, Y_phosphatase; TM=M; SS=N; 5.969387755
 411756; BE294350; Hs.71891; discoidin domain receptor family, member; pkinase, F5_F8_type_C; TM=Y; SS=M; 5.95184136
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin; TM=Y; SS=M; 5.951550388
 453459; BE047032; Hs.257789; ESTs; none, none; 5.95
 60 456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=N; 5.838
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin, Peptidase_M10; TM=M; SS=M; 5.917857143
 414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase; TM=Y; SS=M; 5.910455487
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked mol; NUDIX; TM=M; SS=M; 5.901886793
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none, none; 5.868362832
 65 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase inhibitor; serpin; TM=Y; SS=M; 5.842
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 11; Euk_porin; TM=M; SS=M; 5.816363636
 439625; AF086453; Hs.58611; ESTs; Fork_head, glycolytic_enzy, Na_sulph_symp; 5.811694203
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 5.81
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 5.806
 70 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; SS=N; 5.804137931
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fs, clone CO; pkinase, Furin-like, Recep_L_domain, none; 5.8
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec, zf-C4, Metallothio_5; TM=M; SS=N; 6.794
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 5.778588808
 439246; A1498072; Hs.351474; membrane-associated tyrosine- and threon; ank, pkinase, UPF0073; 5.763492084
 452461; N78238; Hs.108106; transcription factor; zf-C3HC4, ubiquitin, PHD, YDG_SRA; TM=M; SS=N; 5.728
 75 414883; AA826960; Hs.348669; CDC28 protein kinase 1; CKS; 5.714634146
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fs, clone MA; SH2, STAT, STAT_bind, STAT_pro, none; 5.701666667
 419056; M89957; Hs.89575; CD79B antigen (immunoglobulin-associated; Ig, ITAM; TM=Y; SS=M; 5.692
 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 5.686
 452699; A1826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate_kin, PDZ, SH3; 5.683673469
 80 411030; BE387193; Hs.67895; 7-60 protein; none; TM=M; SS=N; 5.676767677
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (lazarro; none; TM=Y; SS=N; 5.672977625
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 5.666
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB; TM=M; SS=N; 5.655616943

- 427490; Z95152; Hs.176695; mitogen-activated protein kinase 13; pkinase; TM=M;SS=N; 5.6485623
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine; ank.pkinase; UPF0073; 5.648
 452690; A1536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 5.646
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3.pkinase; TM=M;SS=N; 5.642405063
 418703; NM_014448; Hs.87435; Rho guanine exchange factor (GEF) 16; SH3,PH,RhoGEF,Bima_VP3; TM=M;SS=N; 5.636
 426108; A622037; Hs.166468; programmed cell death 5; DUF122; TM=M;SS=N; 5.635087719
 424490; A1728016; Hs.55565; ankyrin repeat domain 3; ank.pkinase; TM=M;SS=N; 5.620930233
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), cat; Metallophos; TM=M;SS=N; 5.608352145
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3.pkinase; TM=M;SS=N; 5.596052632
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C; none; 5.575112108
 435017; AA336522; Hs.12854; angiotensin II, type I receptor-associated; none; TM=Y;SS=M; 5.556910569
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH,lb,Lipase_GDSL; TM=M;SS=N; 5.556195965
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3.pkinase; TM=M;SS=N; 5.555421687
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 5.549751244
 413989; X14043; Hs.75648; phospholipase C, gamma 2 (phosphatidyl); SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDGF; 5.541366907
 406621; X57809; Hs.181125; immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA; TM=M;SS=N; 5.54076087
 417700; M35542; Hs.1101; POU domain, class 2, transcription factor; homeobox,pou; TM=M;SS=N; 5.536
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M;SS=N; 5.52661597
 436576; A458213; Hs.77542; ESTs; 7bm_1,DnaJ; 5.52638191
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR; TM=M;SS=N; 5.519672131
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (I); MIF,sugar_b; none; 5.516453382
 417433; BE270266; Hs.82128; ST4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT; TM=Y;SS=M; 5.514964789
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3,Ig_Y_phosphatase,MAM; TM=Y;SS=M; 5.494202899
 419508; AW997938; Hs.90788; ATP-binding cassette, sub-family C (CFTR); ABC_tran,ABC_membrane; TM=Y;SS=M; 5.471947195
 410608; A1538438; Hs.159087; ESTs; ubiquitin,Integrin_B,UBA; none; 5.465384615
 448633; AA311428; Hs.21635; tubulin, gamma 1; tubulin; TM=M;SS=N; 5.460076046
 408716; A1567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein; UvrD-helicase,RNB,RunT; TM=M;SS=N; 5.450413223
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2,BH4; none; 5.444805195
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none; none; 5.444281625
 422597; BE245909; Hs.118634; ATP-binding cassette, sub-family B (MDR); ABC_tran,ABC_membrane,PRK; TM=Y;SS=N; 5.437931035
 429191; AF065215; Hs.198161; phospholipase A2, group IVB (cytosolic); C2,PLA2_B,mjC; TM=M;SS=N; 5.4375
 449951; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain; none; 5.435211268
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF; TM=M;SS=M; 5.433333333
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; Inducible Ik; pkinase,RIO1; TM=M;SS=N; 5.429657795
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 5.423322684
 423189; M59371; Hs.171598; EphA2; fn3.pkinase,SAM,EPH_Lbd; TM=Y;SS=M; 5.421621622
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae); pkinase; TM=M;SS=N; 5.412
 432527; AW975028; Hs.102754; ESTs; none; none; 5.40625
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7bm_2; TM=Y;SS=M; 5.405504587
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M;SS=N; 5.396
 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 f1, clone PL; 7bm_1; none; 5.391472888
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 5.389250814
 439670; AF088076; Hs.59507; ESTs; Weakly similar to AC004858 3 U1 sm; none; none; 5.382
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD,SET,zf-
 CXXC,EGF,ank,notch,VW,FCH,GATase,GMP_synL,C,Occludin,YEATS,metalldio,EB,hema_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT; TM=M;SS=N; 5.373937677
 424848; A1263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin; none; 5.36
 452721; A1269529; Hs.301871; solute carrier family 37 (glycerol-3-phos; MORN,sugar_tr; TM=Y;SS=M; 5.35971223
 405932; ; C15000305; gl3808122[gb]AAC69198.1 [AF0]; ras; TM=M;SS=N; 5.349226804
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated); Ig,ITAM,Zn_clus; TM=Y;SS=M; 5.346153846
 453143; AA382234; Hs.356289; protein tyrosine phosphatase, receptor t; serpin; 5.333667335
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT; TM=M;SS=N; 5.33
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none; none; 5.328
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig; TM=Y;SS=M; 5.316
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig; TM=Y;SS=M; 5.309638554
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD_DAPIN,CARD; TM=M;SS=N; 5.293560606
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor t; fn3_Y_phosphatase,carb_anhydase; TM=Y;SS=M; 5.28
 427316; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 5.278947368
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y;SS=N; 5.274746193
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none; TM=Y;SS=M; 5.272222222
 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1; TM=M;SS=N; 5.27
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH; TM=M;SS=N; 5.251865672
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese; none; 5.248
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y;SS=M; 5.232
 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 5.212418301
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 5.209259259
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphat; Ribosomal_L20,Na_PL_cotrans; TM=Y;SS=N; 5.202
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2; TM=M;SS=N; 5.19979716
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (f; ABC_tran,GTP_EFTU,ABC_membrane; none; 5.199074074
 416602; NM_006159; Hs.367896; Protein kinase C-binding protein NELL2; EGF,wvc,TSPN; 5.198224852
 429556; AW139399; Hs.314807; ESTs; none; TM=M;SS=N; 5.192439863
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND; TM=M;SS=M; 5.190251572
 400617; ; lenglis; none; TM=M;SS=N; 5.18
 413438; AF238083; Hs.68061; sphingosine kinase 1; DAGKc; TM=M;SS=N; 5.172881356
 423527; A1206965; Hs.105861; hypothetical protein FLJ13824; none; TM=M;SS=N; 5.165060241
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR,TPR,RyR,MIR; TM=Y;SS=N; 5.156976744
 437809; AL137723; Hs.6855; Homo sapiens mRNA; cDNA DKFZp434D0818 (f; none; none; 5.154676259
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos; TM=M;SS=N; 5.152360515
 409340; BE174629; Hs.321130; hypothetical protein MGC2771;
 aa_permeases,pyridoxal_deC,bromodomain,PHD,MBO,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN; TM=M;SS=N; 5.144859813
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51; none; 5.142
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,VW,RhoGAP; 5.141534392
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M;SS=N; 5.14
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M;SS=N; 5.13968254

- 431685; AW296135; Hs.267559; vav 3 oncogene; CH,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 5.129476584
- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 5.121527778
- 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type recc; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 5.107438017
- 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,art;TM=M;SS=M; 5.10251046
- 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subu; CDK5_activator,PCI,none; 5.095194085
- 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; Inositol_P,lg;TM=M;SS=N; 5.092
- 435243; AW292886; Hs.348932; hypothetical protein dJ4340.14.3; IRF,none; 5.092
- 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp585F2224 (f; DSPc,none; 5.091922006
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 5.086932806
- 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA; 5.082840237
- 420030; BE503994; Hs.146233; KIAA0418 gene product; SH3,none; 5.080645161
- 444065; AW449415; Hs.10260; Homo sapiens cDNA FLJ11341 fis, clone PL; SH3; 5.063953488
- 421677; H64092; Hs.38282; ESTs; A1pp,Armadio_seg,IBB; 5.056
- 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiose; 5.054133858
- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 5.054
- 423883; AF250238; Hs.134514; ATP-binding cassette, sub-family A (ABC1; ABC_tran,photoRC,SRP54,Ca_channel_B,Pterin_4a;TM=Y;SS=M; 5.051724138
- 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka;TM=M;SS=N; 5.051282051
- 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3_Y_phosphatase;TM=M;SS=N; 5.047311828
- 410026; AJ912061; Hs.55016; hypothetical protein FLJ21935; none,none; 5.04674221
- 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 5.040298508
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_Oxidase;TM=M;SS=M; 5.039039039
- 444895; AJ674383; Hs.22891; solute carrier family 7 (cationic amino; ASC,death,TNFR_c6; 5.037151703
- 413472; BE242870; Hs.75379; solute carrier family 1 (glial high aff; SDF;TM=Y;SS=M; 5.034
- 445272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 5.03030303
- 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Topoisom_bac,Toprim; 5.027885075
- 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase; pkinase,CNH;TM=M;SS=N; 5.014652015
- 415166; NM_003652; Hs.78068; carboxypeptidase Z; Zn_carbOpept,Dioxygenase,Fz; 5.012269939
- 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 5.001811594
- 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_Oxidase; 4.997983871
- 430024; AJ808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 4.994871795
- 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfam; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.987135506
- 423804; AW403448; Hs.1706; Interferon-stimulated transcription fact; IRF,zf-C3H4,IBR,zf-RanBP;TM=M;SS=N; 4.985185185
- 423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm_1;TM=Y;SS=M; 4.984
- 419577; L36531; Hs.91296; Integrin, alpha 8; Integrin_A,FG-GAP;TM=Y;SS=N; 4.968
- 402328; ; Target Exon; pkinase;TM=M;SS=N; 4.96728972
- 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.966334165
- 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.964491363
- 414203; BE262170; Hs.78629; ATPase, Na+ transporting, beta 1 polypep; none,none; 4.961956522
- 409582; R27430; Hs.271565; ESTs; none;Neur_chan_LBD,Neur_chan_membr; 4.946
- 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 4.943181818
- 453449; W16752; Hs.32981; sema domain, immunoglobulin domain (Ig); Ig,Sema,PSI; 4.930508475
- 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,lg; 4.926347222
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10; 4.92
- 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExbB;TM=Y;SS=M; 4.912181303
- 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.910224439
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.909972299
- 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 4.904
- 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;SS=N; 4.897338403
- 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;SS=N; 4.894
- 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1;TM=Y;SS=M; 4.886
- 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanes,none; 4.884
- 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 4.876379691
- 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG; 4.876117497
- 427792; M63928; Hs.180841; tumor necrosis factor receptor superfam; SRP14,TNFR_c6; 4.873684211
- 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,lg,Neuregulin;TM=M;SS=N; 4.872641509
- 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, poly; pkinase,pkinase_C;TM=M;SS=N; 4.869318182
- 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 4.868073879
- 458873; AW150717; Hs.345728; STAT induced STAT inhibitor 3; none,none; 4.861538462
- 437669; AJ358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none,pkinase,pkinase_C; 4.854651163
- 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 4.85
- 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 4.848387097
- 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus; fn3,lg,IRK;TM=Y;SS=M; 4.846153846
- 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.843694494
- 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, poly; pkinase,pkinase_C;TM=M;SS=N; 4.842532468
- 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_CAT_hook,SNF2_N;TM=M;SS=N; 4.842
- 444143; AW747896; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 4.841071429
- 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 4.839464883
- 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.837837838
- 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.833333333
- 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 4.821666667
- 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=M; 4.820936639
- 417949; AL049795; Hs.83004; interleukin 14; none,Armadillo_seg,IBB,WD40; 4.81443299
- 439569; AW602168; Hs.222399; CCEP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 4.81
- 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.805603291
- 432194; AL040801; Hs.273219; breast cancer anti-estrogen resistance 1; SH3; 4.803191489
- 431472; AK001023; Hs.256549; nucleotide binding protein 2 (E.coli Mtr; fer4_NiH,ParA,APS_kinase,AraA,ATPase;TM=M;SS=N; 4.800990099
- 450690; AA296695; Hs.333416; FXYD domain-containing ion transport reg; ATP1G1_PLM_MATB;TM=Y;SS=M; 4.795480881
- 448950; AF288687; Hs.9275; CGI-152 protein; E1-E2_ATPase,Hydrolase;TM=Y;SS=N; 4.776923077
- 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death,TNFR_c6,PH,Xlink,RhoGEF,Metallothio_5;TM=M;SS=M; 4.772196262
- 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.760115607
- 433376; AJ249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.751162791
- 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.748
- 431657; AI345227; Hs.105448; ESTs, Weakly similar to B34087 hypotheti; pkinase,PA28_alpha,PA28_beta,Cu_amine_oxd,Cu_amine_oxdN2,Cu_amine_oxdN3; 4.746

- 412958; BE391579; Hs.75087; Fas-activated serine/threonine kinase; none; 4.736781609
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; lg; pkinase; TM=Y; SS=N; 4.733
 419250; AW770185; Hs.355066; U5 snRNP-specific protein, 116 kD; 7m_1,BAH,zf-CXXC,DNA_methylase; 4.725454546
 417903; NM_002342; Hs.1116; lymphotxin beta receptor (TNFR superfam; TNFR_c6; TM=M; SS=M; 4.718858132
 5 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK_CoaE; 4.718836555
 426059; BE292842; Hs.166120; Interferon regulatory factor 7; IRF; 4.718543046
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.708
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 4.707920792
 10 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX; TM=M; SS=N; 4.707671958
 407143; C14076; Hs.332329; EST; none; TM=Y; SS=M; 4.682675815
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.681818182
 408805; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fls, clone C; SH3,PDZ,Guanylate_kin,none; 4.680440771
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP; TM=M; SS=M; 4.679841897
 15 418836; A1655499; Hs.161712; ESTs; pkinase,Activin_recp,PDZ,ZU5,death; 4.679180887
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; lg,kringle,pkinase,Fz; TM=Y; SS=M; 4.675342466
 414665; AA160873; Hs.356307; serum amyloid A1; zf-C2H2,BTB,K_tetra,none; 4.67447496
 449843; R85337; Hs.24030; solute carrier family 31 (copper transp; none; TM=Y; SS=M; 4.673701299
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (y; none; 4.656756757
 20 417088; M54915; Hs.81170; p1m-1 oncogene; pkinase; TM=M; SS=N; 4.656190476
 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 com; ITAM; TM=M; SS=M; 4.65
 425966; NM_001761; Hs.1973; cyclin F; cyclin_F-box,cyclin_C; TM=M; SS=N; 4.644
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; lg,abhydrolase; 4.640384615
 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4,zf-RanBP,pkinase; 4.630653266
 19 419273; BE271180; Hs.293490; ESTs, Weakly similar to I38022 hypothesis; none,none; 4.628
 453880; A1803166; Hs.135121; ESTs, Weakly similar to I38022 hypothesis; HSP70,none; 4.619047619
 459399; BE407712; Hs.153998; creatine kinase, mitochondrial 1 (ubiquit; none,none; 4.618577075
 412970; AB026438; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPE; 4.616
 433577; AW007080; Hs.284192; ESTs; none,none; 4.614
 444838; AV651680; Hs.208558; ESTs; Integrin_A,FG-GAP,none; 4.612149533
 30 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+pep; PTR2; TM=Y; SS=N; 4.602
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin; 4.596875
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin,none; 4.587931035
 433083; AL042759; Hs.191762; ESTs; SH3,PX; TM=M; SS=N; 4.586
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor; ; lg; TM=Y; SS=M; 4.58557047
 35 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; 4.579087049
 422009; A1742845; Hs.110713; DEK oncogene (DNA binding); SAP; 4.576347305
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 4.57312253
 414561; A1064813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.573015873
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU; TM=M; SS=M; 4.570526316
 40 459053; A1807052; Hs.97792; ESTs; none,7m_2,GPS; 4.569230769
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,lg,FAD_Synth,ldh_C,pkinase; 4.566195373
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham tp_lik; TM=M; SS=N; 4.56056338
 416178; A1085527; Hs.192822; serologically defined breast cancer ant; none; TM=M; SS=N; 4.558
 408051; A1623351; Hs.172148; ESTs; PH,RhoGAP,none; 4.552307692
 45 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ehand,ldl_recept_a; 4.547761194
 438659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7m_1,LRR; TM=Y; SS=N; 4.547169811
 426201; AW182614; Hs.128499; ESTs; SH3,none; 4.541666667
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 4.536
 445229; BE278013; Hs.343828; Homo sapiens mRNA for FLJ00086 protein; ; G-alpha; TM=M; SS=N; 4.530588235
 50 413109; AW368945; Hs.110855; ESTs; PHO4,none; 4.529761905
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolo; EGF_cadherin,Jamninin_G; TM=Y; SS=M; 4.529710145
 402330; ; Target Exon; pkinase,none; 4.528070175
 439238; M47305; Hs.302161; EDG-8 (endothelial differentiation, sph; 7m_1; TM=Y; SS=M; 4.524
 55 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20; 4.523715415
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase; CBS,IMPDL_C,IMPDL_N,NPD; TM=M; SS=N; 4.522900763
 431429; AF072813; Hs.252831; reticulon 3; Reticulon,Fz,lg,kringle,pkinase; TM=Y; SS=N; 4.512
 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 4.512
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS; TM=M; SS=N; 4.51
 60 449101; AA205847; Hs.23016; G protein-coupled receptor; 7m_1; TM=Y; SS=M; 4.506
 408157; AA047685; Hs.62946; ESTs; none,pkinase; 4.504
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILY; TM=M; SS=Y; 4.50215208
 431326; AW970580; Hs.188689; KIAA0728 protein; none,none; 4.501
 428072; BE258602; Hs.182366; heat shock protein 75; HATPase_c,HSP90; TM=M; SS=N; 4.48828125
 65 416149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 4.484375
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypept; p450; TM=Y; SS=M; 4.48
 445143; U29171; Hs.378918; casein kinase 1, delta; zf-C3HC4,Filamin,zf-B_box,NHL,pkinase,zf-MZ; TM=M; SS=N; 4.478092784
 421071; A1311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen; none; TM=Y; SS=M; 4.477337111
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none; TM=M; SS=N; 4.478
 38774; AA431620; Hs.379034; hypothetical protein MGC2745; none,none; 4.474874372
 70 410726; A1623859; Hs.15936; ESTs; pkinase,pro_Isomerase,none; 4.47
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator,none; 4.468
 426485; NM_008207; Hs.170040; platelet-derived growth factor receptor; lg; 4.464944649
 433646; AA603319; Hs.155195; ESTs; pou,homeobox,lg_chan,ANF_receptor; 4.458
 410293; AK000047; Hs.61950; hypothetical protein; K_tetra; TM=M; SS=N; 4.453020134
 75 453464; A1884911; Hs.32899; receptor (calcitonin) activity modifying; none; TM=Y; SS=N; 4.448198198
 410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galac; SH3,PDZ,Guanylate_kin,none; 4.446927374
 441455; AJ271671; Hs.7854; zinc/fon regulated transporter-like; Zip; TM=Y; SS=M; 4.445010183
 453084; RA0334; Hs.89463; potassium large conductance calcium-act; none,none; 4.436480187
 443303; U87318; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20; TM=M; SS=M; 4.433411215
 80 411825; AK000334; Hs.352415; solute carrier family 39 (zinc transport; SNF,Zip; TM=Y; SS=N; 4.432765152
 428376; AF116665; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase; TM=M; SS=N; 4.428571429
 429592; AB029041; Hs.209646; KIAA1118 protein; Troponin,Exo_endo_phos,IQ; TM=M; SS=N; 4.428
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); ank,DAGKa,DAGKc,DAG_Pe-bind; TM=M; SS=N; 4.426229508

- 427138; N77624; Hs.173717; phosphatidic acid phosphatase type 2B; PAP2; none; 4.4234375
 414496; W73853; Hs.355424; ESTs; pkinase; F5_F8_type_C_adh_short; none; 4.42114094
 429432; A1678059; Hs.202676; synaptonemal complex protein 2; none; TM=M; SS=N; 4.42
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M; SS=N; 4.419207317
 5 446700; AW208257; Hs.156326; Human DNA sequence from clone RP11-145L2; none; TM=M; SS=N; 4.418181818
 435411; AW444619; Hs.138211; ESTs; none; pkinase; 4.414
 414581; AA256213; Hs.72010; ESTs; none; Cam_acyltransf; Choline_kinase; SCO1-SanC; Glycos_transf_3; Glycos_trans_3N; 4.41
 10 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death; DED; 4.408523909
 442259; A1690269; Hs.201345; ESTs; Acetyltransf; RhoGAP; FCH; SH3; Kelch; fn3; 4.406
 415860; D56051; Hs.78888; diazepam binding inhibitor (GABA receptor; ACBP; TM=M; SS=N; 4.404678363
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc; TM=M; SS=N; 4.404
 404440; ; NM_021048; Homo sapiens melanoma antigen; MAGE; TM=M; SS=N; 4.4
 435542; AA687376; Hs.351226; ESTs; SH3; Ig; pkinase; PH; spectrin; RhoGEF; none; 4.394
 15 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar; Ir; TM=Y; SS=N; 4.39028777
 435732; AF29178; Hs.123136; leucine rich repeat and death domain con; none; none; 4.38490566
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L: 7bm_1; none; 4.382129278
 425749; AW328587; Hs.159448; surfell 2; none; 4.382
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; SS=N; 4.381422925
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS; TM=Y; SS=M; 4.380681818
 20 418137; T79326; Hs.331967; olfactory receptor, family 2, subfamily; none; 7m_3; sushi; ANF_receptor; 4.376
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm; pkinase; 4.370247934
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; Ig; Rhabd_glycop; TM=Y; SS=M; 4.37
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y; SS=M; 4.367777778
 25 403912; ; C5000394; gll12737280[ret]XP_006682.2; k; none; TM=M; SS=N; 4.367684478
 425268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20; yeast; pkinase; 4.366348449
 434263; N34895; Hs.79187; ESTs; Ig; none; 4.358527132
 404760; ; Target Exon; cadherin; TM=M; SS=M; 4.356
 413076; U10564; Hs.75168; wee1 (S. pombe) homolog; pkinase; TM=M; SS=N; 4.35472973
 30 420757; X78592; Hs.99915; androgen receptor (dihydrotestosterone r; hormone_rec; zf-C4; Androgen_recep; TM=M; SS=N; 4.354
 426812; AF106365; Hs.172613; solute carrier family 12 (potassium/chlor; none; TM=Y; SS=N; 4.353244838
 431674; AA098901; Hs.301642; G-protein coupled receptor; none; GCV_H; 4.35
 431886; L77954; Hs.271980; mitogen-activated protein kinase 6; pkinase; TM=M; SS=N; 4.347893916
 447719; BE387402; Hs.19333; hypothetical protein FLJ10349; adenylatekinase; ATP-bind; TM=M; SS=N; 4.346007605
 35 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerev; Acetyltransf; TM=M; SS=N; 4.344
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none; none; 4.334722222
 411768; NM_013371; Hs.71979; Interleukin 19; IL10; 4.322
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2; TM=M; SS=N; 4.320359281
 425964; AW889928; Hs.8071; progesterone membrane binding protein; homeobox; none; 4.318867925
 40 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; mm; TM=M; SS=N; 4.316573557
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; 4.316
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none; Cys_knot; 4.314726682
 438899; AF085833; Hs.135624; ESTs; none; P13_P14_kinase; P13Ka; P13K_C2; P13K_rbd; P13K_p85B; 4.314084507
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos; TM=M; SS=M; 4.312121212
 45 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4; TM=M; SS=N; 4.304407714
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg; HEAT; TM=M; SS=N; 4.304
 430017; AA263172; Hs.35; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=M; SS=M; 4.302
 447224; BE617125; Hs.142076; gb:601441664f1 NIH_MGC_65 Homo sapiens c; none; NA; NA; 4.302
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase; UBA; KA1; TM=M; SS=N; 4.301639344
 50 454042; H22570; Hs.47860; hypothetical protein FLJ20093; Ig; pkinase; LRR; LRRNT; LRRCT; none; 4.30141844
 446143; BE245342; Hs.306079; sec61 homolog; NUDIX; secY; E1_dehydrog; transfeL_pyr; TM=Y; SS=M; 4.300872093
 428991; BE313077; Hs.93135; ESTs; Weakly similar to ALU2_HUMAN ALU S; none; mm; 4.292620865
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2; TM=M; SS=N; 4.290258449
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none; TM=M; SS=M; 4.288405797
 55 421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10; DDP; ehfand; CH; spectrin; serpin; TM=M; SS=N; 4.284
 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK; 4.28057554
 453941; U39817; Hs.36820; Bloom syndrome; DEAD; helicase_C; HRDC; TM=M; SS=N; 4.28
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor; ; Tropomyosin; pkinase; LRR; LRRCT; Hydantoinase_B; Hydantoinase_A; TM=M; SS=N; 4.277477478
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF; laminin_Nterm; Integrin_B; 4.276162791
 60 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none; none; 4.273927393
 438012; AA393254; Hs.43619; ESTs; Armadillo_seg; none; 4.273134328
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; SS=N; 4.273109244
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41; ERM; pkinase; LRR; LRRCT; MAM; Nucleoplasmin; Tropomyosin; OPR; filament; bZIP; G-gamma; M; DUF164; TM=M; SS=N; 4.272123894
 65 415214; A1445236; Hs.125124; EphB2; fn3; pkinase; SAM; EPH; Ibd; TM=Y; SS=M; 4.268
 438233; W52448; Hs.56147; ESTs; Neur_chan_LBD; Neur_chan_membr; MAGE; 4.26284585
 429019; AA443280; Hs.279907; myosin IIIA; myosin_head; pkinase; PRK; IQ; TM=M; SS=N; 4.262
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; kln; kln_C; SH3; pkinase; UBA; TM=M; SS=N; 4.258695652
 453655; AW860427; Hs.342874; transforming growth factor, beta receptor; zona_pellucida; none; 4.257208766
 417414; AA434589; Hs.357676; dUTP pyrophosphatase; dUTPase; KRAB; 4.251785714
 70 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase; LIM; PDZ; zf-PARP; TM=M; SS=N; 4.249116608
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase; DAG_PE-bind; PH; TM=M; SS=N; 4.247692308
 404883; ; ENSP00000216009; Sodium-glucose cotranspo; SSF; TM=Y; SS=M; 4.242424242
 412507; L36645; Hs.73964; EphA4; fn3; pkinase; SAM; EPH; Ibd; TM=Y; SS=M; 4.239285714
 75 411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none; none; 4.237313433
 436957; AA902488; Hs.122952; ESTs; none; DAGKa; DAGKa_RA; DAG_PE-bind; 4.236
 452568; AA805634; Hs.300870; Homo sapiens mRNA: cDNA DKFZp547M072 (fr; P13_P14_kinase; TM=M; SS=M; 4.23537415
 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT; TM=M; SS=N; 4.234793187
 432728; NM_006979; Hs.278721; HLA class II region expressed gene KE4; Zip; lip_chan; TM=Y; SS=M; 4.234545455
 416350; AF188622; Hs.189507; phospholipase A2, group IID; phoslip; TM=M; SS=Y; 4.234
 80 409533; AW969543; Hs.144609; mitogen-activated protein kinase kinase; Peptidase_C48; none; 4.230666667
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 4.228009259
 403362; ; NM_001815; Homo sapiens actin, gamma 2; ; actin; 4.22688478
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen; COLFI; TSPN; Jaminin_G; CorA; 4.226388889

- 428897; AJ245719; Hs.194385; hypothetical protein FLJ20234; SH2;TM=M;SS=N; 4.224731183
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; GH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.223684211
 418566; C21220; Hs.321717; hypothetical protein FLJ10875; zf-C2H2,BTB,K_tetra,7tm_1; 4.222807018
 454098; W27953; Hs.217493; Plakophilin; none;none; 4.22
 5 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); pkinase,FHA,DnaJ;TM=M;SS=N; 4.21875
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 4.217130215
 436756; Z18364; Hs.198298; v-src avian sarcoma (Schmidt-Ruppin A-2); none;none; 4.216
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 4.215163934
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; ehband; 4.212041885
 10 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; none,DS,UPF0139,Glyco_hydro_38; 4.207407407
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rm;TM=M;SS=N; 4.206
 432284; AA532807; Hs.287740; ESTs; pkinase;none; 4.205454546
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase,RJO1;TM=M;SS=N; 4.204142012
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypothet; ABC_tran,ABC_membrane,Ig,MHC_II_beta,SRP54,proleasome,ABC_membrane,ABC_tran; 4.202572347
 15 412817; AL037159; Hs.74619; proleasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 4.202061856
 425394; AA356730; Hs.323949; kangal 1 (suppression of tumorigenicity; transmembrane4,none; 4.195014663
 449335; AW150717; Hs.345728; STAT induced STAT inhibitor 3; SH2;TM=M;SS=N; 4.192248062
 415023; AA932146; Hs.355397; Homo sapiens clone TCCOA00164 mRNA sequ; none;NA;NA; 4.192
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 4.191878981
 20 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.189922481
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y;SS=N; 4.188333333
 434633; AI189587; Hs.120915; ESTs; SH3,PH,RhoGAP,none; 4.187106918
 452908; AB001451; Hs.30965; neuronal Shc adaptor homolog; SH2,PID,Zn_carbOpept;TM=M;SS=N; 4.186885246
 25 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 3.930957684
 432201; AJ538613; Hs.298241; Transmembrane protease, serine 3; ldl_receptLa,trypsin;TM=Y;SS=M; 3.893103448
 428969; AF120274; Hs.194689; artemin; TGF-beta; 3.884030418
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; Ig;TM=Y;SS=M; 3.831669044
 432305; M62402; Hs.274313; insulin-like growth factor binding prote; thyroglobulin_1,IgFBP,A2M_N;TM=M;SS=N; 3.742996346
 30 405547; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.676
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 3.634
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 3.662
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q,Collagen; 3.49
 405546; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.422661871
 35 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none;none; 3.402
 404210; ; NM_005936; Homo sapiens myeloid/lymphoid; FHA,PDZ,RA,DIL;TM=M;SS=N; 3.368807339
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C; 3.213402062
 418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); none;TM=M;SS=N; 3.084
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M;SS=N; 1.65

40 TABLE 17B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418869	12769_14	AA229762 AA230035

50 TABLE 17C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 55 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
405932	7767812	Minus	123525-123713
400517	9796686	Minus	49996-50346
402328	4464263	Minus	13758-13922,14558-14752
405545	1054740	Plus	118677-118807,119091-119298,121626-12182
402330	4464283	Minus	15325-15380,15484-15588,15842-15915
404440	7528051	Plus	80430-81581
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
70 404760	7767724	Plus	223266-223352,224472-224585
404883	5101762	Minus	94626-94730,96998-97069
403362	8571772	Plus	64099-64260
405547	1054740	Plus	124361-124520,124914-125050
405546	1054740	Plus	124010-124183
75 404210	5006248	Plus	169926-170121

80 Table 18A: 194 Up-Regulated Genes in Uterine Cancer Versus Normal Adult Tissues

Table 18A lists about 194 genes up-regulated in uterine cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" uterine cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" uterine cancer level was set to the 2nd highest amongst uterine cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst non-malignant tissues. In order to remove gene-specific background

levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor vs. normal tissue			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	449034	AI624049		gb:ts41a09.x1 NCI_CGAP_U11 Homo sapiens cDNA	55.7
	435094	AI560129	Hs.277523	EST	45.2
	438817	AI023799	Hs.163242	ESTs	42.6
	421478	AI683243	Hs.97258	ESTs	35.2
	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	27.3
20	450451	AW591528	Hs.202072	ESTs	26.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252	24.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49) (HG38)	24.2
	438993	AA828995	Hs.52520	Integrin; beta 8	16.7
	436775	AA731111	Hs.291891	ESTs	14.3
25	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA clo	13.5
	441377	BE218239	Hs.202656	ESTs	13.5
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	12.3
	400292	AA250737	Hs.72472	BMPRII-bone morphogenetic protein receptor Ib	10.7
	403899			predicted exon	10.1
30	442438	AA995998		gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens cDNA	10.0
	447350	AI375572	Hs.1939	HER4 (o-erb-B4)	9.8
	453964	AI961486	Hs.12744	ESTs	9.7
	443830	AI142095	Hs.143273	ESTs	9.1
	459325	AW088369	Hs.282184	ESTs	9.0
35	415245	N59650	Hs.27252	ESTs	8.9
	446608	N75217	Hs.257846	ESTs	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
	433426	H69125	Hs.133525	ESTs	8.7
	437960	AI669586	Hs.222194	ESTs	8.5
40	441091	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H]	8.3
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [Hs]	7.3
	447835	AW591623	Hs.164129	ESTs	7.2
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO10	7.1
	412925	AI089319	Hs.179243	ESTs	7.0
45	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane receptor (robo2)	7.0
	428272	W25140	Hs.110667	ESTs	6.9
	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM	6.3
	437938	AI950087		ESTs; Weakly similar to Gag-Pol polyprotein	6.2
	420610	AI683183	Hs.99348	distal-less homeo box 5	6.2
50	448672	AI955511	Hs.225106	ESTs	6.1
	452461	N78223	Hs.108106	transcription factor	6.1
	413335	AI613318	Hs.48442	ESTs	6.1
	449611	AI970394	Hs.197075	ESTs	6.0
	449260	AA741180	Hs.29879	ESTs	6.0
55	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0
	432113	AA935065	Hs.152385	ESTs	5.9
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
60	426465	AI758948		gb:ty16807.x1 NCI_CGAP_U13 Homo sapiens cDNA	5.7
	446704	AI337228	Hs.197083	ESTs	5.5
	419503	AA243642	Hs.137422	ESTs	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
65	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.3
	445258	AI635931	Hs.147613	ESTs	5.3
	440901	AA909358	Hs.128612	ESTs	5.3
	434636	AA083764	Hs.241334	ESTs	5.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone LNG020	5.2
70	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.2
	459583	AI907673		gb:LL-BT162-080399-004 BT162 Homo sapiens cDN	5.2
	436787	AA908554	Hs.192766	ESTs	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	5.1
	428771	AB028992	Hs.193143	KIAA1069 protein	5.1
75	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
	405609			predicted exon	5.0
	410102	AW248508	Hs.279727	ESTs;	5.0
	433283	BE041135	Hs.175622	ESTs	4.8
80	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 18	4.8
	410247	AF181721	Hs.61345	RU2S	4.7
	422589	AA312735	Hs.179725	ESTs	4.7
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cat93620	4.7
	407275	AI354186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens cDNA	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	4.6
	451105	AI761324		gb:w60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	4.6

	453816	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	4.6
	424115	AA335497	Hs.293965	ESTs	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	4.6
5	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	4.5
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	4.5
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG076	4.4
	458861	AI630223		PHD finger DNA binding protein isoform 1 (int)	4.4
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	4.3
10	420149	AA255920	Hs.88095	ESTs	4.3
	433479	AW511459	Hs.249972	ESTs	4.3
	449416	AI651016	Hs.246311	ESTs	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone HEP106	4.3
	450109	AI539295	Hs.17967	ESTs	4.3
15	436954	AA740151	Hs.130425	ESTs	4.3
	415511	AI732617	Hs.182362	ESTs	4.3
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM40	4.3
	406411			predicted exon	4.2
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)	4.2
20	416456	H57052	Hs.176626	hypothetical protein EDAG-1	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07	4.1
	452249	BE394412	Hs.61252	ESTs	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	4.1
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUB	4.1
25	434988	AI418055	Hs.161160	ESTs	4.1
	423515	AA327017	Hs.162204	ESTs	4.0
	435407	AI149774	Hs.117178	ESTs	4.0
	440886	AW511032	Hs.190516	ESTs	4.0
	444783	AK001468	Hs.62180	ESTs	4.0
	452039	AI922988	Hs.172510	ESTs	4.0
30	407300	AA102616	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT0614	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	4.0
	449433	AI672096	Hs.9012	ESTs	3.9
	419335	AW960146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP20	3.9
35	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp5861518	3.9
	453098	AW294631	Hs.11325	ESTs	3.9
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.9
	445034	AW293376	Hs.160323	ESTs	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.8
40	422219	AW978073		gb:EST390182 MAGE resequences	3.8
	440304	BE159984	Hs.125395	ESTs	3.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228	3.8
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK	3.8
	400250			predicted exon	3.8
45	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	3.8
	420092	AA814043	Hs.88045	ESTs	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFP2	3.8
	437212	AI765021	Hs.210775	ESTs	3.8
	409887	AW502161		gb:U1-HF-BR0p-aj-g-12-0-ULr1 NIH_MGC_62	3.7
50	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.7
	427119	AW880582	Hs.114574	ESTs	3.7
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	3.7
	434539	AW748078	Hs.214410	ESTs	3.7
	424717	H03754	Hs.152213	wingless-type MMTV integration site family	3.7
55	412078	X69699	Hs.73149	paired box gene 8 (PAX-8)	3.7
	447342	AI199268	Hs.19322	ESTs, Weakly similar to IIII ALU SUBFAMILY J	3.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.7
	446619	AU076843	Hs.313	secreted phosphoprotein 1 (osteopontin)	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDNA clo	3.7
60	443613	AI079356		gb:ac39b09.s1 Soares_NhHMPu_S1 Homo sapiens c	3.6
	441285	NM_002374	Hs.167	microtubule-associated protein 2	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	3.6
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	3.6
	441484	AA935481	Hs.58972	ESTs	3.6
65	415802	AA169515	Hs.6008	ESTs	3.6
	448112	AW245919	Hs.301018	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	3.6
	402606			predicted exon	3.6
	407905	AW103655	Hs.252905	ESTs	3.6
70	424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone LNG025	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	3.6
	451842	AI820539	Hs.267087	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.6
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	3.6
	431731	BE265322	Hs.211374	ESTs, Weakly similar to SP49_HUMAN SPLICEOSOM	3.6
75	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal sh	3.6
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	3.6
	406030			predicted exon	3.5
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA Libr	3.5
80	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.5
	437641	AA811452	Hs.291911	ESTs	3.5
	415211	RB4730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	3.4
	443450	N66045	Hs.133529	ESTs	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	3.4
	451254	AI571016	Hs.172967	ESTs	3.4

5	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMB810	3.4
	427778	AA412323	Hs.105323	ESTs	3.3
	435031	AJ632091	Hs.116877	ESTs	3.3
	407356	AF026942		gb:Homo sapiens cjb33 mRNA, partial sequence.	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187J11 on c	3.3
	431548	AJ834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	3.2
	432415	T16971	Hs.289014	ESTs	3.2
	423126	AA322245	Hs.290165	ESTs	3.2
10	433420	AJ674093	Hs.293951	ESTs	3.2
	435174	AA687378	Hs.194524	ESTs	3.2
	444743	AA045848	Hs.11817	nrdix (nucleoside diphosphate linked motety X	3.2
	452588	AA889120	Hs.110637	Homeo box A10	3.2
	427304	AA761526	Hs.163853	ESTs	3.2
15	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from cl	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	3.1
	419356	AJ656166	Hs.7331	ESTs	3.1
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [3.1
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase 1	3.1
20	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone COL064	3.1
	405174			predicted exon	3.1
	403776			predicted exon	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily, m	3.1
	431255	AA497043	Hs.115665	ESTs	3.1
25	442353	BE379594	Hs.49136	ESTs	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (formerl	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens cDNA c	3.1
	406400			kallikrein 8 (neurosin/ovastin)	3.0
30	439949	AW978197	Hs.292073	ESTs	3.0
	430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186 Homo sapi	3.0
	401517			predicted exon	3.0
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	3.0
	435267	N23797	Hs.110114	ESTs	3.0
35	426384	AJ472078		ESTs	3.0
	422797	AB033064	Hs.120908	KIAA1238 protein	3.0
	428832	AA578229		gb:nl22b12.s1 NCI_CGAP_HSC1 Homo sapiens cDNA	3.0
	449722	BE280074	Hs.23960	cyclin B1	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	3.0
40	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	3.0

TABLE 18B

	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
45			
50	409745	115237_1	AA077391 AJ347618 AJ361453 AJ088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450
	409867	1156530_1	AW502161 AW502587 AW502345
	422219	213547_1	AW978073 AW978072 AA807550 AA306567
	422689	218986_1	AW856665 AA315008 AW954733
	426384	266211_1	AJ472078 AA377209 AA865807
55	428465	287684_1	AJ758948 AA379527 AA379948 AA379262 AW963933
	428832	296144_1	AA578229 AA436432 AA481375 AA481363
	430704	322217_1	AW813091 AW206655 AA484440
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	437938	44573_2	AJ950087 N70208 R97040 N36809 AJ308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
60			AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
			AA527794 AJ560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AJ741346 AI689062 AA282915
			AW102698 AJ872193 AJ763273 AW173586 AW150329 AI653832 AJ762688 AA988777 AA488892 AJ356394 AW103813 AI539642 AA642789 AA856975
			AW505512 AJ961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669
			AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628
			N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AJ373032 AI564269 F00531 H83488 W37181 W78802 R66056
65			AJ002839 R67840 AA300207 AW959581 T63226 F04005
	438993	467851_1	AA828995 AA834879 AI926361
	442438	542469_1	AA959998 AI916584 R61781 T77332 F07756 F08149 F07647
	443613	575391_1	AJ079356 W23287
70	449034	794817_1	AJ624049 AW117770 AI858360
	451105	859083_1	AJ761324 AW880941 AW880937
	452771	930983_1	T05477 T07855 AJ917711
	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1	AW813350 AW816082 AW813476 AW813383
75	455666	1349545_1	BE065813 BE065788 BE065889 BE065832
	458154	491768_1	AW816379 AA888282 AA879046 AA879195
	458861	798085_1	AJ630223 AJ630470

TABLE 18C

80	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

5	Pkey	Ref	Strand	Nt_position
	401517	7677912	Plus	29278-29770
	402606	9909429	Minus	81747-82094
	403776	7770611	Minus	1414-1513,1624-1756
10	403899	7381715	Minus	9144-9350
	405174	7108030	Minus	102814-103063
	405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
	406030	8312328	Minus	96123-96547
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
15	406411	9256407	Plus	7400-7527

Table 19A: 225 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, UTERINE Cancer Versus Normal Adult Tissues

Table 19A lists about 225 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	R1
35	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	TM	27.3
	438993	AA828995	Hs.52620	integrin; beta 8	SS,TM,integrin_B	16.7
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stroma	SS,hemopexin	12.3
	446508	N75217	Hs.257846	ESTs	TM	8.9
	433426	H69125	Hs.133525	ESTs	TM	8.7
40	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clo	TM,PAX	7.1
	408562	AI436323	Hs.31141	Roundabout homolog 2 transmembrane	SS,TM,ig,fn3	7.0
	420610	AI683183	Hs.99348	distal-less homeo box 5	TM,homeobox	6.2
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rab	TM,kinesin	6.0
	443715	AI583187	Hs.9700	cyclin E1	TM,cyclin	6.0
	432113	AA935065	Hs.152385	ESTs	TM	5.9
45	419503	AA243642	Hs.137422	ESTs	TM	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated memb	TM,Lamp	5.4
	436076	AI193277	Hs.120954	ESTs	TM	5.4
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	TM,hemopexin	5.3
50	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.2
	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo s	TM	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	TM,hormona_rec,zf-C4	5.1
	405609			predicted exon	TM,Myosin_tail,myosin_head	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazol	TM	5.0
55	410102	AW248508	Hs.279727	ESTs	SS,TM,	5.0
	433283	BE041135	Hs.176522	ESTs	TM	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gen	TM	4.8
	410247	AF181721	Hs.61345	RU2S	TM	4.7
	422589	AA312735	Hs.179725	ESTs	TM	4.7
60	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_U14 Homo sap	TM	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	TM,Uteroglobulin	4.6
	453616	NM_003462	Hs.33846	dynelin, axonemal, light intermediat	TM,Ribosomal_S27e	4.6
	424115	AA335497	Hs.293965	ESTs	TM	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	TM,WH2	4.6
65	458861	AI630223		PHD finger DNA binding protein iso	TM,PHD	4.4
	449416	AI651016	Hs.246311	ESTs	SS,TM,	4.3
	420149	AA255920	Hs.88095	ESTs	TM	4.3
	433479	AW511459	Hs.249972	ESTs	TM	4.3
	457551	AW821319	Hs.268928	Homo sapiens cDNA: FLJ23296 fis, cl	TM	4.3
70	406411			predicted exon	TM,vwa,FG-GAP	4.2
	416456	H57052	Hs.176626	hypothetical protein EDAG-1	TM	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192	TM	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	TM	4.1
	434988	AI418055	Hs.161160	ESTs	TM	4.1
	444783	AK001468	Hs.62180	ESTs	TM,PH	4.0
75	440886	AW511032	Hs.190516	ESTs	TM,FG-GAP	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HU	TM,Glyco_transf_29,TEA	4.0
	445034	AW293376	Hs.160323	ESTs	TM	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box	TM,HMG_box	3.8
80	400250			predicted exon	TM,Hist_deacetyl	3.8
	428227	AA321649	Hs.2248	interferon-gamma induced protein	TM,IL8	3.8
	415138	C18356	Hs.78045	Issue factor pathway inhibitor 2 T	TM,Kunitz_BPT1,G-gamma	3.8
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	TM,WW	3.7
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	TM	3.7

5	413472	BE242870	Hs.75379	solute carrier family 1 (glial high	TM,SDF	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SU	TM	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopon	TM,Osteopontin	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length inser	TM	3.7
	441285	NM_002374	Hs.167	microtubule-associated protein 2	TM,tubulin-binding	3.6
10	409731	AA125985	Hs.56145	thymosin, beta, identified in neuro	TM,Thymosin	3.6
	441484	AA935481	Hs.58972	ESTs	TM,fn3,lg_Y_phosphatase	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrity	SS,Peptidase_M10	3.6
	407905	AW103655	Hs.252905	ESTs	SS,TM,Ephrin	3.6
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular	SS,TM	3.6
15	402606			predicted exon	TM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1	TM	3.6
	437641	AA811452	Hs.291911	ESTs	TM	3.5
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFA	TM,IO,Rlla	3.4
	443450	N66045	Hs.133529	ESTs	TM	3.4
20	457438	NM_014053	Hs.270594	FLVCR protein	TM	3.4
	435031	AI632091	Hs.116877	ESTs	TM,RhoGEF,PH	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-1	TM	3.3
	435174	AA687378	Hs.194624	ESTs	TM,SPRY	3.2
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linka	TM,muT	3.2
25	433420	AI674093	Hs.293961	ESTs	TM	3.2
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E23	TM	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	TM	3.1
	403776			predicted exon	SS,TM,IL8	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) supe	TM,TNF	3.1
30	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, cl	TM,Ets	3.1
	405174			predicted exon	TM	3.1
	431255	AA497043	Hs.115685	ESTs	TM	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog	TM,homeobox	3.1
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	TM,trypsin,pro_isomerase	3.1
35	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapi	TM	3.1
	406400			kalikrein 8 (neurosinovasin)	TM,trypsin	3.0
	401517			predicted exon	TM,HMG14_17	3.0
	417830	AW504786	Hs.132808	epithelial cell transforming sequen	TM	3.0
	435267	N23797	Hs.110114	ESTs	TM	3.0
40	449722	BE280074	Hs.23960	cyclin B1	TM,cyclin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2	TM,ank	3.0
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297	TM,SNF2_N	3.0
	441794	AW197794	Hs.253338	ESTs	TM,ank	2.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractura	TM,EGF,TB	2.9
45	431130	NM_006103	Hs.2719	epididymis-specific; whey-acidic pr	SS,wap	2.9
	418113	AI272141	Hs.83484	ESTs	TM,HMG_box	2.9
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome	TM,TEA	2.9
	431989	AW972870	Hs.291069	ESTs	SS	2.9
	400284			Estrogen receptor 1	TM,hormone_rec,zf-C4	2.9
50	438578	AA811244	Hs.164168	ESTs	TM,formyl_transf,AIRS,GARS	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	TM,Transglutamin_N	2.8
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 fis, clo	TM	2.8
	431870	AW449902	Hs.105500	ESTs	TM,MHC_IJg	2.8
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276	TM	2.8
55	439777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 (M.mus	TM	2.8
	451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	2.8
	433326	AI379486	Hs.159430	ESTs	TM	2.8
	448221	BE622615		gb:601440775T1 NIH_MGC_72 Homo sapi	TM	2.8
	448141	AI471598	Hs.197631	ESTs	TM,bZIP	2.8
60	456311	AA225632	Hs.190016	ESTs	TM,Sec7	2.8
	405454			predicted exon	TM	2.8
	459287	AL078369		gb:DKFZp564G2378_r1 564 (synonym: h	TM	2.8
	438935	H40665	Hs.31584	ESTs	TM	2.7
	421312	AA824627	Hs.291670	ESTs	TM,G-patch	2.7
65	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	TM,ABC_membrane,ABC_tran	2.7
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clo	TM	2.7
	417856	AA210704	Hs.190465	ESTs	SS,sushi	2.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	2.7
	448089	AI467945	Hs.173696	ESTs	SS,TM	2.6
70	446643	AA194417	Hs.282060	ESTs	TM,ClaI_adaptor_s	2.6
	456671	AB011142	Hs.114293	KIAA0570 gene product	TM	2.6
	457256	AA459443	Hs.231816	ESTs	SS	2.6
	438986	AF085888	Hs.269307	ESTs	TM,Spln-Ssty	2.5
	435313	AI769400	Hs.189729	ESTs	TM,MBD	2.5
75	417351	T90278	Hs.15049	ESTs	TM,CH	2.5
	412198	AA937111	Hs.69165	ESTs	TM	2.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	TM,ubiquitin	2.5
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium ph	TM,Na_PL_cotrans	2.5
	418092	R45154	Hs.106604	ESTs	TM,pldnase	2.5
80	410008	AA079552		gb:zm20h12.s1 Stralagene pancreas (TM,FG-GAP	2.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH1_LWEQ	2.5
	431974	AW972689	Hs.200934	ESTs	TM,bZIP	2.5
	438209	AL120659	Hs.6111	KIAA0307 gene product	TM,HUHPAS	2.5
	447578	AA912347	Hs.136585	ESTs	TM	2.5
	414812	X72755	Hs.77367	monokine induced by gamma interfero	SS,IL8	2.5
	421515	Y11339	Hs.105352	GaINac alpha-2, 6-sialyltransferase	TM,Glyco_transf_29	2.4
	416402	NM_000715	Hs.1012	complement component 4-binding prot	TM,sushi	2.4

	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HU	TM	2.4
	426242	H55709	Hs.2250	leukemia inhibitory factor (chole	SS,LIF_OSM	2.4
	417693	AW959741	Hs.40368	adaptor-related protein complex 1,	TM,Cla1_adaptor_6	2.4
	426679	AA431765		gbzw80c03.s1 Soares_testis_NHT Hom	TM,HECT	2.4
5	436311	AA708958	Hs.168732	ESTs	TM	2.4
	426920	AA393351	Hs.132121	ESTs	TM	2.4
	426698	AA394104	Hs.97489	ESTs	TM	2.4
	443426	AF098158	Hs.9329	Homo sapiens mRNA for fls353, compl	TM	2.4
	406815	AA833930	Hs.268036	IRNA isopentenylpyrophosphate trans	TM,IPPT	2.4
10	434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 a	TM	2.3
	432441	AW292425	Hs.163484	EST	TM,Fork_head	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	TM	2.3
	402298			predicted exon	TM,zf-C2H2,KRAB	2.3
	435542	AA687378	Hs.269533	ESTs	TM	2.3
15	442952	A1743261	Hs.131860	ESTs	TM	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM,CKS	2.3
	429228	AI553633	Hs.104985	ESTs	TM	2.3
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	TM,SH3	2.3
20	447570	AI868315	Hs.99669	ESTs	TM,PHD	2.3
	405032			predicted exon	TM,FMO-like	2.3
	416566	NM_003914	Hs.79378	cyclin A1	TM,cyclin	2.3
	420900	AL045633	Hs.44269	ESTs	TM,FAD_binding_5	2.3
	430563	AA481269	Hs.178381	ESTs	TM,ABC_membrane,p450	2.3
25	417372	T99755	Hs.290814	ESTs	TM	2.3
	449083	AI948808	Hs.191144	ESTs	TM	2.3
	410361	BE391804	Hs.62661	guanylate binding protein 1, interf	TM,GBP	2.3
	434131	AI858275	Hs.143659	ESTs	TM	2.3
	431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	2.3
30	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific	TM	2.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	2.3
	445870	AW410053	Hs.13406	syntaxin 18	TM	2.3
	430639	AW025427	Hs.233552	ESTs	TM,pkinase	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	SS,TM,	2.3
35	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	SS,TM,Cu-oxidase	2.2
	411558	AA102670	Hs.70725	*Human GABA-A receptor p1 subunit m	TM,neur_chan	2.2
	408380	AF123050	Hs.44532	diubiquitin	TM,7tm_3,ANF_receptor	2.2
	403721			predicted exon	TM	2.2
	440711	AA804389	Hs.143511	ESTs	TM,rm	2.2
40	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1	TM,efhand	2.2
	422956	BE545072	Hs.122579	ESTs	TM	2.2
	433482	AI953499	Hs.152617	ESTs	TM	2.2
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fls, cl	TM	2.2
	420777	AA280223	Hs.130865	ESTs	TM	2.2
45	446659	AI335381	Hs.226376	ESTs	TM	2.2
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	TM	2.2
	422282	AF019225	Hs.114309	apolipoprotein L	TM	2.2
	431701	AW935490	Hs.14658	ESTs	TM,Occludin	2.2
	426910	AA470023	Hs.190089	ESTs	TM,MMR_HSR1	2.2
50	405638		Hs.153595	predicted exon	SS,TM,EGF_kd_recept_a	2.2
	401833			predicted exon	TM,lon_trans	2.1
	436679	AI127487	Hs.120451	ESTs, Weakly similar to unnamed pro	TM	2.1
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 pr	TM	2.1
	410664	NM_006033	Hs.65370	lipase, endothelial	SS,TM,Ribosomal_L22,lipase	2.1
55	449378	AW664026	Hs.59892	ESTs	TM	2.1
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	TM	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase	SS,TM,Branch	2.1
	431832	AW276866	Hs.192715	ESTs	TM,Ets,SAM_PNT	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating prot	TM,kinesin_abhydrolase_2	2.1
60	423049	X59373	Hs.188023	ESTs	TM,homeobox	2.1
	427510	Z47542	Hs.179312	small nuclear RNA activating comple	TM	2.1
	418076	RB1388	Hs.6724	ESTs	TM	2.1
	413670	AB000115	Hs.75470	hypothetical protein, expressed in	TM	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	TM	2.1
65	439031	AF075079		gb:Homo sapiens full length insert	TM	2.1
	431060	AF039307	Hs.249171	homeo box A11	TM,homeobox	2.1
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HU	TM	2.1
	419978	NM_001454	Hs.93974	forkhead box J1	TM,Fork_head	2.1
	404535	Z25684	Hs.121483	chloride channel 1, skeletal muscl	SS	2.1
70	445181	AW338972	Hs.147471	ESTs	TM	2.1
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM,Hydrolase	2.1
	443591	AI078281	Hs.179240	ESTs	TM	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN	TM,trypsin	2.1
	424310	AA338648	Hs.50334	ESTs	TM	2.0
75	450193	AI916071	Hs.224623	ESTs	TM,pkinase	2.0
	436009	H57130	Hs.120925	ESTs	SS,TM,Ephrin	2.0
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fls, cl	TM	2.0
	419833	AA251131	Hs.220697	ESTs	TM,WHEP-TRS	2.0
	437655	AA759263	Hs.14041	ESTs	TM,trap	2.0
80	411828	AW161449	Hs.72290	wingless-type MMTV integration site	TM,wnt	2.0
	440052	AI633744	Hs.195648	ESTs	TM,PAC	2.0
	410718	AI920783	Hs.191435	ESTs	TM,SQS_PSY	2.0
	404767			predicted exon	TM	2.0
	447462	AW337214	Hs.158973	ESTs	TM	2.0

5	442255	A1701857	Hs.202388	ESTs	TM	2.0
	410292	AA843087	Hs.124194	ESTs	TM	2.0
	442748	A1016713	Hs.135787	ESTs	TM	2.0
	458760	A1498631	Hs.111334	ferritin, light polypeptide	TM,HCO3_cotransp	2.0
	409789	D11928	Hs.76845	phosphoserine phosphatase-like	TM,Hydrolase	2.0
	401324			predicted exon	TM,myosin_head	2.0
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	SS	2.0
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	TM,zf-CCHC	2.0
10	421379	Y15221	Hs.103982	small inducible cytokine subfamily	SS,TM,IIL8	2.0

TABLE 19B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Pkey	CAT number	Accession
20	409457	1132521_1	AW818081 AW392887 AW514700 AW392881
	410008	116812_1	AA079552 BE142525 BE142527
	422689	219896_1	AW856665 AA315006 AW954733
	426679	294049_1	AA431765 AA432015
	438993	467651_1	AA826995 AA834879 AI926361
25	439031	46798_1	AF075079 H48601 H48795
	448221	75534_-1	BE622615
	454392	116882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1	AW813350 AW816082 AW813476 AW813383
	458154	491768_1	AW816379 AA888282 AA879046 AA879195
30	458861	798085_1	AI630223 AI630470
	459287	977129_1	AL079369 D81804

TABLE 19C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	401324	9863791	Plus	234057-234174
	401517	7677912	Plus	29278-29770
45	401933	3810668	Minus	48725-49057,51864-51955,52424-52589
	402298	6598824	Plus	36758-37953
	402606	9909429	Minus	81747-82094
	403721	7528046	Minus	156647-157366
	403776	7770611	Minus	1414-1513,1624-1756
50	404767	7882827	Minus	23244-23759
	405032	7107731	Minus	131945-132224
	405174	7108030	Minus	102814-103063
	405454	7656675	Plus	133807-134053
55	405609	6757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
	405636	5123990	Plus	66384-66587
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
60	406411	9256407	Plus	7400-7527

Table 20A: 58 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, Uterine Cancer Versus Normal Adult Tissues

Table 20A lists about 56 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g. kinase, peptidase, isomerase, transporters). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
75	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	7tm_1	24.2
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin)	hemopexin	12.3
80	447350	AI375572	Hs.172634	HER4 (c-erb-B4)	kinase	9.8
	420610	AI683183	Hs.99348	distal-less homeobox 5	homeobox	6.2
	405609			predicted exon	Myosin_tail,myosin_head	5.0
	458881	NM_007358	Hs.31016	PHD finger DNA binding protein	PHD	4.4
	410153	BE311926	Hs.16830	Homo sapiens cDNA FLJ12691 fis, clone	NA	4.3

5	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	NA	4.1
	444783	AK001468	Hs.62180	ESTs	PH	4.0
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	HMG_box	3.8
	413472	BE242870	Hs.75379	solute carrier family 1	SDF	3.7
	443613	AI079356	Hs.21807	gbx239b09.s1 Soares_NhHMPu_S1 Homo s	zf-C2H2	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	Peptidase_M10	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF125780 1 re	NA	3.6
	435031	AI632091	Hs.116877	ESTs	RhoGEF,PH	3.3
10	417411	AW500008	Hs.6956	Human DNA sequence from clone RP1-187	NA	3.3
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrola	NA	3.1
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	trypsin,pro_isomerase	3.1
	406400	AA343629	Hs.104570	kalikrein 8 (neurosin/ovasine)	trypsin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	ank	3.0
15	441794	AW197794	Hs.253338	ESTs	ank	2.9
	402373	AL135225	Hs.301855	dopachrome tautomerase (dopachrome de	TEA	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	Transglutamin_N	2.8
	448141	AI471558	Hs.197531	ESTs	bZIP	2.8
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	guanylate_cyc	2.7
20	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	ABC_membrane,ABC_tran	2.7
	448435	BE293439	Hs.182278	calmodulin 2	NA	2.6
	417351	T90278	Hs.15049	ESTs	CH	2.5
	430372	AI206173	Hs.211375	ESTs	SH3,efhand,C2,PH	2.5
	431974	AW972689	Hs.200934	ESTs	bZIP	2.5
25	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hy	ank	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1	Glyco_transf_29	2.4
	403095			predicted exon	homeobox,PAX	2.4
	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate transfe	IPPT	2.4
	435615	Y15065	Hs.4975	potassium voltage-gated channel	ion_channel	2.3
30	402298			predicted exon	zf-C2H2,KRAB	2.3
	418203	X54942	Hs.83758	CDC28 protein kinase 2	CKS	2.3
	430563	AA481269	Hs.178381	ESTs	ABC_membrane,p450	2.3
	447570	AI668315	Hs.99669	ESTs	PHD	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamil	NA	2.3
35	415539	AI733881	Hs.72472	BMPR-Ib;	bone morphogenetic protein NA	2.2
	422095	AI668872	Hs.288966	ceruloplasmin (ferroxidase)	Cu-oxidase	2.2
	408380	AF123050	Hs.44532	diubiquitin	ANF_receptor,sushi,7tm_1	2.2
	440711	AA904389	Hs.143511	ESTs	rm	2.2
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-	efhand	2.2
40	418506	AA084248	Hs.85339	G protein-coupled receptor 39	NA	2.2
	410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22, lipase, PLAT	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1	Branch	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein	kinesin,PHD,abhydrolase_2	2.1
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-dom	rm,NTF2	2.1
45	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscle	NA	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2	trypsin	2.1
	446342	BE298665	Hs.14846	Cationic amino acid transporter (ecto	NA	2.0
	458760	AI498631	Hs.111334	ferritin, light polypeptide	HCO3_cotransp,zf-C3HC4	2.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	2.0
50	401324			predicted exon	myosin_head	2.0

TABLE 20B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT number	Accession
443613	575391_1	AI079356 W23287
458861	798085_1	AI630223 AI630470

TABLE 20C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
402298	6598824	Plus	36758-37953
403095	8954339	Plus	150025-150240,151564-151690
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 21A: 270 Up-Regulated Genes, Uterine Cancer Versus Normal Uterus

Table 21A lists about 270 genes up-regulated in uterine cancer compared to normal uterus. These were selected as for Table 18A, except that the ratio was greater than or equal to 5.0, and the denominator was the median value for six non-malignant uterine specimens.

Pkey: Unique Eos probe/identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor vs. normal tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	449034	AI624049		gb:ts41a09.x1 NCL_CGAP_U11 Homo sapiens	55.7
	435094	AI560129	Hs.277523	EST	45.2
15	438461	AW075485	Hs.286049	phosphoserine aminotransferase	19.5
	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel	15.6
	441633	AW958544	Hs.112242	ESTs	15.2
	429183	AB014604	Hs.197955	KIAA0704 protein	14.6
20	436775	AA731111	Hs.291891	ESTs	14.3
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	14.0
	446921	AB012113	Hs.16530	CC chemokine SCYA18 (MIP-4) (PARC)	13.0
	413753	U17760	Hs.301103	Laminin, beta 3 (niclin (125kD), kalinin	12.9
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, l	12.2
25	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	12.0
	453891	AB037751	Hs.35353	Homo sapiens mRNA full length insert cDN	11.7
	425196	AL037915	Hs.155097	carbonic anhydrase II	11.4
	444863	AW384082	Hs.301323	ESTs	11.3
	449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	11.1
30	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	10.9
	449801	AA477355	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	10.3
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.3
	414812	X72755	Hs.77367	monokine induced by gamma interferon	10.2
	410381	BE391804	Hs.62661	guanylate binding protein 1, interferon-	10.1
35	423645	AI215632	Hs.147487	ESTs	10.1
	442438	AA995998		gb:os26b03.s1 NCL_CGAP_Kid5 Homo sapiens	10.0
	415786	AW419196	Hs.257924	ESTs	10.0
	458017	AA813426	Hs.192034	ESTs, Weakly similar to KIAA0705 protein	10.0
	435525	AI831297	Hs.123310	ESTs	9.9
40	413335	AI613318	Hs.48442	ESTs	9.7
	420297	AI628272	Hs.88323	ESTs	9.6
	452799	AI948829	Hs.213786	ESTs	9.6
	434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	9.4
	408243	Y00787	Hs.624	interleukin 8	9.3
45	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	9.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	9.2
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	9.2
	443830	AI142095	Hs.143273	ESTs	9.1
	442547	AA306997	Hs.268362	ESTs, Weakly similar to hypothetical pro	9.0
50	421633	AF121860	Hs.106260	sorting nexin 10	9.0
	403381			0	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
	440500	AA972165	Hs.150308	ESTs	8.7
	436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulat	8.7
55	431668	AW969610	Hs.151179	ESTs	8.7
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	8.7
	424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino	8.6
	425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	8.6
	428862	NM_000346	Hs.2316	SRY (sex-determining region Y)-box 9	8.5
60	438986	AF085888	Hs.269307	ESTs	8.4
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	8.4
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	8.3
	415992	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	8.2
	431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, co	8.2
65	409865	AW502208		gb:U1-HF-BR0p-aju-e-09-0-UI.r1 NIH_MGC_5	8.0
	448158	AI627292	Hs.190877	ESTs	8.0
	401519			0	7.9
	441730	AI243276	Hs.149017	ESTs	7.9
	432441	AW292425	Hs.163484	EST	7.8
70	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	7.8
	438424	AI912498	Hs.25895	ESTs, Weakly similar to PI-3 kinase [Hs	7.8
	447342	AI199258	Hs.19322	ESTs; Weakly similar to [Hs] ALU SUBFAM	7.7
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	7.7
	423081	AF262992	Hs.123159	sperm associated antigen 4	7.8
75	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	7.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.6
	459142	AI903396		gb:RC-BT029-120199-219_1 BT029 Homo sapi	7.5
	411094	BE066142		gb:CM4-BT0320-221199-047-g10 BT0320 Homo	7.5
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	7.5
80	452607	AI160029	Hs.61438	ESTs	7.5
	443171	BE281128	Hs.9030	TONDU	7.4
	459081	W07808		gb:zb03a12.r1 Soares_fetal_Jung_NbHL19W	7.4
	431195	AA503083	Hs.79742	ESTs	7.4
	444459	AI680624	Hs.148576	ESTs	7.4

5	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	7.3
	414918	AI219207	Hs.72222	Hypothetical protein FLJ13459	7.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	7.3
	448865	R35027		gb:yg60g02.r1 Soares Infant brain 1N18 H	7.3
	409219	AA393383	Hs.133331	ESTs	7.3
10	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	7.2
	403485			0	7.2
	408350	AW183350	Hs.250127	ESTs	7.2
	445873	AA250970	Hs.251948	Homo sapiens cDNA: FLJ23107 fis, clone L	7.1
	400995			0	7.1
15	406086			0	7.1
	403378			0	7.0
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	7.0
	422038	R39098	Hs.192028	ESTs	7.0
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in card	6.9
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.9
	427494	AI628365	Hs.130412	ESTs, Weakly similar to sre-2 [C.elegans	6.9
	429272	W25140	Hs.110667	ESTs	6.9
	427258	AA400091	Hs.39421	ESTs	6.9
	449309	AW589823	Hs.224189	ESTs	6.9
25	400104			0	6.9
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	6.8
	404767			0	6.8
	406690	M29540	Hs.220529	CEA (carcinoembryonic antigen-related ce	6.8
	439750	AL359053	Hs.57664	ESTs	6.8
30	403127	AI904493	Hs.99890	polymerase (DNA directed), delta 1, cata	6.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.8
	425858	AA364923		gb:EST75602 Pineal gland II Homo sapiens	6.8
	421712	AK000140	Hs.107139	hypothetical protein	6.7
	456903	D49441	Hs.155981	mesothelin	6.7
35	414564	AA164803	Hs.71994	ESTs	6.7
	457942	AW665665	Hs.153034	ESTs	6.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.7
	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.7
	445537	AJ245671	Hs.12844	EGF-like domain; multiple 6	6.7
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	6.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.6
	410664	NM_006033	Hs.65370	lipase, endothelial	6.6
	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibito	6.6
	406400			kallikrein 8 (neuropsin/ovasin)	6.6
45	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	6.5
	441460	AI962478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN I	6.5
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta pol	6.5
	424349	AF141289	Hs.145550	solute carrier family 7 (cationic amino	6.5
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.4
50	445258	AI635931	Hs.147613	ESTs	6.4
	456032	AW957446	Hs.301711	ESTs	6.4
	404727			0	6.4
	422810	AA317400		gb:EST19374 Retina II Homo sapiens cDNA	6.4
	440044	AW665167	Hs.259563	EST	6.4
55	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	6.4
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	6.4
	422170	AI791949	Hs.112432	anti-Müllerian hormone	6.4
	449611	AI970394	Hs.197075	ESTs	6.4
	402539	AW502761	Hs.30909	KIAA0430 gene product	6.3
60	456983	AI081687	Hs.170225	thymopoietin	6.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.3
	457887	AI240007	Hs.148812	ESTs	6.3
	431765	AF124249	Hs.268541	novel SH2-containing protein 1	6.3
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR	6.2
65	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ22389 fis, clone H	6.2
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	6.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	6.2
	413982	BE503035	Hs.279193	ESTs	6.2
	458091	AF150286		gb:AF150286 Human mRNA from cd34+ stem c	6.2
70	402104			0	6.2
	428771	AB028992	Hs.193143	KIAA1069 protein	6.1
	435313	AI769400	Hs.189729	ESTs	6.1
	441668	AI188346	Hs.301776	ESTs	6.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.1
75	427308	D26067	Hs.174905	KIAA0033 protein	6.1
	423069	W15613	Hs.1613	adenosine A2a receptor	6.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.1
	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	6.1
	449409	AI650935	Hs.301694	ESTs	6.1
80	400855			0	6.1
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192 Homo	6.0
	414869	AA157291	Hs.72163	ESTs	6.0
	439662	H97552	Hs.269060	ESTs	6.0
	445181	AW338972	Hs.147471	ESTs	6.0
	437129	AL049327		gb:Homo sapiens mRNA; cDNA DKFZp564E016	6.0
	440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0

	422355	AW403724	Hs.140	Immunoglobulin heavy constant gamma 3	5.9
	405291			0	5.9
	432113	AA935065	Hs.152385	ESTs	5.9
	441238	AA923489	Hs.130432	ESTs	5.9
5	424418	BE503432	Hs.66170	HSKM-B protein	5.9
	453028	AB006532	Hs.31442	RecQ protein-like 4	5.8
	407137	T97307	Hs.199067	EST	5.8
	443462	AJ064690	Hs.171176	ESTs	5.8
10	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens c	5.8
	456311	AA225632	Hs.190016	ESTs	5.8
	446501	AJ302616	Hs.150819	ESTs	5.8
	433921	AA618174		gb:uq14/01.s1 NCI_CGAP_Thy1 Homo sapiens	5.8
	409615	AW444861		gb:UH-H-BI3-ajz-a-04-0-UI.s1 NCI_CGAP_Su	5.8
	459360	BE384526		gb:601277913F1 NIH_MGC_20 Homo sapiens c	5.8
15	403824			0	5.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	5.8
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabknes	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
	426465	AI758948		gb:ty16107.x1 NCI_CGAP_UI3 Homo sapiens	5.7
20	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780.1 refn	5.7
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.7
	405392			0	5.7
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	5.7
25	449796	AA004321	Hs.194397	ESTs	5.7
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.7
	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3	5.7
	404220			0	5.6
	420973	AA743415	Hs.291368	ESTs	5.6
30	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	5.6
	442549	AI751601	Hs.8375	TNF receptor-associated factor 4	5.6
	409867	AW502161		gb:UH-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_5	5.6
	451110	AI955040	Hs.301584	ESTs	5.6
	418216	AA662240	Hs.283099	AF15q14 protein	5.6
35	411897	AW875066		gb:RC6-PT0001-180100-021-F04 PT0001 Homo	5.6
	456161	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	5.6
	406536			0	5.6
	432540	AB21517	Hs.105866	ESTs	5.6
	446315	NM_016293	Hs.14770	bridging Integrator 2	5.6
40	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	5.6
	406685	M18728		gb:Human nonspecific crossreacting antiq	5.5
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	5.5
	402430			0	5.5
45	446704	AI337228	Hs.197083	ESTs	5.5
	435282	AA677428	Hs.189731	ESTs	5.5
	426062	N57014	Hs.44013	ESTs	5.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	5.5
	456002	AI828729	Hs.191450	ESTs, Weakly similar to type II membrane	5.5
50	409613	AW444816	Hs.171537	Homo sapiens cDNA: FLJ21596 fis, clone C	5.5
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	5.5
	434609	R76593		gb:y80c11.r1 Soares placenta Nb2HP Homo	5.5
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	5.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	5.4
55	400379	NM_018432	Hs.283076	Homo sapiens ovarian cancer related prot	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
	432119	T80289		gb:yd03h04.r1 Soares infant brain 1N1B H	5.4
	417175	R44558	Hs.94002	ESTs	5.4
	445774	AI254165	Hs.145504	ESTs	5.4
60	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	5.4
	411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	5.4
	445262	AW205650	Hs.253503	ESTs	5.4
	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cD	5.4
	434756	AA827650	Hs.259307	ESTs	5.3
65	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	5.3
	439949	AW979197	Hs.292073	ESTs	5.3
	414995	C18200		gb:C18200 Human placenta cDNA (TFujhwara	5.3
	428071	AF212848	Hs.182339	transcription factor ESE-3B	5.3
	412323	AW937143		gb:PM1-DT0041-281299-001-r01 DT0041 Homo	5.3
70	434283	AW235341	Hs.58715	mouse thiamin pyrophosphokinase homolog	5.3
	447798	AA25049	Hs.119629	ESTs, Moderately similar to ALU1_HUMAN A	5.3
	401723			0	5.3
	406270			0	5.3
	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	5.3
75	415757	AA830854	Hs.187810	ESTs	5.3
	430051	AA64611	Hs.52515	transducin (beta)-like 2	5.2
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-like	5.2
	455953	AI907673		gb:IL-BT152-080399-004 BT152 Homo sapien	5.2
	449009	BE044755	Hs.224812	ESTs	5.2
80	424001	W67883	Hs.137476	KIAA1051 protein	5.2
	409479	BE163800	Hs.136912	ESTs	5.2
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	5.2
	435928	H64345	Hs.183981	ESTs	5.2
	447397	BE247676	Hs.18442	E-1 enzyme	5.2

5	449183	AW445022	Hs.196985	Homo sapiens cDNA: FLJ21135 fis, clone C	5.2
	410146	AW592655		gb:U45112x1 Soares_NFL_T_GBC_S1 Homo s	5.2
	458164	AI208666	Hs.192081	ESTs	5.2
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	5.1
	439509	AF086332	Hs.58314	ESTs	5.1
	422569	BE552132	Hs.118442	cyclin C	5.1
	430664	AW969834		gb:EST381912 MAGE resequences, MAGK Homo	5.1
	411231	AW833501		gb:QV4-TT0008-091199-025-e09 TT0008 Homo	5.1
10	412194	AW900282	Hs.115412	Homo sapiens cDNA FLJ13881 fis, clone TH	5.1
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.1
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.1
	433279	AW971745		gb:EST383834 MAGE resequences, MAGL Homo	5.1
	454112	NM_000885	Hs.301806	ESTs	5.1
15	423261	Z43509		gb:HSC1EA031 normalized infant brain cDN	5.1
	434084	AI061640	Hs.192768	hypothetical protein PRO1905	5.1
	446115	AI733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	5.1
	416719	H79731		gb:yu81f112r1 Soares fetal liver spleen	5.1
	421462	AF016495	Hs.104624	aquaporin 9	5.1
20	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	5.1
	403383			0	5.1
	430832	AI073913	Hs.100686	ESTs, Weakly similar to secreted cement	5.1
	435070	AK000073		gb:Homo sapiens cDNA FLJ20066 fis, clone	5.0
	416969	AI815443	Hs.283404	organic cation transporter	5.0
25	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
	439031	AF075079		gb:Homo sapiens full length insert cDNA	5.0
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	5.0
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	5.0
30	449986	AW864502		gb:PM4-SN0016-120400-004-b12 SN0016 Homo	5.0
	418717	AI334430	Hs.86984	ESTs	5.0
	438769	AA830684	Hs.163426	ESTs	5.0
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1	5.0
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase	5.0

35 TABLE 21B

Pkey: Unique Eos probaset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

40	Pkey	CAT number	Accession
45	409615	1143425_1	AW444861 BE074994 BE074968 BE074992
	409865	1156518_1	AW502208 AW502366 AW502148
	409867	1156530_1	AW502161 AW502587 AW502345
	410148	1178974_1	AW592655 R05927 R06916
	411094	1231982_1	BE066142 AW817074
	411231	1236356_1	AW833501 AW833506 AW833722 AW833332 AW833509 AW833511 AW833767 AW833339
	411426	1245515_1	BE141714 AW845993 AW845989
50	411897	1264907_1	AW875066 AW875079 AW875075 AW875062 AW875061 AW875074
	412323	1288770_1	AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173 AW937159 AW937139 AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179 AW937156 AW937140 AW937135 AW937170
55	412517	130281_1	BE271584 AA112511
	414484	1452830_1	BE314385
	414539	1460320_1	BE379046 BE395459
	414995	1511736_1	C18200 D78681 T82025
	416719	1611345_1	H79731 H79732
60	422731	220507_1	AL138411 AL138412 AA315860
	422810	221630_1	AA317400 AA434584
	423261	226553_1	Z43509 H09001 AA375202 AW954383
	425858	257265_1	AA364923 AW963483 BE182774 C21461
	426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933
65	430664	321423_1	AW869834 AA528493 AA483165 AW969842
	432119	34170_1	T80289 AF052168
	433279	381800_1	AW971745 AA581359 AA581358
	433921	377350_1	AA618174 AI114549 R36464 R36465
	434609	38950_1	R76593 AF147390 R76594
70	436070	41426_1	AK000073 AA380183 AA380181 AW963533
	437129	43343_1	AL049327 AA847105
	439031	46798_1	AF075079 H48601 H48795
	442438	542469_1	AA95998 AI916584 R61781 T77332 F07756 F08149 F07647
	448865	78535_1	R35027 R12034 BE407120
75	449034	794817_1	AI624049 AW117770 AI858360
	449986	821463_1	AW864502 AW884369 AI678780
	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1	AW813350 AW816082 AW813476 AW813383
	455604	1337197_1	BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169
80	458091	472385_1	AF150286 AA835857
	459081	889426_1	W07808 AI822066
	459142	918906_1	AI903396 AI903361 AI903360

TABLE 21C

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
10	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
15	400855	1931571	Minus	17801-18228
	400995	8099094	Plus	141186-141601
	401519	6649315	Plus	157315-157950
	401723	7656694	Plus	147273-147503
20	402104	8119072	Plus	122409-122600
	402430	9796372	Minus	62382-62552
	403378	9438244	Minus	44264-44443
	403381	9438267	Minus	26009-26178
25	403383	9438267	Minus	119837-121197
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403824	9798468	Plus	473-887
	404220	6706820	Plus	46107-46439
30	404727	8081050	Plus	115534-115747
	404767	7882827	Minus	23244-23759
	405291	3845420	Plus	19999-20473,20672-21036,21147-21285,21378-21667
	405392	6624069	Minus	116167-116289,118879-119030
	406086	7107817	Plus	9418-9573
	406270	7534217	Plus	13136-13591
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	406536	7711478	Plus	25655-25782

TABLE 22A: 430 SIGNIFICANTLY DOWN-REGULATED GENES, UTERINE CANCER VERSUS NORMAL UTERUS

35 Table 22A lists about 430 genes significantly down-regulated in uterine cancer compared to normal uterus. These were selected as for Table 21A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 14 (i.e. 14-fold down-regulated in tumor vs. normal uterus).

40	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
45	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of tumor vs. normal tissue		
	Pkey	ExAccn	UnigeneID	Unigene Title
50	414063	H26904	Hs.75736	apolipoprotein D
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A, member 14
	407815	AW373860	Hs.301716	ESTs
	452547	AA335295	Hs.74120	adipose specific 2
55	415165	AW887604	Hs.78065	complement component 7
	453655	AW960427	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE
	429350	AJ754534	Hs.131987	ESTs
	407228	M25079	Hs.155376	hemoglobin, beta
60	425869	AA524547	Hs.160318	FXD domain-containing ion transport regulator
	416585	X54162	Hs.79386	telomodin 1 (smooth muscle)
	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (from c
	417542	J04129	Hs.82269	progesterone-associated endometrial protein (p
65	412295	AW088826	Hs.22971	ESTs
	421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (from c
	429707	W76631	Hs.211819	matrix metalloproteinase 23B
70	416950	AL049798	Hs.80552	dermatopontin
	408221	AA912183	Hs.47447	ESTs
	406791	AJ220684	Hs.272572	hemoglobin, alpha 2
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome
75	407938	AA905097	Hs.85050	phospholamban
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)
	412524	AA417813	Hs.11177	ESTs
	452426	AJ904823	Hs.31297	Homo sapiens cDNA: FLJ23001 fis, clone LNG002
80	414290	AJ568801	Hs.71721	ESTs
	439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone HEP018
	400258		Hs.79064	deoxyhypusine synthase
	414807	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)
	410023	AB017169	Hs.57929	sfil (Drosophila) homolog 3
	407663	NM_016429	Hs.37482	COP22 for nonclathrin coat protein zeta-COP
	410286	AJ739159	Hs.61898	DKFZP586N2124 protein
	418986	AJ123555	Hs.81798	ESTs
	409060	AJ815867	Hs.50130	necdin (mouse) homolog
	435569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)
	420674	NM_000055	Hs.1327	butyrylcholinesterase
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, member
	450810	BE207588	Hs.25511	transforming growth factor beta 1 induced tra
	438150	AA037534	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE

5	430468	NM_004673	Hs.130699	ESTs	31.5
	453060	AW294092	Hs.21594	ESTs	31.3
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular	30.8
	422126	AW973784	Hs.112028	Misshapen/NIK-related kinase	30.5
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform	30.3
10	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDNA clo	30.3
	402520				29.9
	418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase receptor	29.7
	443906	AA348031	Hs.7913	ESTs	29.7
	450958	AL137669	Hs.25700	Homo sapiens mRNA; cDNA DKFZp434M0435 (from c	29.4
15	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-type 12-	29.4
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob dise	29.4
	429507	NM_003102	Hs.2420	superoxide dismutase 3, extracellular	29.2
	400545				29.1
	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	29.1
20	429942	AI338993	Hs.134535	ESTs	28.9
	438303	AB028998	Hs.6147	KIAA1075 protein	28.7
	419971	AA400027	Hs.296234	ESTs, Highly similar to mitogen-activated pro	28.7
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	28.7
	452877	AI250789	Hs.32478	ESTs	28.6
25	412442	AI983730	Hs.26530	serum deprivation response (phosphatidylerin	28.6
	424378	W28020	Hs.184367	GTPase activating protein-like	28.6
	421823	N40850	Hs.28625	ESTs	27.9
	447786	BE620810	Hs.39619	hypothetical protein LOC57333	27.6
	400023			AFX control: 18S ribosomal RNA	27.5
30	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	27.2
	414134	X60188	Hs.861	mitogen-activated protein kinase 3	27.1
	428451	AW970451	Hs.98570	ESTs	26.9
	435520	AA297990	Hs.9315	HNOEL-iso protein	26.6
	437179	AA393508	Hs.171409	serologically defined colon cancer antigen 8	26.4
35	441481	AA935303	Hs.270553	ESTs	26.0
	450227	BE388192	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone COL001	25.6
	403731				25.5
	452814	AI092790	Hs.65016	hypothetical protein FLJ21935	25.5
	410036	R57171	Hs.57975	calsequestrin 2, cardiac muscle	25.5
40	416854	H40164	Hs.80296	Purkinje cell protein 4	25.4
	418421	R58620	Hs.85050	phospholamban	25.4
	407000	U12139		gb:Human alpha1(XI) collagen (COL11A1) gene,	25.3
	421803	NM_012205	Hs.108441	3-hydroxyanthranilate 3,4-dioxygenase	25.3
	445613	BE550889	Hs.158491	ESTs	25.1
45	432302	AA345857	Hs.274307	KIAA1442 protein	24.8
	420796	L34355	Hs.99331	sarcoglycan, alpha (50kD dystrophin-associata	24.8
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL021	24.7
	417302	BE245812	Hs.8941	ESTs	24.6
	421913	AI934355	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	24.6
50	440130	AI083899	Hs.157527	ESTs	24.5
	431967	AJ243653	Hs.283404	organic cation transporter	24.5
	424580	AA446539	Hs.35092	ESTs	24.4
	406907	Z25427		gb:H.sapiens protein-serine/threonine kinase	24.2
	443745	AB039670	Hs.8728	ALEX1 protein	24.1
55	429101	AW452174	Hs.173780	ESTs	23.5
	410691	AW239226	Hs.65450	reticulon 4	23.4
	408853	AW291484	Hs.254967	ESTs	23.3
	407979	AA046306	Hs.62827	ESTs	23.1
	446619	AJ867182	Hs.202255	ESTs	22.8
60	424585	AA464840		gb:zx43h11.1.r1 Soares_total_fetus_Nb2HF8_9w Ho	22.7
	407891	AA486620	Hs.41135	Endomucin 2	22.6
	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma virus (FB	22.5
	426990	AL044315	Hs.173094	Homo sapiens mRNA; cDNA DKFZp564H142 (from cl	22.5
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelial cell)	22.1
65	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like	22.0
	423690	AA329648	Hs.23804	ESTs	22.0
	402865				21.9
	417387	AW021102	Hs.21509	ESTs	21.9
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	21.9
70	459722			Homo sapiens cDNA: FLJ23449 fis, clone HSI058	21.8
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	21.8
	402195				21.7
	418213	AW978753	Hs.127327	ESTs	21.6
	440274	R24595	Hs.7122	scrapie responsive protein 1	21.6
75	455818	AJ733747		gb:zn86d04.y5 Stratagene lung carcinoma 93721	21.4
	420861	AI039044	Hs.88827	Homo sapiens mRNA for FLJ00033 protein, parti	21.4
	405228				21.3
	441292	AF131218	Hs.7765	chromosome 16 open reading frame 5	21.3
	432553	AA553334	Hs.211095	ESTs	21.3
80	417098	AB017365	Hs.173859	frizzled (Drosophila) homolog 7	21.2
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	21.2
	405313				21.1
	410243	D83402	Hs.289008	ESTs, Weakly similar to alternatively spliced	21.1
	413186	AU077141	Hs.75231	solute carrier family 16 (monocarboxylic acid	21.1
	425954	AK000533	Hs.164476	hypothetical protein FLJ20626	21.0
	421770	AA374192	Hs.108124	ribosomal protein L41	21.0
	435265	AA779958	Hs.185932	ESTs	20.8

	430038	AL050284	Hs.227782	DKFZP586M1019 protein	20.7
	430233	AW367802	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (from c	20.7
	436130	AA341497	Hs.31408	ESTs	20.7
5	434843	R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary prol	20.7
	429303	AW137635	Hs.44238	ESTs	20.6
	442422	AI344415	Hs.156082	ESTs	20.5
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific prot	20.5
	435869	AF255910	Hs.54650	ESTs, Weakly similar to (define not availabl	20.5
10	447384	AI377221	Hs.40528	ESTs	20.5
	440610	AI733098	Hs.130800	ESTs	20.5
	445806	AL137516	Hs.13323	hypothetical protein FLJ22059	20.4
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	20.4
	436467	AW450278	Hs.91681	ESTs	20.3
15	440191	AI990417	Hs.116107	Homo sapiens genomic DNA, chromosome 21q, sec	20.2
	417511	AL049176	Hs.82223	chordin-like	20.2
	406976	M50299		gb:Human alpha-1 collagen type II gene, exons	20.1
	443547	AW271273	Hs.23767	ESTs	20.1
	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo sapi	20.1
20	419313	AA843387	Hs.87279	ESTs	20.1
	408322	AW181985	Hs.249986	ESTs	20.0
	448422	BE263813		gb:601194177F1 NIH_MGC_7 Homo sapiens cDNA cl	20.0
	403121				19.9
	424198	AB029010	Hs.143026	KIAA1087 protein	19.9
25	459080	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein D (AU	19.9
	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [H.sapiens	19.9
	445029	AF196481	Hs.12256	midline 2	19.9
	424382	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from c	19.8
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal mono	19.7
30	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYDROXY	19.6
	435891	AW249394	Hs.5002	copper chaperone for superoxide dismutase	19.6
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	19.6
	400637				19.5
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (car	19.4
35	430310	U60115	Hs.239069	four and a half LIM domains 1	19.4
	402741				19.4
	401703				19.3
	409229	H60333	Hs.251928	nuclear pore complex interacting protein	19.3
	453856	AA804789	Hs.19447	Homo sapiens mRNA for FLJ00106 protein, parti	19.3
40	430342	NM_005938	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (l	19.3
	404033				19.2
	411939	AI365585	Hs.146246	ESTs	19.2
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	19.1
	452669	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced	19.1
45	439698	AW779654	Hs.55876	ESTs	18.9
	416253	BE250659	Hs.15463	ESTs	18.9
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo sapien	18.9
	408877	AA479033	Hs.130315	ESTs	18.9
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24kD	18.9
50	417054	AF017050	Hs.174151	aldehyde oxidase 1	18.8
	404654				18.8
	420174	AI824144	Hs.23912	ESTs	18.8
	400626				18.7
	406150				18.7
55	457835	BE256338	Hs.192375	ESTs, Highly similar to dJ127B20.3 [H.sapiens	18.6
	420105	AW015571	Hs.32244	ESTs	18.6
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S. cere	18.5
	423282	AL137563	Hs.126378	putative ABC transporter	18.5
	424097	M13981	Hs.1734	Inhibin, alpha	18.5
60	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from c	18.5
	427605	NM_000997	Hs.179779	ribosomal protein L37	18.4
	406535				18.4
	418947	W52990	Hs.22860	ESTs	18.4
	414323	NM_014759	Hs.239500	KIAA0273 gene product	18.3
65	457111	AA482027	Hs.142569	ESTs	18.3
	418373	AW760770	Hs.84344	CGI-135 protein	18.3
	424461	D83542	Hs.148090	cadherin 15, M-cadherin (myotubule)	18.2
	451565	NM_000897	Hs.456	leukotriene C4 synthase	18.2
	407751	BE276096	Hs.38205	from HeLa cyclin-dependent kinase 2 interacti	18.2
70	432031	AF039196	Hs.284126	hairless (mouse) homolog	18.1
	404608	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	18.1
	451962	AW078832	Hs.226806	ESTs	18.1
	424100	AI793080	Hs.123525	ESTs, Weakly similar to NGAL RAT NEUTROPHIL G	18.1
	451509	AI969529	Hs.171637	Homo sapiens cDNA: FLJ21937 fis, clone HEP044	18.1
75	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker protein	18.0
	429924	W39693	Hs.226138	Homo sapiens mRNA; cDNA DKFZp566H2448 (from c	17.9
	423780	AA352013		gb:EST59935 Infant brain Homo sapiens cDNA 5'	17.9
	427030	AA397600	Hs.97531	ESTs	17.9
	439872	T81058		gb:yd26c08.r1 Scores fetal liver spleen 1NFLS	17.9
80	407836	T78340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone CAE112	17.9
	451427	AI091441	Hs.26401	tumor necrosis factor (ligand) superfamily, m	17.9
	424462	AU076866	Hs.148101	serum constituent protein	17.9
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidylerin	17.8
	422319	AW403342	Hs.115232	splicing factor 3a, subunit 2, 66kD	17.8

	400489				17.8
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein, parti	17.8
	449282	AL048056	Hs.23437	Homo sapiens cDNA FLJ13555 fis, clone PLACE10	17.7
5	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (from c	17.7
	429790	AK001352	Hs.221737	hypothetical protein FLJ10490	17.7
	422796	AW897265		gb:CA0-NN0057-150400-335-e04 NN0057 Homo sapi	17.7
	427980	AA418305		gb:zv96g05.s1 Soares_NhHMPu_S1 Homo sapiens c	17.6
	409543	AW410200		gb:th05b12.x1 NIH_MGC_17 Homo sapiens cDNA cl	17.6
10	440206	AI762232	Hs.46794	ESTs	17.6
	455904	BE156173		gb:QV0-HT0367-201299-079-a02 HT0367 Homo sapi	17.5
	427707	NM_005578	Hs.180398	LIM domain-containing preferred translocation	17.5
	437140	AA312799	Hs.283689	activator of CREM in testis	17.5
	417637	AA204969	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEM8810	17.5
15	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor type,	17.4
	417808	AF177909	Hs.12828	twety (Drosophila) homolog 1	17.4
	426232	Z70024	Hs.168157	nuclear transcription factor Y, gamma	17.4
	440747	AW297226	Hs.137840	ESTs, Moderately similar to SIX1_HUMAN HOMEOB	17.4
	415307	F05232	Hs.27495	prostate cancer associated protein 7	17.3
20	407049	X72632		(NONE)	17.3
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT2RM40	17.3
	411085	AF022991	Hs.68398	period (Drosophila) homolog 1	17.3
	443104	AA088470	Hs.83135	p53-responsive gene 6	17.2
	424106	AA412442	Hs.98132	ESTs	17.2
25	446716	AA436575	Hs.16602	ESTs	17.1
	448677	AI560769	Hs.227051	ESTs	17.0
	434919	AI821740	Hs.116531	ESTs	17.0
	401171	AA360954	Hs.27268	Homo sapiens mRNA; cDNA DKFZp564N196 (from cl	17.0
	456804	AI421645	Hs.139851	caveolin 2	17.0
30	453621	AW749983		gb:QV3-BT0537-280100-070-e04 BT0537 Homo sapi	16.9
	413419	BE063686	Hs.48938	Homo sapiens cDNA: FLJ21802 fis, clone HEP007	16.9
	426515	BE394222	Hs.231444	ESTs	16.9
	428937	T82221	Hs.56729	lymphocyte-specific protein 1	16.9
	424562	AI420859	Hs.150557	basic transcription element binding protein 1	16.9
35	444655	AF088886	Hs.11590	cathepsin F	16.9
	447424	AI681105	Hs.181641	ESTs	16.8
	425439	D38024	Hs.157425	double homeobox, 2	16.8
	446707	AI591214	Hs.156336	ESTs	16.8
	405324				16.8
40	434340	AI193043	Hs.128685	ESTs	16.8
	422942	AF054839	Hs.122540	telraspan 2	16.8
	421820	AW662990	Hs.108675	heme-binding protein	16.8
	420037	BE299598	Hs.135569	ESTs, Weakly similar to NEUROD (H.sapiens)	16.7
	428818	AI131291	Hs.98866	ESTs	16.7
45	426485	NM_006207	Hs.170040	platelet-derived growth factor receptor-like	16.7
	404947				16.6
	412677	AW029608	Hs.17384	ESTs	16.6
	401551				16.6
	408053	AW139474	Hs.246862	ESTs	16.6
50	425016	AA376049	Hs.154162	ADP-ribosylation factor-like 2	16.6
	418179	X51630	Hs.1145	Wilms tumor 1	16.6
	418994	AA296520	Hs.89546	Selectin E (endothelial adhesion molecule 1)	16.5
	457514	AA775208	Hs.136423	ESTs	16.5
	426275	BE151551		gb:RC0-HT0297-201199-031-f12 HT0297 Homo sapi	16.5
55	457924	AL390142	Hs.288697	Homo sapiens cDNA FLJ13861 fis, clone THYR010	16.5
	430712	AW044647	Hs.196284	ESTs	16.5
	455144	AW875942		gb:CM1-PT0013-131299-067-b10 PT0013 Homo sapi	16.4
	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory rece	16.4
	426712	AW173177	Hs.197755	ESTs	16.4
60	429954	AI918130	Hs.21374	ESTs	16.4
	446208	BE258323	Hs.225795	ESTs, Highly similar to OTX1_HUMAN HOMEOBOX P	16.4
	442792	AI352340	Hs.131194	ESTs	16.3
	420485	AF218586	Hs.288835	cell death-inducing DFFA-like effector b	16.3
	426767	AA384398	Hs.192491	ESTs	16.3
65	436960	L05779	Hs.113	epoxide hydrolase 2, cytoplasmic	16.3
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	16.3
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo sapi	16.3
	433457	AA830194	Hs.199417	Homo sapiens mRNA for FLJ00027 protein, parti	16.2
	402316				16.2
70	409736	AA076628		gb:P07H07 Chromosome 7 Placental cDNA Librar	16.2
	407964	AW130334	Hs.281111	ESTs	16.2
	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN ALU SU	16.2
	426507	AI684745	Hs.165983	hypothetical C2H2 zinc finger protein FLJ2250	16.2
	413724	AA131466	Hs.23767	Homo sapiens cDNA FLJ12666 fis, clone NT2RM40	16.2
75	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4H855Y Ho	16.1
	413055	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-induc	16.1
	435977	AL138079	Hs.5012	brain-specific membrane-anchored protein	16.1
	442208	AW296984	Hs.255595	ESTs, Weakly similar to PSF_HUMAN PTB-ASSOCIA	16.1
	402426				16.0
80	412399	N53816	Hs.14394	hypothetical protein FLJ20157	16.0
	413200	AA127395	Hs.222414	ESTs	16.0
	404597				15.9
	453143	AA382234	Hs.170121	protein tyrosine phosphatase, receptor type,	15.9
	455984	BE177442		gb:RC1-HT0595-200400-012-01 HT0595 Homo sapi	15.9

5	416193	T25400		gb:PTH069 HTC0L1 Homo sapiens cDNA 5'3' sim	15.9
	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR	15.9
	441785	AW138139	Hs.244598	ESTs	15.9
	413784	BE165819		gb:CMO-HT0486-220300-301-d12 HT0486 Homo sapi	15.9
	429092	AI190884	Hs.178226	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.8
10	408499	AW205323	Hs.253475	ESTs	15.8
	453754	AW972580	Hs.172753	ESTs	15.8
	450826	U43030	Hs.25537	cardiotrophin 1	15.8
	428486	AW583497	Hs.184604	pancreatic polypeptide	15.7
	405895				15.7
15	409108	AA339443	Hs.48793	ESTs	15.7
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	15.6
	422948	AW810824	Hs.21351	ESTs	15.6
	447852	AW504781		gb:U1-HF-BN0-ah-c-04-0-ULr1 NIH_MGC_50 Homo	15.6
	419084	AA496539	Hs.179902	transporter-like protein	15.6
20	456771	AW016739	Hs.232201	ESTs	15.6
	438564	AA381553	Hs.198253	major histocompatibility complex, class II, D	15.6
	448705	H05072	Hs.124984	ESTs, Moderately similar to unnamed protein p	15.6
	454460	X66945	Hs.748	fibroblast growth factor receptor 1 (fms-rela	15.5
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.5
25	426759	AI590401	Hs.21213	ESTs	15.5
	453769	R35261	Hs.24947	ESTs	15.4
	434179	AI743448	Hs.116177	ESTs	15.4
	404111				15.4
	402056				15.4
30	458602	AI262208	Hs.276489	ESTs	15.3
	427530	AA405093	Hs.126519	ESTs	15.3
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	15.3
	400632				15.3
	443918	AA305475	Hs.22660	Homo sapiens cDNA FLJ11658 fis, clone HEMBA10	15.3
35	432037	AW450592	Hs.300459	ESTs	15.3
	412921	BE009345	Hs.128942	ESTs	15.3
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein (H.sapi	15.3
	441704	AI458766	Hs.201988	ESTs	15.3
	414272	AI651603	Hs.46998	ESTs	15.3
40	448224	R48700	Hs.20733	EH-domain containing 2	15.2
	404611	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	15.2
	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp434A1010 (from c	15.2
	454719	BE006547		gb:RC2-BN0130-040400-011-b03 BN0130 Homo sapi	15.2
	446973	H95724	Hs.4283	ESTs	15.2
45	457760	AA668123	Hs.134170	ESTs	15.2
	440144	AW082297	Hs.88523	ESTs	15.2
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1, parti	15.2
	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN ALU SU	15.2
	404244				15.1
50	402959				15.1
	435487	W07343	Hs.182538	phospholipid scramblase 4	15.1
	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo sapiens cDNA c	15.0
	455916	BE156710		gb:QVD-HT0368-310300-181-d01 HT0368 Homo sapi	15.0
	448943	AI608810	Hs.193288	ESTs	15.0
55	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	15.0
	454082	AF283508	Hs.63168	cell death regulator even	14.9
	453308	AW959731	Hs.32538	ESTs	14.9
	458823	AW207574	Hs.179501	ESTs	14.9
	452532	AI905811	Hs.110757	DNA segment on chromosome 21 (unique) 2056 ex	14.9
60	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	14.9
	409473	AL137716	Hs.296567	Homo sapiens mRNA; cDNA DKFZp434D2030 (from c	14.8
	449779	AA004258	Hs.25218	ESTs, Weakly similar to ALUB_HUMAN !!! ALU C	14.8
	457546	AA568484	Hs.153632	ESTs	14.8
	403368				14.8
65	432163	AK000440	Hs.272799	hypothetical protein FLJ20433	14.8
	421531	AA713505	Hs.291769	ESTs	14.8
	428283	AI439096	Hs.25832	Homo sapiens mRNA; cDNA DKFZp564P116 (from cl	14.8
	443528	AK001778	Hs.9547	hypothetical protein FLJ10916	14.8
	402399				14.8
70	410545	U32324	Hs.64310	Interleukin 11 receptor, alpha	14.8
	450300	AL041440	Hs.58210	ESTs	14.8
	403552				14.7
	406929	U04690		gb:Human olfactory receptor (OR17-210) gene,	14.7
	436365	AW444548	Hs.163118	ESTs	14.7
75	402550				14.7
	441782	AW140126	Hs.132357	ESTs	14.7
	415672	N53097	Hs.193579	ESTs	14.7
	430582	AI215509	Hs.143964	ESTs	14.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin	14.7
80	432683	AW995441	Hs.10475	ESTs	14.7
	441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na glucose c	14.6
	447481	AF052151	Hs.18686	Mouse Mammary Tumor Virus Receptor homolog	14.6
	405114				14.6
	401082				14.6
	454316	AW366144		gb:QV0-HT0101-061099-032-b12 HT0101 Homo sapi	14.6
	421572	AA531607	Hs.125143	ESTs, Weakly similar to POL2 MOUSE RETROVIRUS	14.6
	424591	R55704	Hs.150958	hypocretin (orexin) receptor 1	14.6

5	441503	AW172263	Hs.185202	ESTs	14.6
	416199	R83537		gb:q12a08.r1 Soares fetal liver spleen 1NFLS	14.6
	420360	U83171	Hs.97203	small inducible cytokine subfamily A (Cys-Cys	14.6
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	14.5
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, member	14.5
10	405100				14.5
	454012	M76424	Hs.37014	carbonic anhydrase VII	14.5
	402457				14.5
	454613	AW810814		gb:MR2-ST0129-201099-004-a01 ST0129 Homo sapi	14.5
	429821	AL056749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (from cl	14.5
15	431073	BE254470	Hs.249186	cone-rod homeobox	14.5
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing leucine	14.5
	401223				14.4
	438627	AI087335	Hs.123473	ESTs	14.4
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.4
20	437217	AW779241	Hs.155316	ESTs	14.4
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G protein	14.4
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-biphosp	14.4
	413237	AI468574	Hs.171965	ESTs	14.4
	412975	T70958	Hs.75106	clusterin (complement lysis inhibitor, SP-40,	14.4
25	426488	X03350	Hs.4	alcohol dehydrogenase 2 (class I), beta polyp	14.4
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	14.4
	405479				14.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedia C)	14.3
	426316	NM_002430	Hs.301852	Human DNA sequence from clone 437G10 on chrom	14.3
30	412171	AW897452		gb:CM0-NN0058-150400-337-b08 NN0058 Homo sapi	14.3
	447241	BE382838	Hs.19322	ESTs	14.3
	402100				14.2
	438286	AW139266	Hs.134807	Homo sapiens cDNA FLJ12057 fis, clone HEMBB10	14.2
	407947	AI500332	Hs.102367	ESTs, Weakly similar to hTcd-4 [H.sapiens]	14.2
35	402275				14.2
	402358				14.2
	439524	AA838771	Hs.124407	ESTs	14.2
	444455	AI149879	Hs.175024	Homo sapiens cDNA: FLJ23447 fis, clone HSI033	14.2
	455314	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	14.2
40	427872	AA835058	Hs.21111	ESTs	14.2
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	14.2
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene homolo	14.2
	442682	AI014545	Hs.231027	EST	14.1
	457033	AF029674	Hs.173422	KIAA1605 protein	14.1
45	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	14.1
	401007				14.1
	458274	AF149297	Hs.8087	NAG-5 protein	14.1
	454106	D19687	Hs.245146	ESTs	14.1
	432928	AA570454	Hs.186467	ESTs, Moderately similar to ALU1_HUMAN ALU SU	14.1
50	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin/ bet	14.1
	433887	AW204232	Hs.279522	ESTs	14.1
	434927	H46612	Hs.293815	ESTs, Weakly similar to PLM_HUMAN PHOSPHOLEMM	14.1
	404282				14.1
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor II	14.0
55	424823	NM_006226	Hs.153322	phospholipase C, epsilon	14.0
	408107	AA806754	Hs.62835	ESTs	14.0
	401577				14.0
	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-rich p	14.0
	408104	AW972927	Hs.293968	ESTs	14.0
60	404642				14.0
	400675				14.0
	406059				14.0
	448386	AB037750	Hs.21061	KIAA1329 protein	14.0
	407287	AI678812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	14.0

TABLE 22B

65	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
70	Pkey	CAT number	Accession	
	408922	109017_1	R87388 R84328 AA058916	
	409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309	
75	409736	115189_1	AA078628 R09051 AA078197 AA077334 AW748808 AW748807	
	412171	1280759_1	AW897452 Z20302 D55805 D52877 D60432	
	413784	1389150_1	BE165819 BE165853 W01388	
80	414213	1426375_1	BE297765 BE262061 BE302686 T83915	
	416193	1577102_1	T25400 H26834 H44554 R73193	
	416199	1577561_1	R83537 W80940 H27368	
	417998	171375_1	AW967420 AA210915 AA236991 AA210916	
	418464	1759038_2	R87580	
	418556	1767868_1	T02850	
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361	
	423780	231952_1	T06241 AA326794 AL138130 AW407975 AW999277	
			AA352013 AA330878 AA339379 AW966303	

5	424585	241151_1	AA464840 AA343628
	426275	263712_1	BE151551 AA373783 BE182852 BE008826 BE008827 BE008781 BE008699
	427980	285225_1	AA418305 AI264351
	439872	47823_1	T81058 AL357200 T70270
	442197	535550_1	AW837912 AW837934 AA984475 AW997490
	447852	73973_1	AW504781 BE620394
	448422	762770_1	BE263813 BE253504 AI500202 BE251145
	453621	974526_1	AW749983 AL045823
10	454316	1109350_1	AW366144 AW366154 AW366142 AW366151 AW366140 AW366155 BE141715 BE141718 BE141698
	454613	1226904_1	AW810814 AW810787 AW810854 AW810773 AW810735 AW810785 AW810660 AW810834 AW810874 AW810723
			AW810881 AW810791 AW810644 AW810659 AW810676
	454719	1230646_1	BE006547 AW815578 AW815311 AW856304
	455144	1254914_1	AW875942 AW858234 AW875938 AW875941 AW858235 AW875958
	455818	137219_1	AI733747 AA129802
15	455904	1382290_1	BE156173 BE156305 BE156196
	455916	1382748_1	BE156710 BE156726 BE156712
	455984	1397288_1	BE177442 BE177439 BE177445 BE177448 BE177444 BE177433
20	TABLE 22C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
25	NI_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand NI_position
30	400489	8954013	Plus 131475-131652
	400545	9800107	Minus 124618-124881
	400625	7228177	Minus 117266-117441
	400632	3818355	Plus 72875-73447,75874-76425
	400637	8894326	Plus 68901-69507
	400675	8118750	Plus 11223-11816
35	401007	8117333	Minus 140821-141050
	401082	3242744	Plus 22937-23494,27677-27966
	401223	8099088	Plus 148940-150214
	401551	8096896	Minus 189824-190728
	401577	9280797	Minus 139377-139674,141195-141281,142217-142340
40	401703	4826475	Plus 135-1229
	402056	8084234	Plus 207002-207288
	402100	8117697	Plus 133649-133792
	402195	7689778	Minus 147901-148884
45	402275	2935596	Minus 31055-31233,33680-33771,34345-34411,38890-39125,39779-39943
	402316	7527774	Minus 10751-10919,18817-19052,22131-22328
	402358	8886976	Minus 131788-132729
	402399	1905915	Minus 24502-24656,24986-25102
	402426	9796361	Minus 73590-73824
50	402457	9796782	Minus 16513-16577,16838-16926
	402520	7596899	Minus 171761-171996
	402550	7652009	Minus 80413-80673
	402741	9212200	Minus 18603-18760,19719-19890
	402865	9716300	Plus 3197-3429,3722-3914,5795-5987,6802-6961,8653-8815,9292-9660
55	402959	9368493	Plus 36729-37084
	403121	9180223	Plus 4059-4258
	403368	4388738	Plus 70286-70429,75165-75258
	403552	6862638	Minus 117504-117662
	403731	7543752	Minus 144000-144518
60	404033	8122195	Plus 7976-8158
	404111	9408736	Plus 161506-161781
	404244	5672609	Minus 98173-98517
	404282	2276311	Plus 61503-62205
	404597	9958262	Minus 114369-114599
65	404642	9796810	Plus 102999-103145
	404654	9797010	Plus 6275-6527
	404947	7382205	Plus 29740-30105,30176-30412
	405100	8076846	Plus 144114-144234
	405114	8096938	Minus 97013-97560
70	405228	7248990	Plus 92234-95905
	405313	3638954	Plus 68924-69093
	405324	3342751	Minus 5475-5677
	405479	6453391	Plus 1668-1844
	405895	7677903	Minus 66990-67484
75	406059	9103984	Minus 13856-14004
	406150	9886026	Minus 59331-59701
	406535	7711477	Plus 83135-83362

80 TABLE 23A: 626 genes upregulated in uterine cancer relative to normal body tissues

Table 23A lists about 626 genes upregulated in uterine cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis

was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

5	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
	Pred.Protdomains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
10	UniGene Title:	UniGene gene title
	R1	95th percentile of uterine cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
15	Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Protdomains; R1	
		428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 35.11
		420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobin; 22.80
20		439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 21.66
		425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homolog 4; none; 21.11
		421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 20.20
		437938; A1950087; Hs.369628; gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapien; none,none; 19.83
		406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 17.68
25		446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; 17.60
		418281; U09550; Hs.1154; oviductal glycoprotein 1, 120kD (mucin 9; Glyco_hydro_18; TM=M; SS=M; 17.48
		431130; NM_006103; Hs.2719; HE4; epikidymis-specific, whey-acidic pr; wap; TM=M; SS=Y; 16.59
		400301; X03635; Hs.1657; estrogen receptor 1; F-box, hormone_rec, zf-C4, Oest_recep, adh_zinc, ketoacyl-synt, CAAA, E7, RFX_DNA_binding; TM=M; SS=N; 16.11
30		419356; A1656166; Hs.7331; hypothetical protein FLJ22316; Asparaginase_2, none; 15.90
		433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 15.39
		417931; W95642; Hs.82961; trefol factor 3 (intestinal); trefol; 15.39
		400284; ; NM_000125; Homo sapiens estrogen recepto; hormone_rec, zf-C4, Oest_recep; TM=M; SS=M; 15.23
		456662; NM_002448; Hs.1494; msh (Drosophila) homeo box homolog 1 (fo; homeobox, none; 15.04
35		438817; A1023799; Hs.163242; ESTs; none, none; 13.72
		453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 13.67
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 13.51
		458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (S; HMG_box; TM=M; SS=N; 13.44
40		410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M; SS=M; 13.41
		421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans, K_tetra, asp; 13.27
		449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp; TM=M; SS=M; 12.76
		436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin; TM=Y; SS=M; 12.69
		450693; AW450461; Hs.203965; ESTs; Sema, lg, none; 12.52
		415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN, sugar_tr; TM=Y; SS=M; 12.46
45		413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 12.23
		431629; AU077025; Hs.265827; interferon, alpha-inducible protein (cik; none; TM=M; SS=Y; 12.09
		417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 12.08
		407786; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 11.91
		444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 11.86
50		446608; N75217; Hs.175622; ESTs; Armadillo_seg, HEAT_PBS; TM=M; SS=M; 11.72
		447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022 hypothetical; none, UQ_con; 11.59
		420181; A1380089; Hs.158951; ESTs; none, lg, kinase, LRR, LRRCT; 11.49
		451253; H48299; Hs.26126; claudin 10; PMP22_Claudin, Peptidase_M1, K_tetra; TM=Y; SS=M; 11.45
		453968; AA847843; Hs.62711; High mobility group (nonhistone chromoso; HMG_box, none; 11.42
55		448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec, MIP; TM=M; SS=M; 11.37
		421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 11.08
		452367; U71207; Hs.29279; eyes absent (Drosophila) homolog 2; Hydrolase; 11.01
		409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 10.95
		415138; C18356; Hs.285944; tissue factor pathway inhibitor 2; Kunitz_2PTI, none; 10.91
60		416558; U03272; Hs.79432; fibrillin 2 (congenital contractural ara; EGF, TB, granulin, PSI, EB, TIL; TM=M; SS=M; 10.81
		411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_membr; TM=Y; SS=M; 10.72
		438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 10.66
		425071; NM_013989; Hs.154424; delodinae, lodothyronine, type II; T4_delodinae; TM=M; SS=Y; 10.66
		430832; A1073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior; none, none; 10.52
		451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF, WIF; 10.50
65		421478; A1683243; Hs.97258; ESTs, Moderately similar to S29539 ribos; none, none; 10.50
		409231; AA446644; Hs.692; GA733-2 antigen; epithelial glycoprotein; thyroglobulin_1; TM=Y; SS=M; 10.35
		443785; AW449952; Hs.190125; basic-helix-loop-helix-PAS protein; HLH_PAS; TM=M; SS=N; 10.34
		409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M_SMC_N, SMC_C, DUF164, none; 10.34
70		431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 10.34
		415539; A173881; Hs.72472; NAME OMITTED ... receptor kinase; pklnase, Activin_rec, PDZ, ZU5, death; 10.31
		411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.24
		423873; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin, Peptidase_M10; TM=M; SS=M; 10.24
		441377; BE218239; Hs.202656; ESTs; none, none; 10.17
75		400292; AA250737; Hs.72472; NAME OMITTED ... receptor kinase; pklnase, Activin_rec, PDZ, ZU5, death; 10.17
		452594; AU076405; Hs.29981; solute carrier family 28 (sulfate transp; xan_ur_permease, Sulfate_transp, STAS, HMG_box; 10.12
		429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic ; C2, PLA2_B; TM=M; SS=N; 9.87
		413859; AW992355; Hs.8384; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT, none; 9.87
		408562; A1436323; Hs.31141; roundabout (axon guidance receptor, Dros; lg, fn3; TM=M; SS=N; 9.86
		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3; TM=Y; SS=M; 9.72
80		438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 9.68
		411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none, none; 9.53
		450451; AW591528; Hs.202072; ESTs; none, none; 9.53
		456062; A1866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none, none; 9.50

- 418113; A1272141; Hs.83484; SRY (sex determining region Y)-box 4; HMG_box,homeobox;TM=M;SS=N; 9.38
 412791; A1131192; Hs.143199; ESTs; Weakly similar to S72481 probable ; pkinase,PBD,none; 9.36
 432435; BE218866; Hs.282070; ESTs; none,none; 9.35
 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyma); trypsin;TM=M;SS=M; 9.32
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM; 9.19
 410407; X66839; Hs.63287; carbonic anhydrase IX; carb_anhydrase;TM=M;SS=M; 9.19
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 9.17
 453459; BE047032; Hs.257789; ESTs; none,none; 9.14
 431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 9.05
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 9.00
 413278; BE563085; Hs.833; Interferon-stimulated protein, 15 kDa; ubiqulin; 8.93
 436954; AA740151; Hs.130425; ESTs; none,none; 8.91
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 8.89
 425397; U04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolV,HATPase_c;; 8.85
 407792; A1077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 8.80
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN cDNA 2810; none,none; 8.79
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 8.72
 413385; AK34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO;TM=M;SS=N; 8.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B,Endonuclease,Phosphodiast;TM=Y;SS=M; 8.69
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphat; Ribosomal_L20,Na_Pi_cotrans;TM=Y;SS=N; 8.67
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembrane; EGF,SEA;TM=Y;SS=M; 8.66
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; DPPIV_N_term,Peptidase_S9,none; 8.55
 414812; X72755; Hs.77387; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 8.53
 426187; A1687303; Hs.285529; G protein-coupled receptor 49; 7tm_1,none; 8.49
 448672; A1955511; Hs.374290; ESTs; lig_chan,ANF_receptor,SBP_bac_3;TM=Y;SS=M; 8.44
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 8.40
 443428; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 8.40
 452093; AA447453; Hs.27860; Homo sapiens mRNA; cDNA DKFZp586M0723 (t; 7tm_1,none; 8.33
 407894; AJ278313; Hs.41143; phospholipid-specific phospholipase ; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 8.23
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 8.21
 419508; AW997939; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 8.20
 424441; X14850; Hs.147097; H2A histone family, member X; histone,C8FD_NFYB_HMF;; 8.20
 408243; Y00787; Hs.624; Interleukin 8; IL8,PAS,IL8;TM=M;SS=N; 8.00
 415752; BE314524; Hs.78776; putative transmembrane protein; none;TM=Y;SS=N; 7.99
 422608; AW160644; Hs.118695; potassium voltage-gated channel, subfam; ion_trans,K_tetra;TM=Y;SS=N; 7.99
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; 7.95
 409549; AA159216; Hs.55505; hypothetical protein FLJ20442; Y_phosphatase,DSPc;TM=M;SS=N; 7.95
 424078; AB005625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 7.86
 432179; X75208; Hs.2913; EphB3; EPH_bdb,fn3,pkinase,SAM;TM=Y;SS=M; 7.85
 424581; M62062; Hs.150917; catenin (cadherin-associated protein), alpha Vinculin,DNA_ligase_ZBD;TM=M;SS=N; 7.84
 420610; A1683183; Hs.99348; distal-less homeo box 5; homeobox;TM=M;SS=N; 7.81
 436856; A1469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 7.81
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 7.80
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN;; 7.78
 424399; AJ905687; Hs.348419; AJ905687:IL-BT095-190199-019 BT095 Homo ; none;TM=M;SS=M; 7.65
 418836; A1655499; Hs.161712; ESTs; pkinase,Activin_rec,POZ,ZU5,death; 7.64
 435793; AB037734; Hs.4993; KIAA1313 protein; none;TM=M;SS=N; 7.61
 426201; AW182614; Hs.128499; ESTs; SH3,none; 7.59
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; zf-C3HC4;TM=Y;SS=M; 7.55
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.55
 453464; A1884911; Hs.32989; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 7.54
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,pkinase; 7.52
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 7.38
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 7.36
 414617; A1339520; Hs.288817; ESTs, Moderately similar to N Chain N, M; hexokinase,hexokinase2;TM=Y;SS=N; 7.35
 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 7.33
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 7.30
 409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none;TM=M;SS=M; 7.28
 417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1;; 7.28
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 7.28
 418506; AA084248; Hs.372651; Unknown protein for MGC:29643 (formerly ; none,none; 7.27
 448913; AA194422; Hs.22564; myosin VI; rm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M;SS=N; 7.26
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_Kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.26
 424317; A1865032; Hs.26017; ESTs; none,pkinase; 7.21
 410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP,GBP_C;TM=Y;SS=M; 7.21
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M;SS=N; 7.14
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT;TM=Y;SS=M; 7.05
 423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor; 7tm_1;TM=Y;SS=M; 7.03
 435021; AA922192; Hs.73962; ESTs; EPH_bdb,pkinase,fn3,SAM,none; 7.02
 446163; AA026880; Hs.25252; prolactin receptor; none,NA;NA; 7.01
 447768; X86400; Hs.19520; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=M;SS=N; 7.00
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 6.99
 451035; AU078785; Hs.430; plastin 1 (I isoform); ehfand,CH,Adaptin_N;; 6.99
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide;; 6.95
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 6.93
 432519; A122311; Hs.130704; ESTs, Weakly similar to BCHUIA S-100 pro; none,none; 6.93
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con;TM=M;SS=N; 6.92
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 6.92
 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 6.87
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.87

- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 6.86
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; Skd_Sno; TM=M; SS=M; 6.86
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin; Peptidase_M10; 6.85
 453064; R40334; Hs.89463; potassium large conductance calcium-acti; none, none; 6.83
 5 452046; AB018345; Hs.27657; KIAA0802 protein; none; TM=M; SS=N; 6.79
 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none, none; 6.79
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glut; aldedh, aak kinase; TM=M; SS=N; 6.77
 431470; AA832417; Hs.139650; ESTs; none, Ig, pkinase, LRR, LRRCT; 6.76
 10 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 6.75
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory sur; SH2, none; 6.74
 417886; AA214584; ; ESTs; SPRY, 7tm_3, ANF_receptor, none; 6.72
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; 6.70
 437960; AI669586; Hs.369312; ESTs; none, none; 6.68
 15 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal, Ribosomal_L10, TNFR_c6, DEAD; 6.66
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Idl_recept_a, PKD, MHC; TM=M; SS=Y; 6.65
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex; TM=Y; SS=M; 6.64
 449656; AA002008; Hs.188633; ESTs; PIP5K; none; 6.64
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-induc; pyr_redox; TM=M; SS=N; 6.62
 446063; AI720140; Hs.151079; ESTs; ISK_Channel, none; 6.61
 20 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none, none; 6.60
 421554; AW137676; Hs.97775; ESTs; none, none; 6.59
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (ma; ank; 6.55
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 6.54
 25 448730; AB032983; Hs.21894; KIAA1157 protein; PP2C; TM=M; SS=N; 6.54
 433577; AW007080; Hs.284192; ESTs; none, none; 6.53
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fesiclin, ABC, tran, ABC, membrane, GTP_EFTU; TM=M; SS=M; 6.53
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane protein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 6.52
 430259; BE550182; Hs.375142; RalGEF-like protein 3, mouse homolog; fn3, RA, RasGEF; TM=M; SS=M; 6.52
 30 434263; N34895; Hs.79187; ESTs; Ig, none; 6.49
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPC; TM=M; SS=N; 6.48
 419942; U25138; Hs.93841; potassium large conductance calcium-acti; CaKB; TM=Y; SS=M; 6.47
 421064; AI245432; Hs.101382; tumor necrosis factor, alpha-induced pro; none; TM=M; SS=N; 6.47
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin; TM=Y; SS=M; 6.45
 35 431685; AW296135; Hs.267659; vav 3 oncogene; CH, DAG, PE-bind, PH, RhoGEF, SH2, SH3, DC1; TM=M; SS=N; 6.44
 428832; AA578229; Hs.324239; ESTs; Moderately similar to ZN91_HUMAN Z; Osteopontin; none; 6.39
 438775; AA731111; Hs.372225; ESTs; none, none; 6.39
 424343; AW956360; Hs.4748; adenylate cyclase activating polypeptide; 7tm_2, HRM; none; 6.37
 421071; AI311238; Hs.104476; ESTs; Weakly similar to CGH1E collagen; none; TM=Y; SS=M; 6.37
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH, PAS, IL8; TM=M; SS=N; 6.37
 438993; AA828995; ; gb:od77b08.s1 NCL_CGAP_Ov2 Homo sapiens; EGF, metalthio, integrin_B, PSI; none; 6.27
 40 408400; ; kallikrein 8 (neuprosin/ovasin) (KLK8); trypsin; TM=M; SS=M; 6.27
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 6.26
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-like; H5AR g; Steroid_dh; TM=Y; SS=M; 6.25
 435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none, none; 6.24
 45 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled, Fz, 7tm_2, toxin_2; TM=Y; SS=M; 6.24
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF, sugar_tr, none; 6.23
 436961; AW375974; Hs.156704; ESTs; none, none; 6.23
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M; SS=N; 6.22
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-I; AAA, NB-ARC, PAAD, DAPIN; NA; NA; 6.20
 50 416224; NM_002902; Hs.79068; reticulocalbin 2, EF-hand calcium binding; ehand; 6.20
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49, EGF, Ig, Neuregulin; TM=M; SS=N; 6.19
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 6.19
 452551; L27071; Hs.29877; TXK tyrosine kinase; Beach, WD40, SH2, SH3, pkinase; TM=M; SS=N; 6.14
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; SS=N; 6.12
 55 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 6.11
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 6.11
 449700; L02867; Hs.78358; paraneoplastic antigen; none; TM=M; SS=N; 6.10
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 6.10
 60 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA; TM=M; SS=N; 6.09
 433159; AB035898; Hs.150587; kinesin-like protein 2; bZIP, kinesin; 6.08
 432432; AA541323; Hs.115831; ESTs; Ig, Sema, PSI; none; 6.07
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; SS=N; 6.04
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; SS=N; 6.03
 65 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese, none; 6.00
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing Ig; Ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 6.00
 428677; AI657119; Hs.351582; troponin I, cardiac; none; TM=M; SS=N; 6.00
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; SET, zf-MYND; TM=M; SS=N; 6.00
 70 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, com; C1q, Collagen; 5.99
 419972; AL041465; Hs.182982; golgin-67; none, none; 5.99
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM, PDZ; 5.97
 403362; ; NM_001615; Homo sapiens actin, gamma 2; ; actin; 5.95
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 5.95
 75 420253; AI656055; Hs.96200; neighbor of A-kinase anchoring protein 9; none; NA; NA; 5.93
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 5.93
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; SS=N; 5.92
 450747; AI064821; Hs.129953; ESTs; Highly similar to 1818357A EWS gen; rm, zf-RanBP, GAS2; 5.92
 415211; R64730.comp; Hs.155986; DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; DEAD, helicase_C, rm, Ndr, Cys_kno1, TIL, vwa, vwc, vwd, IQ, Rila, abhydrolase, TGF-beta, DUF139, TPR, DSPc, isp_1, Ribosomal_S21, rvp; TM=M; SS=N; 5.91
 80 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin) receptor; 7tm_1; TM=Y; SS=N; 5.90
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (lazarus; none; TM=Y; SS=N; 5.89
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none; TM=Y; SS=M; 5.89
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 5.89

- 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz, Frizzled, 7tm_2, TM=Y; SS=M; 5.87
 426761; AJ015709; PORIMIN Pro-oncosis receptor inducing me; none; TM=Y; SS=M; 5.85
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none; TM=M; SS=Y; 5.85
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M; SS=N; 5.84
 450502; T08065; Hs.118262; ESTs; lon_trans, lon_trans; 5.84
 442652; AJ005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none; TM=M; SS=N; 5.83
 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M; SS=N; 5.83
 448569; BE382557; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 5.82
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS, AIRS_C; TM=M; SS=N; 5.82
 445133; AW157646; Hs.198689; ESTs; ehfand, spectrin, GAS2, SH3, Plectin, RA, Xylose_Isom, FliD, bZIP, Tropomyosin, Myo-LZ, M, Idh_C, CH, AIP3; TM=M; SS=N; 5.79
 426215; AW963419; Hs.155223; stanniocalcin 2; Stanniocalcin; 5.78
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 5.75
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 5.74
 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox; none; 5.72
 432201; AI538613; Hs.298241; Transmembrane protease, serine 3; Idl_recept_a, trypsin; TM=Y; SS=M; 5.72
 429345; R11141; Hs.198695; hypothetical protein; K_tetra, SAM; 5.72
 449458; AI805078; Hs.208261; ESTs; Frizzled, Fz; none; 5.72
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic); none; TM=Y; SS=M; 5.71
 418848; AI820961; Hs.193465; ESTs; PDZ, pkinase; none; 5.70
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 5.69
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1; TM=M; SS=N; 5.69
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associ; kinesin; TM=M; SS=N; 5.69
 445136; AI348014; Hs.143949; ESTs; Weakly similar to Achaete-Scute ho; lon_trans, lon_trans; 5.69
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP; none; 5.67
 430016; NM_004736; Hs.227656; xantropic and polytropic retrovirus rec; SPX, EXS; TM=Y; SS=N; 5.66
 429538; AI916662; Hs.211577; kinecltin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP, BPL, CETP, B56, M; TM=Y; SS=M; 5.65
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y; SS=M; 5.64
 453950; AA156998; Hs.348037; eukaryotic translation initiation factor; none; 5.64
 425869; M57414; Hs.161305; tachykinin receptor 2; 7tm_1; TM=Y; SS=M; 5.64
 432527; AW975028; Hs.102754; ESTs; none; none; 5.64
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3; none; 5.63
 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; ZOG-Fell_Oxy; TM=M; SS=N; 5.63
 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5, F8_type_C; TM=M; SS=M; 5.61
 440422; AW452696; Hs.130760; myosin phosphatase, target subunit 2; BTB, Kelch, ank; none; 5.58
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 5.58
 432805; X94630; Hs.3107; CD97 antigen; 7tm_2, EGF, GPS, FecCD; TM=Y; SS=M; 5.55
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; Ig, IsoDh, Ribosomal_L6, F-box; TM=Y; SS=M; 5.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40, fn3, Ig; TM=M; SS=N; 5.54
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none; none; 5.54
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 5.53
 441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia vt; FHA, PDZ, RA, DIL; TM=M; SS=N; 5.53
 408051; AI823351; Hs.172148; ESTs; PH, RhoGAP; none; 5.53
 436726; AA324975; Hs.198689; ESTs; Weakly similar to T00079 hypotheti; ehfand, spectrin, GAS2, SH3, Plectin, RA, Xylose_Isom, FliD, bZIP, Tropomyosin, Myo-LZ, M, Idh_C, CH, AIP3; TM=M; SS=N; 5.53
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none; none; 5.52
 428667; AJ375550; Hs.346868; nucleolar protein p40; homolog of yeast; none; none; 5.51
 433907; AW296107; Hs.152686; ESTs; Armadillo_seg; none; 5.50
 442821; BE391929; Hs.8752; transmembrane protein 4; none; 5.50
 422282; AF019225; Hs.114309; apolipoprotein L; MotA, ExbB; TM=Y; SS=M; 5.49
 439820; AL360204; Hs.263853; Homo sapiens mRNA full length insert cDN; none; none; 5.49
 428771; AB028992; Hs.193143; KIAA1069 protein; C2, PI-PLC-Y, PI-PLC-X; TM=M; SS=N; 5.48
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GD1, 7tm_1; none; 5.48
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C1; none; none; 5.48
 408058; AA312329; Hs.42331; ephrin-A4; Ephrin; TM=M; SS=M; 5.47
 422765; AW409701; Hs.1678; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 5.47
 420297; AI628272; Hs.128757; ESTs; Weakly similar to ALU1_HUMAN ALU S; pkinase, TUDOR; none; 5.47
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2, SH3; 5.46
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2, STAT, STAT_bind, STAT_prot; none; 5.45
 441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia vt; pkinase, Recep_L_domain, Furin-like, YLP; none; 5.44
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 5.43
 450402; BE218027; Hs.89969; ESTs; SH3; none; 5.42
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BclA, RUN; TM=M; SS=N; 5.42
 430596; AA531276; Hs.59509; ESTs; pkinase, PP2C; none; 5.42
 412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-recept; Y_phosphatase, Band_41, PDZ; TM=M; SS=N; 5.42
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog); act; PH; none; 5.41
 448379; AI097463; Hs.21035; KIAA1130 protein; none; Zip; 5.41
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; mrx; TM=M; SS=N; 5.41
 411817; BE302900; Hs.72241; mitogen-activated protein kinase kinase ; pkinase; TM=M; SS=M; 5.40
 445413; AA151342; Hs.12677; CGI-147 protein; UPF0099; TM=M; SS=M; 5.39
 451863; AL120634; Hs.331803; ATPase, Ca transporting, plasma membrane; cpn60_TCP1, E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; 5.38
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra, DUF51; none; 5.38
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH_Ib, Lipase, GDSL; TM=M; SS=N; 5.36
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ, Guanylate_kin; 5.34
 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C, G-alpha, arf; TM=M; SS=M; 5.33
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+pep; PTR2; TM=Y; SS=N; 5.33
 435391; AA704588; Hs.58934; ESTs; PIP5K; none; 5.33
 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK; 5.33
 422170; AI791949; Hs.112432; anti-Mullerian hormone; TGF-beta; 5.32
 447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia vt; pkinase, Recep_L_domain, Furin-like, YLP; none; 5.32
 449984; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M; SS=N; 5.31
 426427; M85699; Hs.169840; TTK protein kinase; pkinase; 5.30
 430407; H23551; Hs.30974; ESTs; pkinase, PBD; none; 5.29

- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 5.27
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; Ig,kringle,pkinase,Fz; TM=Y; SS=M; 5.27
 424596; AB020639; Hs.151017; estrogen-related receptor gamma; hormone_rec,zf-C4; TM=M; SS=N; 5.27
 428013; AF151020; Hs.181444; hypothetical protein; none; TM=Y; SS=M; 5.26
 447384; AJ377221; Hs.40528; ESTs; SH3,Sorb; none; 5.26
 441824; AB007871; Hs.7977; KIAA0411 gene product; SH3,RhoGAP; TM=M; SS=N; 5.26
 438493; AJ130740; Hs.6241; phosphoinositide-3-kinase, regulatory su; SH2,SH3,RhoGAP; TM=M; SS=N; 5.26
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; 7tm_2,GPS; TM=Y; SS=M; 5.25
 414359; M62184; Hs.75929; cadherin 11, type 2, OB-cadherin (osteob; cadherin,Cadherin_C_term; TM=Y; SS=M; 5.25
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated gltr; sugar_tr; TM=Y; SS=M; 5.24
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; SS=N; 5.24
 423685; BE350494; Hs.49753; uveal autoantigen with coiled coil domain; ank,bZIP,M,DUF164,AIP3; 5.23
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phos; MORN,sugar_tr; TM=Y; SS=M; 5.23
 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 5.23
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF; 5.23
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAMEPH_bdb; TM=Y; SS=M; 5.23
 426770; AJ948618; Hs.150178; ESTs; Sulfate_transp,STAS; TM=Y; SS=N; 5.23
 422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha; TM=M; SS=N; 5.22
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE; 5.22
 448093; AW977382; Hs.15898; 2,4-dienoyl CoA reductase 2, peroxisomal; adh_short; 5.21
 443646; AB05198; Hs.164226; Thrombospondin 1; EGF,isp_1,vwc,TSPN,isp_3; none; 5.18
 457916; BE085271; Hs.8834; ring finger protein 3; pkinase; none; 5.18
 433933; AJ754389; Hs.355397; Homo sapiens clone TCCIA00164 mRNA sequ; none; NA; NA; 5.18
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 5.17
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,arf; TM=M; SS=M; 5.17
 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail,EGF; 5.16
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 no; none; TM=M; SS=N; 5.15
 454438; AA224053; Hs.172405; cell division cycle 27; SPRY,7tm_3,ANF_receptor; 5.14
 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; none; TM=Y; SS=M; 5.14
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr; TM=M; SS=N; 5.14
 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial; mito_carr; TM=M; SS=N; 5.14
 411704; AJ499220; Hs.71573; hypothetical protein FLJ10074; pkinase; TM=M; SS=N; 5.13
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2; TM=Y; SS=M; 5.13
 454128; AL031259; Hs.367900; programmed cell death 2; zf-MYND; TM=M; SS=N; 5.13
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences, MAGK Homo; none; none; 5.13
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 5.12
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; isp_3,EGF; 5.12
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans; TM=Y; SS=M; 5.11
 436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 5.11
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetase; WHEP-TRS,tRNA-synt_1b; none; 5.10
 453387; AJ990741; Hs.252809; ESTs; Na_Ca_Ex; none; 5.07
 413076; U10584; Hs.75188; weel (S. pombe) homolog; pkinase; TM=M; SS=N; 5.07
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3; TM=M; SS=N; 5.07
 438748; AB85815; Hs.184727; Human melanoma-associated antigen p97 (m; transferin,Guanylate_kin,PDZ,SH3; 5.07
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX; TM=M; SS=N; 5.06
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Map_PNP; 5.06
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none,Ribosomal_S13,Galactosyl_T,Zip,adh_short,zf-C3HC4; 5.06
 421369; NM_005089; Hs.171909; U2 small nuclear ribonucleoprotein auxil; rrm,zf-CCCH,lectin_c,integrin_B; TM=M; SS=N; 5.06
 412170; D16532; Hs.73729; very low density lipoprotein receptor; ldl_recept_L,ldl_recept_Lb,EGF; TM=M; SS=M; 5.06
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank; TM=M; SS=N; 5.05
 421109; L32832; Hs.101842; AT-binding transcription factor 1; HMG14_17,homoeobox,zf-C2H2; TM=M; SS=M; 5.05
 453880; AB03166; Hs.135121; ESTs, Weakly similar to 138022 hypothel; HSP70; none; 5.05
 431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh_C,SH3,pkinase,UBA; TM=M; SS=N; 5.05
 435411; AW444619; Hs.138211; ESTs; none,pkinase; 5.04
 419088; AJ538323; Hs.357688; Integrin, beta 8; Integrin_B; none; 5.04
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX; Tropotin,Exo_endo_phos,JC; TM=M; SS=N; 5.04
 428376; AF119665; Hs.184011; pyrophosphatase (Inorganic); Pyrophosphatase; TM=M; SS=N; 5.03
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPSS; TM=M; SS=M; 5.03
 436415; BE265254; Hs.343258; proliferation-associated 2G4, 38kD; Peptidase_M24,Furin-like,pkinase,Recep_L_domain,ethand; 5.01
 449674; AW444937; Hs.233482; ESTs; C2,PI-PLC-Y,PI-PLC-X; none; 5.01
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,TK; 5.01
 412133; U83460; Hs.104557; solute carrier family 31 (copper transpo; none; TM=Y; SS=N; 5.01
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase; 5.00
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT,pkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-patch; 5.00
 416365; U51311; Hs.79265; suppression of tumorigenicity 5; DENN,dDENN,uDENN; TM=M; SS=N; 5.00
 421351; AU076667; Hs.103755; receptor-interacting serine-threonine ki; CARD,pkinase; TM=M; SS=N; 4.99
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HUH,death,TNFR_c6,Acyl-CoA_hydro; 4.98
 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm,IRK; 4.95
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT; none; none; 4.95
 426310; NM_000909; Hs.169268; neuropeptide Y receptor Y1; 7tm_1; TM=Y; SS=M; 4.85
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase,pkinase; 4.94
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase; TM=M; SS=N; 4.94
 427541; AJ798983; Hs.375935; solute carrier family 35 (CMP-sialic aci; none; none; 4.94
 452792; AB037765; Hs.30652; KIAA1344 protein; thioder; TM=M; SS=M; 4.93
 430713; AA351647; Hs.2642; eukaryotic translation elongation factor; GTP_EFTU,GTP_EFTU_D3,GTP_EFTU_D2; 4.93
 444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP; none; 4.93
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin (neuronal; HNH,cadherin,Cadherin_C_term; TM=M; SS=N; 4.92
 421302; T34462; Hs.103291; neuritin; none; TM=M; SS=Y; 4.91
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase; TM=M; SS=N; 4.91
 408657; AA782601; Hs.378649; ESTs; B56; none; 4.91
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricin_B_lectin; 4.91
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 4.90
 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A,FG-GAP; TM=Y; SS=N; 4.89

- 438564; AA381553; Hs.198253; major histocompatibility complex, class ; Ig,MHC_II_alpha,none; 4.89
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frtzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.88
 434521; NM_002267; Hs.3888; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.88
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity la, re; Ig;TM=Y;SS=M; 4.88
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; perilipin; 4.88
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase_C,PRKAIIP3;TM=M;SS=N; 4.87
 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC,CBS,none; 4.86
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C; Phosphodiester,Somatomedin_B,Endonuclease,none; 4.86
 417656; AJ345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M;SS=N; 4.86
 453864; AW021407; Hs.21058; hypothetical protein; none,none; 4.86
 453082; H18835; Hs.31608; hypothetical protein FLJ20041; Ion_trans;TM=Y;SS=M; 4.85
 413407; AJ356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo_endo_phos;; 4.85
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CoxA;; 4.85
 436652; N32388; Hs.334370; uncharacterized hypothalamus protein HBE; none;TM=M;SS=N; 4.84
 419355; AA428520; Hs.90061; progesterone binding protein; hema_1;TM=Y;SS=M; 4.83
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y;SS=N; 4.83
 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC_tran,ABC_membrane,PRK,Bac_export_3;TM=Y;SS=N; 4.83
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 4.82
 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1); ank;TM=M;SS=N; 4.81
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,pkinase;TM=M;SS=N; 4.81
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.81
 453354; W55946; Hs.234863; Homo sapiens cDNA FLJ12082 fis, clone HE; transmembrane4,none; 4.81
 450883; NM_001348; Hs.25619; death-associated protein kinase 3; pkinase;TM=M;SS=N; 4.79
 429736; AF125304; Hs.212680; tumor necrosis factor receptor superfamily; TNFR_c6;TM=M;SS=M; 4.79
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 4.79
 409960; BE261944; Hs.355264; hexokinase 1; none,none; 4.78
 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1,kazal,A2M,A2M_N;TM=Y;SS=M; 4.78
 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2;TM=Y;SS=M; 4.78
 429305; AF095727; Hs.287832; myelin protein zero-like 1; Ig,transmembrane4;TM=Y;SS=M; 4.78
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPc;TM=M;SS=N; 4.77
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 4.76
 444672; Z95636; Hs.11669; laminin, alpha 5; laminin_EGF,laminin_G,EGF,TNFR_c6,laminin_B,laminin_Nterm,metalthio,Tropomyosin,DUF164,p450;TM=M;SS=N; 4.76
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB;TM=M;SS=N; 4.75
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.75
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;; 4.75
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 4.75
 425548; AA890023; Hs.1906; prolactin receptor; fn3;TM=Y;SS=M; 4.73
 434158; T86534; Hs.14372; ESTs; adenylatekinase,none; 4.73
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothet; none,SH3,myosin_head,IQ; 4.73
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 4.73
 434503; T96231; Hs.17762; ESTs; SH3,Sorb,none; 4.73
 446342; BE298665; Hs.14846; solute carrier family 7 (cationic amino ; none;TM=M;SS=N; 4.72
 427418; AA402587; Hs.356667; LAT1-3TM protein; none,none; 4.71
 449433; AJ672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-bind; Frtzled,Fz,Frtzled,Fz; 4.71
 418910; Z25821; Hs.89466; Homo sapiens, Similar to dodecanoyl-Coen; ECH;; 4.70
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,tRNA-synt_1b,dynamal,dynamain_2,GED,bZIP,M; 4.70
 442199; BE277633; Hs.372542; eloposide-induced mRNA; none;TM=Y;SS=M; 4.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 4.69
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 ; none; 4.69
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death dome; death,DED;; 4.68
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.68
 443323; BE560621; Hs.9222; estrogen receptor binding site associata; none;TM=M;SS=M; 4.68
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor;; Integrin_A,FG-GAP;TM=Y;SS=N; 4.68
 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiester;TM=Y;SS=M; 4.67
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B;; 4.67
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 4.66
 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 4.66
 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2; 4.66
 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-530115; none,none; 4.65
 404287;; FGENESH predicted novel CUB-domain conta; none,none; 4.64
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIP; Ig,Rhbd_glycop;TM=Y;SS=M; 4.63
 426680; AA320160; Hs.171811; adenylate kinase 2; adenylatekinase;TM=M;SS=N; 4.63
 430397; AJ924533; Hs.105607; bicarbonate transporter related protein ; HCO3_cotransp;TM=Y;SS=N; 4.63
 447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of ; SH3,PH;TM=M;SS=N; 4.63
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;SS=N; 4.62
 429126; AW172356; Hs.99083; ESTs; 7tm_1,none; 4.61
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frtzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.60
 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfamily; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.60
 421921; H83353; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10_DDP,ethand,CH,spectrin,serpin;TM=M;SS=N; 4.60
 429083; Y03937; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 4.59
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none,Cys_knot; 4.59
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; Ion_trans;TM=Y;SS=M; 4.59
 409645; AI142265; Hs.55498; geranylgeranyl diphosphate synthase 1; polyprenyl_synt;TM=M;SS=N; 4.59
 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M;SS=N; 4.58
 437212; AJ765021; Hs.210775; ESTs; UDPGT,none; 4.58
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nabulin,UM;; 4.57
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 4.56
 416041; AA345547; Hs.53263; hypothetical protein FLJ13287; WD40;; 4.55
 434511; R28982; Hs.18106; ESTs; pkinase,Glyco_hydro_39; 4.55
 410174; AA306007; Hs.59461; DKFZP434C245 protein; none,DSPc; 4.55
 418758; AW959311; Hs.172021; hypothetical protein DKFZp434J037; pkinase,RIOT;TM=M;SS=N; 4.55
 451367; AA923729; Hs.26322; cell cycle related kinase; pkinase;TM=M;SS=N; 4.54

- 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 4.54
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy; TM=M; SS=M; 4.53
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph); Ham1p_ike; TM=M; SS=N; 4.53
 431992; NM_002742; Hs.2891; protein kinase C, mu; pkinase, DAG_PE-bind, PH; TM=M; SS=M; 4.53
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 4.53
 428005; AW302245; Hs.181390; casein kinase 1, gamma 2; pkinase; TM=M; SS=N; 4.52
 407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras, arf; TM=M; SS=N; 4.52
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 4.51
 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HE; none, none; 4.51
 405484; ; C3002124; g|12737280|ref|XP_006682.2| k; none; 4.50
 443605; H06865; Hs.134131; ESTs; ethand, lon, trans, none; 4.50
 431738; AW237726; Hs.288549; hypothetical protein FLJ14710; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 4.50
 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; 4.49
 418869; AW516565; ; gb|xq01d05.x1 Soares_NHCCc_cervical_tumo; none, RasGAP, WW, IQ; 4.48
 447898; AW96638; Hs.112318; 6.2 kd protein; none, none; 4.48
 450607; AL050373; Hs.25213; hypothetical protein; SH3; TM=M; SS=N; 4.48
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig; TM=Y; SS=M; 4.48
 424823; NM_006226; Hs.153322; phospholipase C, epsilon; C2, PH, PI-PLC-C, PI-PLC-X; TM=M; SS=N; 4.48
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlor; none; TM=Y; SS=N; 4.47
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP; none; 4.47
 435615; Y15065; Hs.4975; potassium voltage-gated channel, KQT-like; lon, trans, KCNQ1_channel; TM=Y; SS=N; 4.47
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR, LY6E, PLA2_inh; 4.47
 428727; AF078847; Hs.78452; general transcription factor IIH, polypep; PHO4, LM; TM=M; SS=N; 4.46
 412760; AW379030; Hs.41324; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 4.46
 409093; BE243834; Hs.50441; CGI-04 protein; Ribosomal_L37ae, pkinase, POLO_box, tRNA-syn1, 1b, dynamin, dynamin_2, CED, hZIP, M; 4.46
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfurylase, PRK, Thymidylate_kin; 4.46
 447434; R16890; Hs.137135; ESTs; pkinase, fn3, Ig, pkinase, fn3; 4.45
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_br; 4.45
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxysterol_BP, pkinase; TM=M; SS=N; 4.44
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec, zf-C4, Metallothio_5; TM=M; SS=N; 4.44
 409686; AK000002; Hs.55879; Homo sapiens mRNA: cDNA DKFZp434L0827 (f; ABC_tran, ABC_membrane; TM=M; SS=M; 4.44
 408113; T62427; Hs.194101; Homo sapiens cDNA: FLJ20669 fis, clone A; 7tm_3, none; 4.44
 436823; AW749865; Hs.117077; ESTs, Weakly similar to I38022 hypotheti; aa_permeases, zf-C2H2, KRAB, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BclA, RUN, TFIIS; TM=M; SS=N; 4.44
 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg; TM=M; SS=N; 4.43
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoca; none, none; 4.43
 417412; X16896; Hs.82112; Interleukin 1 receptor, type I; ig, TIR; TM=M; SS=M; 4.43
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 4.43
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol_P, Ig; TM=M; SS=N; 4.43
 452124; AA454220; Hs.61170; ESTs; pkinase, none; 4.43
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK, PH, Oxysterol_BP; 4.42
 416202; AW964492; Hs.169624; ESTs; none; TM=M; SS=N; 4.42
 441518; AW161697; Hs.294150; ESTs; Y_phosphatase, DSPC; none; 4.42
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg; TM=M; SS=N; 4.42
 431429; AF072813; Hs.252831; reticulon 3; Reticulon, Fz, Ig, kring, pkinase; TM=Y; SS=N; 4.42
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP, Integrin_A, NIF; 4.41
 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none; NA; NA; 4.41
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 4.41
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; 4.41
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C; TM=M; SS=N; 4.41
 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_br; TM=Y; SS=N; 4.41
 458097; AW341135; Hs.68104; ESTs; none, SH3, PID; 4.40
 458248; BE407379; Hs.108082; ESTs, Weakly similar to T31636 hypotheti; C1q, Collagen; TM=M; SS=Y; 4.40
 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death, TNFR_c6, PH, Xlink, RhoGEF, Metallothio_5; TM=M; SS=M; 4.40
 443693; A1344782; Hs.9683; DnaJ (Hsp40) homolog, subfamily C, member; mm, DnaJ, TPR; TM=M; SS=N; 4.40
 437162; AW005505; Hs.5454; thyroid hormone receptor coactivating pr; bromodomain; TM=M; SS=N; 4.39
 453891; AB037751; Hs.301242; Homo sapiens mRNA full length insert cDN; none, none; 4.39
 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none, HSP70; 4.39
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 4.37
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; SS=N; 4.37
 444895; AI674383; Hs.22891; solute carrier family 7 (cationic amino ; ASC, death, TNFR_c6; 4.37
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg; TM=M; SS=M; 4.37
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin, none; 4.37
 418283; S79895; Hs.83942; cathepsin K (pseudosynthesis); Peptidase_C1; 4.37
 445826; BE313754; Hs.13350; Homo sapiens mRNA: cDNA DKFZp586D0918 (f; ig, isp_1, ZU5, Nucleoside_tran; 4.37
 417874; BE616160; Hs.28289; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; SS=N; 4.36
 400257; ; Hs.76366; ENSP0000000452-BAD protein (BCL-2 bindi; none; TM=M; SS=N; 4.36
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT; 4.36
 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.36
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90, HATPase_c, zf-C2H2, PHD; none; 4.36
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; Armadillo_seg, HEAT; TM=M; SS=N; 4.35
 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; SS=N; 4.35
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms; pkinase, Ig, pkinase, Ig, p450, SET, PPWW; 4.35
 445926; AF054284; Hs.334826; splicing factor 3b, subunit 1, 155kd; none; TM=M; SS=N; 4.35
 410726; AI623859; Hs.15936; ESTs; pkinase, pro_isomerase, none; 4.35
 433996; AW135357; Hs.192374; ESTs; HSP90, HATPase_c, UDC; 4.34
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) ; none; TM=M; SS=N; 4.34
 437103; AW139408; Hs.152940; ESTs; Choline_kinase, none; 4.34
 410068; AI633888; Hs.58435; FYN-binding protein (FYN-120/130); SH3; TM=M; SS=N; 4.34
 427349; AA360154; Hs.177415; Finkel-Biskis-Reilly murine sarcoma viru; ubiquitin; TM=M; SS=N; 4.33
 439807; AA376417; Hs.374608; hypothetical protein MGC5244; ; abhydrolase_2; TM=M; SS=M; 4.33
 453308; AW959731; Hs.323099; ESTs; none, pkinase, Actin_vin_rec; 4.33
 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OV; SAM; 4.33

	444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-S; DSPc; TM=M; SS=N; 4.33
	429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase, fn3, none; 4.32
	409121; AA902256; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR; none; 4.32
5	430280; AA361258; Hs.237868; Interleukin 7 receptor, fn3, none; 4.32
	423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbon; HCO3_cotransp; TM=Y; SS=M; 4.29
	425654; AB033022; Hs.158654; KIAA1196 protein; zf-C2H2; TM=M; SS=N; 4.29
	457500; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm, pkinase; TM=M; SS=N; 4.29
	427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 4.29
10	447191; NM_014521; Hs.17667; SH3-domain binding protein 4; SH3; TM=M; SS=N; 4.29
	408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M; SS=N; 4.29
	441130; A1160734; Hs.267604; Homo sapiens PNAS-129 mRNA, complete cds; BTB, Kelch, K_tetra, DSPc; TM=M; SS=N; 4.28
	430057; AW450303; Hs.2534; bone morphogenetic protein receptor, typ; Activin_rec, pkinase; TM=Y; SS=M; 4.28
	430250; NM_016929; Hs.283021; chloride intracellular channel 5; none; TM=M; SS=N; 4.28
15	406774; AW518383; Hs.177592; ribosomal protein, large, P1; 60s_ribosomal; 4.28
	413809; L25851; Hs.851; integrin, alpha E (antigen CD103, human; vwa, integrin_A, FG-GAP; TM=M; SS=Y; 4.27
	443950; A1093577; Hs.255416; hypothetical protein FLJ21986; TTL; TM=M; SS=N; 4.27
	427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE; TM=M; SS=N; 4.27
	412204; A125507; Hs.24937; ESTs; Ig, nm, none; 4.26
20	439506; A1361238; Hs.41136; ESTs; MAM, pkinase, Nucleoplasm, none; 4.26
	451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase, DAG, PE-bind, pkinase_C, OPR; none; 4.26
	452488; N74921; Hs.184389; ESTs; none; TM=M; SS=N; 4.26
	450973; AF102072; Hs.25732; eukaryotic translation initiation factor; W2, MA3, MIF4G; TM=M; SS=N; 4.26
	452437; A026237; Hs.181272; ESTs; eifhand, lon_trans, none; 4.26
25	438204; A1589645; Hs.126690; ESTs; none; 7tm_1; 4.25
	424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24, FKBP; TM=Y; SS=N; 4.25
	430570; A1417881; Hs.292464; ESTs; 7tm_2, Fz, Frizzled, none; 4.25
	445709; H02592; Hs.74280; ESTs; PDZ; none; 4.25
	428134; AA421773; Hs.161008; ESTs; Armadillo_seg, none; 4.24
30	434149; Z43829; Hs.244624; hypothetical protein MGC5469; none; TM=M; SS=M; 4.24
	425118; AU078611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding, THF_DHG_CYH, THF_DHG_CYH_C, CAP_GLY, AAA, LON, Peptidase_C9, bZIP, M_xan, ur_permease, HCO3_cotransp; TM=M; SS=N; 4.24
	433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; 4.24
	447818; W79940; Hs.355279; Homo sapiens clone 24670 mRNA sequence; none, pkinase; 4.24
35	450684; AA872605; Hs.25333; Interleukin 1 receptor, type II; Ig; TM=Y; SS=M; 4.23
	435542; AA887376; Hs.351226; ESTs; SH3, Ig, pkinase, PH, spectrin, RhoGEF; none; 4.23
	426224; BE085860; Hs.374468; karyopherin (importin) beta 2; Armadillo_seg, HEAT; TM=M; SS=N; 4.23
	413284; AU077055; Hs.289107; baculoviral IAP repeat-containing 2; zf-C3HC4, CARD, BIR, death, Ig; TM=M; SS=N; 4.22
	421917; AB028943; Hs.109445; KIAA1020 protein; BTB, zf-C2H2, PI3_P4_kinase, PI3Ka; TM=M; SS=N; 4.22
40	431239; A1039971; Hs.251216; hypothetical protein DKFZp434A196; SH2, ank, WH2; 4.22
	419685; W76083; Hs.134185; ESTs; none; TM=M; SS=N; 4.22
	431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP, Rhabd_glycop, integrin_A; TM=Y; SS=M; 4.22
	425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; 4.21
	422219; AW978073; Hs.1010; regulator of mitotic spindle assembly 1; pkinase, none; 4.21
45	450746; D82673; Hs.278589; general transcription factor II, i; none, SH3, PX; 4.21
	428023; A1038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fcs, clone L; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P4_kinase, FAT, FATC, BoA, RUN; TM=M; SS=N; 4.21
	416907; W60909; ; gbzd29g10.s1 Soares_fetal_heart_NbHH19W; ion_trans, none; 4.21
	411768; NM_013371; Hs.71979; Interleukin 19; IL10; 4.21
50	425262; D87119; Hs.155418; GS3955 protein; pkinase; 4.21
	430035; NM_003463; Hs.227777; protein tyrosine phosphatase type IVA, m; Y_phosphatase, DSPc; TM=M; SS=N; 4.21
	411789; AF245505; Hs.72157; Adicant; Ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 4.15
	416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none, none; 4.14
	419452; A33835; Hs.90572; PTK7 protein tyrosine kinase 7; Ig, pkinase; TM=Y; SS=M; 4.13
55	431745; AW972448; Hs.163425; Novel FGENSESH predicted cadherin repeat; none, none; 4.10
	416965; N26223; Hs.160436; MDAC1; none; NA; NA; 3.94
	426890; AA393167; Hs.41294; ESTs; none, none; 3.88
	442438; AA995998; Hs.370007; gbzcs26b03.s1 NCI_CGAP_Kid5 Homo sapiens; none, DNA_pol_B, DNA_pol_B_exo; 3.86
	412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor; 7tm_1; TM=Y; SS=M; 3.84
60	448243; AW369771; Hs.367688; integrin, beta 8; integrin_B, none; 3.64
	439318; AW837048; Hs.6527; G protein-coupled receptor 56; 7tm_2, CytC_asm, GPS; TM=Y; SS=M; 3.61
	415999; AA172179; Hs.294029; ESTs; none, none; 3.60
	429466; M85835; Hs.12827; ESTs; none, none; 3.45
	407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 3.34
65	400517; ; lengsin; none; TM=M; SS=N; 3.17
	439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 2.88
	426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 2.84
	414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN; TM=M; SS=M; 2.81
	424522; A1134847; Hs.149957; ribosomal protein S6 kinase, 90kD, poly; pkinase, pkinase_C; 2.70
70	438167; R28353; Hs.24266; chemokine binding protein 2 (CCBP2), mRN; none; TM=Y; SS=M; 2.68
	418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestine; cadherin; TM=Y; SS=M; 2.17

TABLE 23B

75	Pkey: Unique Eos probeset identifier number
	CAT number: Gene cluster number
	Accession: Genbank accession numbers
80	Pkey CAT Number Accession
	409745 MH1944_5 BI030997 AA921874 AW188822 BI027862 A1347618 A1361453 A1088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	417886 1031334_1 AA210987 D57294 AA214584 AA207006 D56572
	438993 2580163_1 A1926361 AA634879 AA828995

418859 12789_14 AA229762 AA230035
416907 1112245_1 W60909 W61051 M78905 BG959483

TABLE 23C

Pkey: Unique number corresponding to an Eos probe
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404287	2326514	Plus	53134-53281
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
400517	9796686	Minus	49996-50346

TABLE 24A: 571 GENES UP-REGULATED IN HEAD AND NECK TUMORS COMPARED WITH NORMAL BODY TISSUES

Table 24A lists about 571 genes up-regulated in head and neck tumors compared with normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probe set identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 70th percentile of AI for head and neck cancer samples vs. the 80th percentile of the AI for normal body tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
421155	H87879	Hs.102267	lysyl oxidase	166.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	156.00
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	80.00
438274	AI918906	Hs.55080	ESTs	28.00
401486				121.00
446999	AA151520	Hs.334822	hypothetical protein MGC4485	126.00
423887	AL080207	Hs.134585	DKFZP434G232 protein	13.00
419569	AI971651	Hs.91143	Jagged 1 (Alagille syndrome)	98.00
428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00
420602	AF060877	Hs.99236	regulator of G-protein signalling 20	35.00
445019	AI205540	Hs.281295	ESTs	93.00
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	270.62
449722	BE280074	Hs.23960	cyclin B1	9.81
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	373.00
424086	AI351010	Hs.102267	lysyl oxidase	200.00
447078	AW885727	Hs.301570	ESTs	184.00
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	177.00
409506	NM_006153	Hs.64589	NCK adaptor protein 1	170.00
426471	M22440	Hs.170009	transforming growth factor, alpha	158.00
413268	AL039079	Hs.75255	regulator of G-protein signalling 1	155.00
419948	AB041035	Hs.93847	NADPH oxidase 4	140.00
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	139.00
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	111.00
452785	AW392555	Hs.18878	hypothetical protein FLJ21620	109.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	106.00
416283	NM_005429	Hs.79141	vascular endothelial growth factor C	95.00
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	92.00
449101	AA205847	Hs.23016	G protein-coupled receptor	92.00
442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	86.00
438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothe	85.68
414132	AI801235	Hs.48480	ESTs	85.00
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	83.00
402047	AK001921	Hs.169575	hypothetical protein MGC2550	80.00
414972	BE263782	Hs.77695	KIAA0008 gene product	74.00
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	74.00
416661	AA634543	Hs.79440	IGF-1I mRNA-binding protein 3	71.00
427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	70.19
449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	66.25
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	66.00
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	64.00
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	63.00
432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothe	60.00
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	58.00
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	57.00
418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	57.00
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	54.00
452188	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothe	54.00
423020	AA383092	Hs.1608	replication protein A3 (14kD)	49.00

	422426	W79117	Hs.58559	ESTs	49.00
	405747	AI925153	Hs.217493	annexin A2	46.00
	445828	F05802	Hs.81907	ESTs	46.00
5	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamily	44.00
	452909	NM_015368	Hs.30985	pannexin 1	43.95
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	43.00
	458027	L49054	Hs.85195	myeloid leukemia factor 1	43.00
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	43.00
10	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	42.00
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	40.00
	433859	AW896758	Hs.273789	ESTs	38.00
	426753	T89832	Hs.170278	ESTs	37.00
	400792	AA635082	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	36.00
	402034				35.00
15	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	34.00
	458424	AI084049	Hs.206761	ESTs	34.00
	435159	AA668879	Hs.116649	ESTs	33.00
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	32.00
20	444361	W76027	Hs.23920	hypothetical protein FLJ11105	31.00
	439128	AI949371	Hs.153089	ESTs	29.20
	420795	AA323037	Hs.128645	sorting nexin 16	26.00
	422505	AL120862	Hs.124165	ESTs	25.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	24.00
25	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	22.10
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	19.00
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	19.00
	414869	AA157291	Hs.21479	ubiquitin 1	17.37
	453049	BE537217	Hs.30343	ESTs	16.00
30	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	14.00
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	13.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	10.00
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	9.60
35	414231	AI468004	Hs.278956	hypothetical protein FLJ12929	9.00
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	8.09
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	8.07
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.07
	417791	AW965339	Hs.111471	ESTs	8.04
40	436486	AA742221	Hs.120633	ESTs	7.23
	432731	R31178	Hs.287820	fibronectin 1	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	5.18
	435039	AW043921	Hs.130526	ESTs	5.00
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.25
45	457001	J03258	Hs.2062	vitamin D (1,25-dihydroxyvitamin D3) re	4.24
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	3.74
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.19
	458531	AA367718	Hs.159083	ESTs	3.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.53
50	411388	X72925	Hs.69752	desmocollin 1	1.00
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14235 fis, clone NT	1.00
	429370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	1.00
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	1.00
	449467	AW205006	Hs.197042	ESTs	1.00
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00
	453637	NM_002589	Hs.34073	BH-proteoglycan (brain-heart)	1.00
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	517.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	618.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	226.00
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	278.00
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	56.11
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	264.00
	424717	H03754	Hs.152213	wingless-type MMTV integration site faml	124.00
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.00
65	420159	AI572490	Hs.59785	Homo sapiens cDNA: FLJ21245 fis, clone C	1.00
	415511	AI732817	Hs.182362	ESTs	1.00
	406467				141.00
	422330	D30783	Hs.115263	epiregulin	98.00
	452461	N78223	Hs.108106	transcription factor	159.00
70	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypothei	1.00
	413324	V00571	Hs.75294	cardiotropin releasing hormone	1.00
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (7.60
	443211	AI128388	Hs.143655	ESTs	99.00
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00
75	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	3.00
	439926	AW014875	Hs.137007	ESTs	2.79
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	94.00
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	1.22
	448062	AW295923	Hs.255472	KIAA1843 protein	1.00
80	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.27
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00
	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	89.00
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	1.00

	449773	R76294	Hs.302383	ESTs	1.00
	443054	AJ745185	Hs.8939	yes-associated protein 65 kDa	90.00
	432097	X51730	Hs.2905	progesterone receptor	1.00
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	0.38
	430184	AB013802	Hs.234790	contactin 5	1.00
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.23
	415025	AW207091	Hs.72307	ESTs	1.00
	416575	W02414	Hs.38383	ESTs	1.00
10	443171	BE281128	Hs.9030	TONDU	0.92
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	20.30
	400844				0.60
	409402	AF208234	Hs.695	cystatin B (stafin B)	1.96
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.38
15	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.60
	400751				1.34
	436361	AA825814	Hs.149065	ESTs	0.92
	455612	BE042896	Hs.274848	ESTs	0.81
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	1.55
20	404148				0.77
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	1.00
	446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.47
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.92
	442994	AJ026718	Hs.16954	ESTs	0.40
25	415327	H22769		gbym54c02.r1 Soares infant brain 1N18 H	0.47
	418624	AJ734080	Hs.104211	ESTs	1.90
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	0.54
	401747			Homo sapiens keratin 17 (KRT17),	7.22
	442432	BE093589	Hs.38178	hypothetical protein FLJ23458	5.10
30	418259	AA215404	Hs.137289	ESTs	1.28
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	8.13
	403381				21.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoiesi	0.00
	418216	AA662240	Hs.283099	AF15q14 protein	11.29
35	444649	AW207523	Hs.197628	ESTs	0.10
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	4.64
	402230				1.64
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.97
40	447334	AA515032	Hs.91109	ESTs	0.62
	432829	W60377	Hs.57772	ESTs	0.86
	418686	Z36830	Hs.87268	annexin A8	8.44
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.68
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	2.22
45	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	78.00
	425721	AC002115	Hs.159309	uroplakin 1A	0.88
	420370	Y13645	Hs.97234	uroplakin 2	0.87
	417720	AA205825	Hs.208087	ESTs	5.83
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.sa	1.07
	431753	X76029	Hs.2841	neuromedin U	7.00
50	402075				288.00
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	363.00
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.81
	405064				1.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	2.00
55	441233	AA972965	Hs.135568	ESTs	1.00
	456034	AW450979		gb:U1-H-BI3-ata-a-12-0-UI.s1 NCL_CGAP_Su	1.23
	414221	AW450979		gb:U1-H-BI3-ata-a-12-0-UI.s1 NCL_CGAP_Su	0.65
	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1.00
	405494				1.00
60	407189	AA598927		gb:aa37e03.s1 Gessler Wilms tumor Homo s	1.00
	403085				1.00
	408633	AW963372	Hs.45677	PRO2000 protein	2.46
	435257	AA677026	Hs.191217	ESTs	1.00
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00
65	445182	AW169787	Hs.147474	ESTs	0.50
	417275	X63578	Hs.295449	parvalbumin	1.00
	418406	X73501	Hs.84905	cytokeratin 20	1.00
	421110	AJ250717	Hs.1355	cathapsin E	1.00
	406081				2.13
70	449448	D60730	Hs.57471	ESTs	123.00
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.37
	408243	Y00787	Hs.624	interleukin 8	3.35
	436246	AW450963	Hs.119991	ESTs	51.00
	440304	BE159984	Hs.125395	ESTs	1.00
75	402778				1.00
	406117				1.00
	406360				71.00
	435347	AW014873	Hs.116963	ESTs	1.00
80	445550	AJ242754	Hs.137306	ESTs	1.00
	451359	H85334	Hs.336623	ESTs	1.00
	419559	Y07828	Hs.91096	ring finger protein	1.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	58.00
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00
	402901				0.85

5	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	0.87
	417715	AW969587	Hs.86366	ESTs	5.12
	442577	AA292998	Hs.163900	ESTs	2.19
	418857	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.54
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.11
10	412610	X90908	Hs.74126	fatty acid binding protein 6, foal (gas	1.27
	414683	S78296	Hs.76688	hypothetical protein MGC12702	0.67
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.03
	403903				0.87
	405033				0.13
15	422282	AF019225	Hs.114309	apolipoprotein L	2.13
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.59
	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.69
	459702	AI204995			1.00
20	446082	AI274139	Hs.156452	ESTs	0.60
	400843				0.76
	417409	BE272506	Hs.82109	syndecan 1	1.78
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	1.20
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.50
25	404875				0.80
	436293	AI601188	Hs.120910	ESTs	1.40
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.03
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.94
	404977			Insulin-like growth factor 2 (somatomedi	0.99
30	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.10
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	0.85
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.20
	420876	AA918425	Hs.177744	ESTs	0.85
	422119	AI277829	Hs.111862	KIAA0590 gene product	0.71
35	400846			sortilin-related receptor, L(DLR class)	0.75
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	4.01
	430152	AB001325	Hs.234642	aquaporin 3	1.74
	402777				0.70
	417151	AA194055	Hs.293858	ESTs	0.99
40	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.48
	405034	AL035754	Hs.2474	tol-like receptor 1	1.00
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	18.68
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.94
	453134	AA032211	Hs.118493	ESTs	0.70
45	440006	AK000617	Hs.6844	hypothetical protein FLJ20510	2.19
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	0.25
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.74
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.07
	438315	R56795	Hs.82419	ESTs	0.65
50	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	1.18
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	0.85
	444444	AI149332	Hs.14855	ESTs	0.59
	407581	R48402	Hs.173508	P3ECSL	0.82
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	0.92
55	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	0.62
	446024	AB040946	Hs.284227	KIAA1513 protein	0.92
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.42
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.68
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	1.57
60	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.08
	446009	AI989885	Hs.231926	ESTs	1.00
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	0.98
	415949	H10562	Hs.21691	ESTs	0.61
	420281	AI623693	Hs.191533	ESTs	7.01
65	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	0.72
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.21
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	0.99
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	0.54
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.06
70	426900	AW163564	Hs.142375	ESTs	0.48
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	0.83
	402305				0.89
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.04
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
75	436608	AA628980	Hs.192371	down syndrome critical region protein DS	0.65
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	0.63
	405932				1.76
	401760				2.61
	452240	AI591147	Hs.61232	ESTs	453.00
80	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.04
	421373	AA808229	Hs.167771	ESTs	17.00
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.16
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.68
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.19
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.73
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal kd	1.00
	454789	BE156314		gb:QV0-HT0387-150200-114-d02 HT0387 Homo	1.00

	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	0.06
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.45
	418067	AI127958	Hs.83393	cystatin E/M	1.41
5	441801	AW242799	Hs.86366	ESTs	140.00
	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	2.45
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	58.00
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	1.17
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	0.86
10	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	0.91
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	1.00
	453204	R10799	Hs.191990	ESTs	1.13
	437240	AA747537		gb:u85c05.s1 NCI_CGAP_GCB1 Homo sapiens	1.00
	405531				0.92
15	440249	AI246590	Hs.337275	ESTs	1.32
	426783	Z19084	Hs.172210	MUF1 protein	1.17
	434192	AW387314	Hs.34371	ESTs	1.00
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	87.14
	402001				37.00
20	433967	AF113018	Hs.284302	PRO1621 protein	1.00
	451592	AI805416	Hs.213897	ESTs	10.00
	422170	AI791949	Hs.112432	anti-Müllerian hormone	0.67
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	1.00
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.99
25	441940	AW298115	Hs.128152	ESTs	0.88
	425048	H05468	Hs.164502	ESTs	0.33
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.01
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.06
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.45
30	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.62
	410348	AW182663	Hs.95469	ESTs	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	0.04
	414907	X90725	Hs.77597	pdk (Drosophila)-like kinase	1.04
	441795	N58115	Hs.21137	AD024 protein	10.00
35	418583	AA604379	Hs.86211	hypothetical protein	1.22
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	106.67
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	2.30
	441495	AW294603	Hs.127039	ESTs	0.44
	417933	X02308	Hs.82962	thymidylate synthetase	2.48
40	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.00
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazzaro	1.44
	430034	X60155	Hs.227767	zinc finger protein 41	1.00
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.87
45	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	0.54
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	2.27
	417599	AA204688	Hs.136201	ESTs	1.01
	438366	AA805760	Hs.303567	ESTs	1.00
	438746	AI885815	Hs.184727	ESTs	1.47
50	409691	T89983	Hs.246042	Homo sapiens, clone MGC:5437, mRNA, comp	1.00
	408827	AW275730	Hs.254825	ESTs	1.00
	414735	BE468016	Hs.281904	ESTs	1.00
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	5.21
	412719	AW016610	Hs.129911	ESTs	494.00
55	417034	NM_006183	Hs.80962	neurotensin	1.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	23.36
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.98
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	7.50
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	9.77
60	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	445.00
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakines	13.93
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	12.77
	452838	U65011	Hs.30743	preferentially expressed antigen in meta	45.00
	418663	AK001100	Hs.41690	desmocollin 3	10.89
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.29
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	0.88
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	38.31
	421948	L42583	Hs.334309	keratin 6A	36.81
	431848	BE019924	Hs.271580	uroplakin 1B	1.37
70	424098	AF077374	Hs.139322	small proline-rich protein 3	8.85
	453964	AI961486	Hs.12744	ESTs	0.40
	446858	AI814373	Hs.164175	ESTs	1.18
	443648	AI085377	Hs.143610	ESTs	2.15
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	4.39
75	431384	BE158000		gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.18
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.22
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	164.00
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	9.85
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.59
80	441020	W79283	Hs.35962	ESTs	5.76
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.97
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.09
	444371	BE540274	Hs.239	forkhead box M1	2.44
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.39

5	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.53
	426440	BE382756	Hs.169502	solute carrier family 2 (facilitated glu	1.67
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	2.30
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.04
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.11
10	401781				11.07
	401780				9.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62
	417389	BE260964	Hs.82045	midkine (neurile growth-promoting factor	1.12
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	947.00
15	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.79
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.16
	440704	MS9241	Hs.162	insulin-like growth factor binding prote	1.08
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.20
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	2.53
20	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	72.00
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	19.86
	409103	AF251237	Hs.112208	XAGE-1 protein	0.47
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	0.66
	428471	X57348	Hs.184510	stratlin	3.39
25	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.61
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.31
	451541	BE279383	Hs.26557	plakophilin 3	1.82
	418203	X54942	Hs.83758	CDC28 protein kinase 2	5.60
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.78
30	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.01
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.18
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.58
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.63
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.25
35	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	11.88
	430677	Z26317	Hs.94560	desmoglein 2	1.38
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.09
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.09
	422963	M79141	Hs.13234	ESTs	2.28
40	418462	BE001596	Hs.85266	Integrin, beta 4	1.40
	450832	AW970602	Hs.105421	ESTs	13.31
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.25
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.89
	458933	AI638429	Hs.24763	RAN binding protein 1	1.54
45	439394	AA149250	Hs.56105	ESTs	3.89
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.77
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.52
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.11
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
50	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.84
	440325	NM_003812	Hs.7184	a disintegrin and metalloproteinase doma	0.61
	439606	W79123	Hs.58561	G protein-coupled receptor 87	303.00
	453684	AA355925	Hs.36232	KIAA0186 gene product	10.55
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38
55	451743	AW074266	Hs.23071	ESTs	2.90
	413129	AF292100	Hs.104613	RP42 homolog	2.38
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	5.92
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.18
60	416819	U77735	Hs.80205	pim-2 oncogene	1.01
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	0.67
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.19
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.55
	425397	J04088	Hs.158346	topoisomerase (DNA) II alpha (170kD)	3.06
65	413004	T35901	Hs.75117	Interleukin enhancer binding factor 2, 4	1.64
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	7.04
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	203.00
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33
	430337	M36707	Hs.239600	catmodulin-like 3	1.32
70	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	81.00
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.03
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	28.00
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.24
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.40
75	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.55
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00
	418678	NM_001327	Hs.167379	concentrin antigen	0.82
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00
	427335	AA448542	Hs.251677	G antigen 7B	0.91
80	409420	Z15008	Hs.54451	laminin, gamma 2 (necilin (100kD), kalini	6.53
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	1.35
	421917	AB028943	Hs.109445	KIAA1020 protein	0.94
	404440				38.57
	409582	R27430	Hs.271565	ESTs	3.19
	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.45
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.61
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	1.95

	408380	AF123050	Hs.44532	diubiquitin	7.23
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.35
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	0.81
	446102	AW168067	Hs.252956	ESTs	1.03
5	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	137.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.91
	423761	NM_006194	Hs.132576	paired box gene 9	36.00
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.35
10	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	207.00
	440659	AF134160	Hs.7327	claudin 1	3.06
	434360	AW015415	Hs.127780	ESTs	3.89
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoma	1.28
	438898	AI819863	Hs.106243	ESTs	1.73
	441553	AA281219	Hs.121296	ESTs	1.47
15	418379	AA218940	Hs.137516	fidgin-like 1	40.42
	436396	AI683487	Hs.152213	wingless-type MMTV integration site faml	14.25
	429413	NM_014058	Hs.201877	DESC1 protein	5.17
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.95
20	415380	F07953	Hs.16085	putative G-protein coupled receptor	0.18
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.09
	429538	BE182592	Hs.11261	small proline-rich protein 2A	6.14
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00
25	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	44.00
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	149.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	127.00
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	20.00
	404996				147.00
30	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	54.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	139.00
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR	22.00
	438702	AI879064	Hs.54618	ESTs	1.00
35	444378	R41339	Hs.12569	ESTs	1.00
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	41.00
	407839	AA045144	Hs.161566	ESTs	7.50
	439223	AW238299	Hs.250618	UL16 binding protein 2	3.39
	409041	AB033025	Hs.50081	KIAA1199 protein	245.00
40	429228	AI553633	Hs.337139	ESTs	10.89
	409757	NM_001898	Hs.123114	cystatin SN	3.19
	411089	AA458454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	0.78
	436511	AA721252	Hs.291502	ESTs	0.23
	449207	AL044222	Hs.23255	nucleoporin 155kD	1.68
45	453331	AI240665	Hs.8895	ESTs	5.21
	409935	AW511413	Hs.278025	ESTs	0.75
	428969	AF120274	Hs.194689	artemin	1.17
	445443	AV653838	Hs.322971	ESTs	1.00
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	11.42
50	401785				2.76
	412723	AA648459	Hs.335951	hypothetical protein AF301222	107.00
	450701	H39960	Hs.288457	Homo sapiens cDNA FLJ12280 fis, clone MA	2.17
	405770				2.42
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.24
	420783	AI859838	Hs.99923	lectin, galactoside-binding, soluble, 7	4.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.85
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.44
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.33
60	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.11
	427441	AA412605	Hs.178053	SPANX family, member C	5.00
	403478				0.78
	400842				0.16
	441525	AW241867	Hs.127728	ESTs	0.79
65	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	1.50
	405646				1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	0.79
	431413	AA504777	Hs.105293	ESTs	1.00
	401994				3.25
70	402420				0.05
	404298				0.64
	404927				88.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	0.96
	436961	AW375974	Hs.156704	ESTs	3.58
75	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	0.92
	426067	AW664691	Hs.97053	ESTs	0.97
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	0.66
	426897	AW976570	Hs.97387	ESTs	1.29
	443892	AI889572	Hs.134791	ESTs	1.00
	413223	AI732182	Hs.191866	ESTs	0.79
80	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.51
	423394	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	2.59
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.39
	420758	AW297536	Hs.33053	ESTs	0.89

5	423816	AL031985	Hs.133034	hypothetical protein	1.00
	447534	AW953935	Hs.30837	ESTs	1.88
	451919	W05086	Hs.114256	ESTs, Weakly similar to I78885 serine/th	0.11
	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell	0.92
	403715				0.89
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	37.00
	436839	AA767346	Hs.291614	ESTs	1.00
10	413582	AW295647	Hs.71331	hypothetical protein MGC5350	59.00
	413573	AI733859	Hs.149089	ESTs	78.00
	430686	NM_001942	Hs.2633	desmoglein 1	127.08
	438993	AA828995		gbxod77b08.s1 NC1_CGAP_Ov2 Homo sapiens	1.00
	448243	AW369771	Hs.52620	Integrin, beta 8	133.00
15	444783	AK001468	Hs.62180	enilfin (Drosophila Scraps homolog), act	232.00
	426427	M86699	Hs.169840	TTK protein kinase	66.00
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	148.00
	445537	AJ245871	Hs.12844	EGF-like domain, multiple 6	40.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.00
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	108.00
	400288	AA032279	Hs.61635	six transmembrane epithelial antigen of	159.00
	415989	AI267700	Hs.317584	ESTs	196.00
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	32.44
	453160	AI263307	Hs.239884	H2B histone family, member L	7.00
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.13
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	45.00

TABLE 24B

30	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accessions:	Genbank accession numbers	
35	Pkey	CAT number	Accessions
	411880	1263110_1	AW872477 BE088101 T05990
	412296	1288043_1	AW936233 AW936272
	413804	1390710_1	T64682 BE168190 BE168256
40	414221	142696_1	AW450979 AA136653 AA136556 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
	415327	1534137_1	H22769 R35182 Z43545 F05783 N92089 H71928
	427260	276598_1	AA663848 AA400100 AA401424
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
45	431384	33264_1	BE158000 BE157999 H75671 H70965 C18895 BE386512 BE385815 BE390298 AI341995 BE074534 AA055592 AA132265 AI733757 AA134504 BE145037 AA055887 BE070191 R66492 AW858018 AW858058 AW817057 AW862031 AW861688 AW862029 AW858805 AW858792 AW862028 AW858017 AW819164 AW853698 AI522161 AW854789 AW817408 BE152005 AJ732411 AA133084
	432222	343347_1	AI204995 AW827539 AW969908 AW440778 AA528756
	437214	434730_1	BE092336 BE092259 BE092497 BE092051 AA746882 AI336378
	437240	435139_1	AA747537 BE089068 BE089070
50	438993	467651_1	AA828995 AA834879 AI926361
	439780	47673_1	AL109688 R23665 R26578
	444163	593658_1	AI126098 AI184746 AI148521
	451844	888230_1	T61430 AI820546 AI821336
	453823	982526_1	AL137967 BE064160 BE064186
55	454789	1234742_1	BE156314 BE156316 AW820750
	456034	142696_1	AW450979 AA136653 AA136556 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 24C

65

Pkey:

Ref:

Strand:

NT_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

70

Pkey

Ref

Strand

NT_position

400751

7331445

Minus

35395-35533

400842

1927148

Plus

90462-90573

400843

9188605

Plus

5863-5970,7653-7764,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958

400844

9188605

Plus

24746-24872,25035-25204

75

400846

9188605

Plus

39310-39474

401486

7341763

Plus

32585-32756,36281-36540,40791-40933,44018-44179

401747

9789672

Minus

118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011

401760

9929699

Plus

83126-83250,85320-85540,94719-95287

80

401780

7249190

Minus

28397-28617,28920-29045,29135-29298,29411-29567,29705-29787,30224-30573

401781

7249190

Minus

83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814

401785

7249190

Minus

165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942

401994

4153858

Minus

42904-43124,43211-43336,44607-44763,45199-45281,46337-46732

402001

9501818

Plus

68052-68223

5	402034	7684482	Minus	86227-86451
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402230	9966312	Minus	29782-29932
	402305	7328724	Plus	40832-41362
	402420	9796339	Plus	129750-129919
	402777	9588235	Plus	126786-126948
	402778	9588235	Plus	128560-128702
	402901	8894222	Minus	175426-175667
10	403085	8954241	Plus	165035-165334,165420-165713
	403381	9438267	Minus	26009-26178
	403478	9958258	Plus	116458-116564
	403715	7239669	Plus	85128-85292
	403903	7710671	Minus	101165-102597
15	404148	9863703	Plus	78218-78418,79571-79709
	404298	9944263	Minus	73591-73723
	404440	7528051	Plus	80430-81581
	404875	9801324	Plus	96588-96732,97722-97831
	404927	7342002	Plus	68690-69563
	404977	3738341	Minus	43081-43229
20	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405033	7107731	Minus	142358-142546
	405064	7658416	Plus	81207-81416
	405494	8050952	Minus	70284-70518
25	405531	9665194	Plus	35602-35803
	405646	4914350	Plus	741-969
	405770	2735037	Plus	61057-62075
	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
30	406117	9142932	Plus	54304-54584
	406360	9256107	Minus	7513-7673
	406467	9795551	Plus	182212-182958

35 TABLE 25A: 691 genes upregulated in head and neck cancer relative to normal body tissues

40 Table 25A lists about 691 genes upregulated in head and neck cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

45 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 85th percentile of head and neck cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

50 Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Prod.Domains; R1

55 422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; ehand,S_100;TM=M;SS=N; 46.25
 408522; AJ541214; Hs.46320; Small proline-rich protein SPRK [human, ; none;Comifin; 40.37
 417366; BE185289; Hs.1076; small proline-rich protein 1B (comifin); Comifin;TM=M;SS=N; 38.94
 401781; ; Target Exon; filament;TM=M;SS=N; 29.74
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.54
 401780; ; NM_005557; Homo sapiens keratin 16 (foca; filament;TM=M;SS=N; 28.58
 60 424098; AF077374; Hs.139322; small proline-rich protein 3; Comifin;TM=M;SS=N; 28.55
 421948; L42583; Hs.334309; keratin 6A; filament;RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 25.74
 428471; X57348; Hs.184510; stratifin; 14-3-3;TM=M;SS=N; 23.65
 417079; U65590; Hs.811134; Interleukin 1 receptor antagonist; IL1; 21.02
 421574; AJ000152; Hs.105924; defensin, beta 2; Defensin_beta;TM=M;SS=M; 20.83
 65 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyperkeratosis); filament,bZIP,UvrD-helicase,TBCA;TM=M;SS=N; 20.72
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt;TM=M;SS=Y; 19.63
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 19.53
 420783; AB59838; Hs.99923; lectin, galactoside-binding, soluble, 7; Gal-bind_lectin;TM=M;SS=N; 19.12
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ehand,S_100,S_100,ehand; 17.93
 70 416091; AF295370; Hs.283082; defensin, beta 3; Defensin_beta;TM=M;SS=M; 17.63
 431211; M86849; Hs.323733; gap junction protein, beta 2, 26kD (conn; connexin;TM=Y;SS=M; 16.94
 429259; AA420450; Hs.380088; Plakophilin; none;none; 14.92
 417515; L24203; Hs.82237; ataxia-telangiectasia group D-associated; zf-B_box,zf-UBR1;TM=M;SS=N; 14.75
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none;TM=M;SS=M; 14.45
 75 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase_M10,Atacina,PG_binding_1; 13.02
 409532; W74001; Hs.55279; serine (or cysteine) proteinase inhibitor; serpin; 12.82
 406621; X57809; Hs.181125; immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M;SS=N; 12.81
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin_C_term;TM=Y;SS=M; 12.45
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL6; 11.71
 80 401760; ; Target Exon; none;bromodomain; 11.68
 407839; AA045144; Hs.161566; ESTs; cadherin,cadherin; 11.65
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 11.56
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6,lactamase_B; 11.31

- 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 11.03
 424012; AW368377; Hs.137569; tumor protein 63 kDa with strong homolog; SAM_P53; TM=M; SS=N; 10.75
 430630; AW269920; Hs.2621; cystatin A (stein A); cystatin; TM=M; SS=N; 10.58
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 10.30
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.25
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M; SS=N; 9.84
 446989; AK001898; Hs.16740; hypothetical protein FLJ11038; none; TM=Y; SS=N; 9.74
 402075; ; ENSP00000251056; Plasma membrane calcium; none; 9.50
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 9.50
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (connexin 3; connexin; TM=Y; SS=M; 9.48
 439310; AF086120; Hs.102793; ESTs; casein_kappa_kinase; none; 9.43
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; SS=N; 9.33
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh; TM=M; SS=M; 9.14
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (23Q/240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose_Isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,ldh,C,CH,AlP3; TM=M; SS=N; 9.12
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 9.11
 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin; TM=M; SS=M; 8.66
 452240; AJ591147; Hs.61232; ESTs; none; none; 8.57
 429228; AJ536363; Hs.356828; ESTs; none; none; 8.46
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin,Peptidase_M10,Astacin; 8.44
 425071; NM_013989; Hs.154424; deliodinase, iodothyronine, type II; T4_deliodinase; TM=M; SS=Y; 8.15
 407242; M18728; ; gb:Human nonspecific crossreacting antig; lg; TM=M; SS=M; 8.05
 407944; R34008; Hs.239727; desmocollin 2; cadherin, Cadherin_C_term,Ha1a_C2; TM=Y; SS=M; 7.90
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 7.82
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrylsin, ; Peptidase_M10; 7.82
 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M; SS=N; 7.77
 413753; U17760; Hs.75517; laminin, beta 3 (necin (125kD), kallinin; laminin_EGF,laminin_Nterm; 7.76
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz_BPTI,fn3,vwa,Collagen,beta-lactamase; TM=M; SS=M; 7.71
 430686; NM_001942; Hs.2633; desmoglein 1; cadherin, Cadherin_C_term; TM=Y; SS=M; 7.69
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf; TM=M; SS=N; 7.54
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P4_kinase,FAT,FATC,BolA,RUN; TM=M; SS=N; 7.53
 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin_C_term; none; 7.30
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide,TGF-beta; none; 7.28
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin; TM=Y; SS=M; 7.26
 412719; AW016610; Hs.816; ESTs; none; none; 7.17
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteoopontin, ; Osteopontin; 7.10
 423961; D13666; Hs.136348; perlestin (OSF-Zos); Fasciclin; TM=M; SS=M; 7.09
 427666; A1791495; Hs.180142; calmodulin-like skin protein (CLSP); ehand; TM=M; SS=N; 7.08
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 7.06
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin,Peptidase_M10; TM=M; SS=M; 7.03
 401747; ; Homo sapiens keratin 17 (KRT17); none,bromodomain; 7.01
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT; none; 6.98
 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg; TM=M; SS=N; 6.96
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (collagenase; hemopexin,Peptidase_M10; 6.87
 417715; AW969587; Hs.86366; ESTs; none; none; 6.72
 422440; NM_004812; Hs.116724; aldo-keto reductase family 1, member B10; aldo_ket_red,ROK; TM=M; SS=N; 6.50
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin,Peptidase_M10; TM=M; SS=M; 6.39
 418844; M52982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT; TM=M; SS=N; 6.38
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B, ; Sulfotransfer; 6.38
 425397; J04088; Hs.156348; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolv,HATPase_c; 6.35
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank; TM=M; SS=N; 6.30
 409420; Z15008; Hs.54451; laminin, gamma 2 (necin (100kD), kallini; laminin_B,laminin_EGF; 6.28
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin; ras; TM=M; SS=N; 6.27
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 6.23
 424587; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2,hemopexin,Peptidase_M10; 6.22
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; SS=N; 6.21
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3; TM=Y; SS=M; 6.12
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase inhibitor; serpin; 6.08
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none; none; 6.08
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 6.04
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fg; none; 5.81
 439223; AW238299; Hs.250618; UL16 binding protein 2; Idl_recept_a,PKD,MHC_F; TM=M; SS=Y; 5.77
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_Oxidase; TM=M; SS=M; 5.72
 454098; W27953; Hs.217493; Plakophilin; none; none; 5.71
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40; TM=M; SS=N; 5.70
 435505; AF200492; Hs.211238; Interleukin-1 homolog 1; IL1; TM=M; SS=N; 5.69
 406685; M18728; ; gb:Human nonspecific crossreacting antig; lg; TM=M; SS=M; 5.67
 430280; AA361258; Hs.237668; interleukin 7 receptor; fn3; none; 5.63
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none; TM=Y; SS=M; 5.61
 449722; BE280074; Hs.23960; cyclin B1; cyclin,cyclin_C; TM=M; SS=N; 5.61
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 5.60
 452862; AW378065; Hs.8587; ADAMTS2 (a disintegrin-like and metallo; Pep_M12B_propep,isp_1,Reprolysin; none; 5.58
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,arf; TM=M; SS=M; 5.57
 411265; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy; TM=M; SS=M; 5.55
 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpepLPropep_M14; 5.54
 416819; U77735; Hs.80205; pim-2 oncogene; kinase; 5.48
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (stromelysin ; hemopexin,Peptidase_M10,Astacin; 5.47
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; lg,Rhbd_glycop; TM=Y; SS=M; 5.46
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2; TM=Y; SS=M; 5.42
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 5.35
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 5.28
 418462; BE001596; Hs.85266; integrin, beta 4; fn3,Integrin_B,Catx-beta,EGF; TM=M; SS=M; 5.26

- 429554; NM_012275; Hs.207224; Interleukin 1, delta; IL1; TM=M; SS=N; 5.14
- 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN_HIN; TM=M; SS=N; 5.13
- 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none; TM=M; SS=N; 5.11
- 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosophila, mous; NHL; TM=M; SS=N; 5.11
- 5 428227; AA321649; Hs.2248; smad inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 5.08
- 436396; AJ583487; Hs.152213; wingless-type MMTV integration site famt; wnt; none; 5.07
- 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig; TM=M; SS=M; 5.05
- 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase, LIM, PDZ, zf-PARP; TM=M; SS=N; 5.04
- 10 414035; Y00630; Hs.75718; serine (or cysteine) proteinase inhibitor; serpin; 5.00
- 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH, death, TNFR_c6, Acyl-CoA_hydro; 4.96
- 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 4.93
- 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkines; kinesin, Tropomyosin; TM=M; SS=N; 4.92
- 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF, MAM; 4.91
- 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfam; 60s_ribosomal, Ribosomal_L10, TNFR_c6, DEAD; 4.90
- 15 436553; AW407157; Hs.181125; immunoglobulin lambda locus; Ig, HSP70, Ppx-GppA; TM=M; SS=N; 4.89
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 4.84
- 430024; AJ808780; Hs.227730; integrin, alpha 6; Integrin_A, FG-GAP; TM=Y; SS=M; 4.81
- 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none, none; 4.80
- 20 444371; BE540274; Hs.239; forkhead box M1; Fork_head; TM=M; SS=N; 4.75
- 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.74
- 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.69
- 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP, Rhabd_glycop, Integrin_A; TM=Y; SS=M; 4.69
- 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none, pkinase, fn3, Ig; 4.68
- 25 418067; AJ127958; Hs.83393; cystatin E/M; cystatin; 4.66
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plant_thionins; 4.64
- 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 4.62
- 410418; D31382; Hs.63325; transmembrane protease, serine 4; ldl_recept_a, trypsin; TM=Y; SS=M; 4.60
- 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin_G, CoA; 4.60
- 30 438113; AJ467908; Hs.8882; ESTs; 7tm_1, none; 4.60
- 418140; BE613838; Hs.83551; microfilament-associated protein 2; none; TM=M; SS=M; 4.57
- 408380; AF123050; Hs.44532; diubiquitin; ubiquitin; TM=M; SS=N; 4.55
- 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.50
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 4.50
- 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death, DED; 4.49
- 35 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1; TM=Y; SS=M; 4.48
- 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD, helicase_C, rrm, Ndr, Cys_knot, TIL_vwa, vwc, vwd, IO, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, lrp_1, Ribosomal_S21, rvp; TM=M; SS=N; 4.47
- 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.47
- 411789; AF245505; Hs.72157; Adilcan; Ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 4.47
- 40 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.47
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 4.45
- 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; 4.43
- 418322; AA284168; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPc; TM=M; SS=N; 4.42
- 409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none; TM=M; SS=M; 4.41
- 45 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gene; none, none; 4.40
- 450701; H39960; Hs.288467; hypothetical protein XP_098151 (leucine; none, LRRCT, LRR; 4.40
- 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2, SH3, pkinase; TM=M; SS=N; 4.38
- 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytolactin); EGF, fn3, fibrinogen_C, toxin_2, Keratin_B2; TM=M; SS=Y; 4.38
- 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 4.32
- 50 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; none; TM=M; SS=N; 4.32
- 411573; AB028000; Hs.70823; KIAA1077 protein; Sulfatase; TM=M; SS=N; 4.31
- 408243; Y00787; Hs.624; Interleukin 8; HLH, PA5, IL8; TM=M; SS=N; 4.31
- 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 4.30
- 55 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC, none; 4.29
- 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, jg, FAD_Synth, lkh, lkh_C, pkinase; 4.29
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig; TM=Y; SS=M; 4.29
- 404996; ; Target Exon; Peptidase_C1; TM=M; SS=M; 4.29
- 416539; Y07809; Hs.79358; epithelial membrane protein 1; PMP22, Claudin, oxidored_q5_N; TM=Y; SS=M; 4.28
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosome; ABC_tran, SMC_N, SMC_C, DUF164, none; 4.25
- 60 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg, HEAT; TM=M; SS=N; 4.25
- 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A, FG-GAP; TM=Y; SS=N; 4.24
- 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 4.24
- 439720; AJ935202; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_tr; 4.23
- 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M; SS=M; 4.23
- 65 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB alpha; TGF-beta, TGF-beta_propeptide, Tub; 4.20
- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA, ABC_tran, CoaE; TM=M; SS=N; 4.20
- 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 4.19
- 407137; T97307; ; gb:yeS3h05.s1 Soares fetal liver spleen; GDA1_CD39, none; 4.18
- 70 419235; AW470411; Hs.288433; neurotrophin; none, none; 4.18
- 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIG, Integrin_B; TM=Y; SS=M; 4.18
- 456908; AF117646; Hs.156637; Cas-BR-M (murine) ectropic retroviral tr; zf-C3HC4, Cbl_N, Cbl_N2, Cbl_N3; TM=M; SS=N; 4.17
- 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX; TM=M; SS=M; 4.17
- 400288; X06258; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A, FG-GAP; TM=Y; SS=N; 4.14
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 4.13
- 75 445417; AK001058; Hs.12680; a disintegrin-like and metalloprotease w; lrp_1, Reprolysin, Pep_M12B_propept, none; 4.12
- 433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase; pkinase, zf-C4, CNH, ERM; TM=M; SS=N; 4.12
- 424490; AJ278016; Hs.55565; ankryrin repeat domain 3; ank, pkinase; TM=M; SS=N; 4.09
- 419121; AA374372; Hs.89626; parathyroid hormone-like hormone; none, none; 4.08
- 80 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF, vwc, TSPN; 4.07
- 424008; R02740; Hs.137655; putative chemokine receptor; GTP-binding; 7tm_1; TM=Y; SS=M; 4.07
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 4.06
- 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 4.03
- 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, Integrin_B; TM=Y; SS=N; 4.02

- 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 4.02
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic; sugar_tr; TM=Y;SS=M; 4.01
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 4.01
 406905; Z25424; ; gb:H.sapiens protein-serine/threonine kt; none;none; 3.98
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase doma; Reprolysin,Pep_M12B_propep,disintegrin,Reprolysin,Pep_M12B_propep,disintegrin; 3.98
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 3.96
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y;SS=M; 3.95
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase, pkinase_C; TM=M;SS=M; 3.95
 417433; BE270266; Hs.82128; ST4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y;SS=M; 3.95
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR_c6; 3.93
 407792; AJ077715; Hs.39384; putative secreted ligand homologous to f; none; TM=M;SS=Y; 3.91
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF; 3.91
 415989; AI267700; Hs.351201; ESTs; none;none; 3.80
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH_1bd; TM=Y;SS=M; 3.90
 443859; NM_013409; Hs.9914; follistatin; kazak; 3.89
 429612; AF052649; Hs.252587; pituitary tumor-transforming 1; none; 3.89
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; 3.88
 450684; AA872605; Hs.25333; Interleukin 1 receptor, type II; lg; TM=Y;SS=M; 3.88
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1, pkinase; TM=M;SS=N; 3.86
 413441; AI929374; Hs.75367; Src-like adapter; SH2, SH3; TM=M;SS=N; 3.84
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP, pkinase, DAG_PE-blind, RBD; 3.83
 436291; BE568452; Hs.344037; protein regulator of cytokinesis 1; none; TM=M;SS=N; 3.82
 417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD; TM=Y;SS=M; 3.81
 427647; W19744; Hs.180069; Homo sapiens cDNA FLJ20653 fis, clone KA; none, pkinase; 3.80
 431629; AU077025; Hs.265827; Interferon, alpha-inducible protein (clo; none; TM=M;SS=Y; 3.80
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2, none; 3.80
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily; IL2; 3.79
 428157; AJ738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2, none; 3.78
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M;SS=N; 3.78
 417720; AA205625; Hs.208067; ESTs; none;none; 3.77
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP; none; 3.77
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino; aa_permeases; TM=Y;SS=M; 3.76
 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGK; TM=M;SS=N; 3.75
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; lg, ITAM, Zn_cus; TM=Y;SS=M; 3.74
 413281; AA861271; Hs.222024; transcription factor BMAL2; HLH, PAS; 3.74
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con; TM=M;SS=N; 3.74
 431890; X17033; Hs.271985; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwa, Integrin_A, FG-GAP; TM=Y;SS=M; 3.74
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; peritipin; 3.73
 426471; M22440; Hs.170009; transforming growth factor, alpha; EGF; TM=M;SS=M; 3.72
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; EGF, vwd, AMOP; 3.72
 450125; AA005418; Hs.158186; ESTs; CIDE-N, 7tm_1, none; 3.71
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; lg; TM=Y;SS=M; 3.70
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; ldl_recept_a, PKD, MHC_1; TM=M;SS=Y; 3.70
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_lr; 3.70
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M;SS=N; 3.69
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3, Y_phosphatase, carb_anhydrase; TM=Y;SS=M; 3.68
 443759; BE390832; Hs.134729; FXYD domain-containing ion transport reg; ATP1G1, PLM, MAT8; TM=Y;SS=M; 3.68
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp, STAS; 3.68
 439625; AF086453; Hs.68611; ESTs; Fork_head, glycolytic_enz, Na_sulph_symp; 3.66
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y;SS=M; 3.66
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen; 3.65
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (; SH3, PH, RhoGEF; TM=M;SS=N; 3.64
 418883; BE387038; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos; TM=M;SS=M; 3.64
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT, MBOAT; TM=Y;SS=M; 3.64
 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase-like; ubiquitin; 3.63
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN cDNA 5730; none; TM=M;SS=N; 3.62
 438746; AJ885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate_kin, PDZ, SH3; 3.62
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M;SS=Y; 3.62
 452696; AI826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate_kin, PDZ, SH3; 3.60
 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc; Galactosyl_T; TM=M;SS=Y; 3.59
 423575; C18863; Hs.163443; intron of perostin (OSF-2os); Fasciclin, none; 3.59
 421391; AW304350; Hs.181958; immunoglobulin superfamily receptor tran; lg, none; 3.58
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; lg, pkinase; TM=Y;SS=M; 3.58
 419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (; SH3, PH, RhoGEF; TM=M;SS=N; 3.58
 431457; NM_012211; Hs.256297; Integrin, alpha 11; FG-GAP, vwa; TM=Y;SS=M; 3.57
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y;SS=M; 3.55
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none; TM=Y;SS=M; 3.55
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E coli Re; none; 3.53
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M;SS=N; 3.53
 429556; AW139399; Hs.314807; ESTs; none; TM=M;SS=N; 3.52
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1; TM=Y;SS=M; 3.52
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin; TM=Y;SS=M; 3.51
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none; TM=Y;SS=M; 3.51
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y;SS=M; 3.49
 425566; AW162943; Hs.250618; UL16 binding protein 2; ldl_recept_a, PKD, MHC_1; TM=M;SS=Y; 3.48
 402447; ; C1000201.gil204418[gb]AA02627.1[L0519; none; TM=Y;SS=M; 3.48
 431183; NM_006855; Hs.250696; KDE1 (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M;SS=M; 3.48
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y;SS=M; 3.48
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3, TPR; TM=M;SS=N; 3.48
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX; Troponin, Exo_endo_phos, IQ; TM=M;SS=N; 3.47
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 3.44
 446051; BE048061; Hs.37054; ephrin-A3; Ephrin_A_deamin, dsrm, z-alpha; 3.43
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin, Reprolysin, Pep_M12B_propep, EGF; TM=Y;SS=M; 3.42

- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Ntam,Integrin_B; 3.42
 411263; BE297802; Hs.69360; kinesin-Iba 6 (mitotic centromere-assoc; kinesin; TM=M;SS=N; 3.42
 430044; AA464510; Hs.152812; ESTs; none;none; 3.42
 425289; AW139342; Hs.155530; Interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN; 3.39
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7m_1; TM=Y;SS=M; 3.39
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino a; eIF6,SDF; TM=M;SS=N; 3.39
 443848; AI085377; Hs.143610; ESTs; Fork_head,none; 3.39
 418869; AW516565; ; gb:qx01d05x1 Soares_NHCeC_cervical_tumor; none,RasGAP,WW,IQ; 3.38
 432179; X75208; Hs.2913; EphB3; EPH_Ibd,fn3,pkinase,SAM; TM=Y;SS=M; 3.38
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell; lg; TM=Y;SS=M; 3.38
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK_CoAE; 3.37
 408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein; ; UvrD-helicase,RNB,RunT; TM=M;SS=N; 3.37
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5; TM=M;SS=N; 3.37
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevis; CDC45; TM=M;SS=N; 3.37
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU; TM=M;SS=M; 3.36
 400298; AA032279; Hs.61635; six transmembrane epithelial antigen of; none; TM=Y;SS=N; 3.35
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3; 3.33
 400261; ; Hs.1802; Eos Control; Ig,MHC_II_beta; TM=Y;SS=M; 3.33
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M;SS=N; 3.32
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none;actin_c; 3.32
 416065; BE267931; Hs.78996; proliferating cell nuclear antigen; PCNA,PCNA_C; TM=M;SS=N; 3.31
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 3.31
 426840; BE244217; Hs.172690; diacylglycerol kinase, alpha (80kD); ehand,DAG_PE-bind,DAGKa,DAGKc,DC1; TM=M;SS=N; 3.31
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc; TM=M;SS=N; 3.31
 418758; AW959311; Hs.172021; hypothetical protein DKFp434J037; pkinase,RIO1; TM=M;SS=N; 3.31
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4; TM=Y;SS=M; 3.31
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT; TM=M;SS=N; 3.30
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; lg,pkinase; TM=Y;SS=M; 3.30
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,Ig,Neuregulin; TM=M;SS=N; 3.28
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox; TM=Y;SS=M; 3.28
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2; TM=M;SS=N; 3.28
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=M; 3.27
 431886; L77564; Hs.271980; mitogen-activated protein kinase 6; pkinase; TM=M;SS=N; 3.27
 430397; AI924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp; TM=Y;SS=N; 3.27
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_P4_kinase,FAT,FATC; TM=M;SS=N; 3.26
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none; TM=M;SS=M; 3.26
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH,none; 3.25
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7m_2; TM=Y;SS=M; 3.25
 405932; ; C15000305:g[3806122]gb[AA069198.1] (AF0; ras; TM=M;SS=N; 3.25
 40205; ; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe); DUF173; 3.25
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M;SS=Y; 3.24
 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activat; pkinase; TM=M;SS=N; 3.23
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; lg; TM=M;SS=M; 3.22
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lg,pkinase,LRR,LRRNT,LRRCT,none; 3.22
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR; TM=M;SS=M; 3.22
 427318; AF186081; Hs.175783; zinc transporter; Zip; TM=Y;SS=M; 3.22
 436075; BE090176; Hs.179902; transporter-like protein; none; TM=Y;SS=M; 3.22
 428698; AA652773; Hs.334838; KIAA1866 protein; none;NA;NA; 3.22
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M;SS=N; 3.22
 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 3.21
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD; TM=M;SS=N; 3.21
 424618; L29472; Hs.1802; major histocompatibility complex, class ; lg,MHC_II_beta; TM=Y;SS=M; 3.20
 438564; AA381553; Hs.198253; major histocompatibility complex, class ; lg,MHC_II_alpha,none; 3.20
 456181; L36463; Hs.1030; ras inhibitor, RA,SH2,VPS9; TM=M;SS=N; 3.20
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH; TM=M;SS=N; 3.19
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP; TM=M;SS=N; 3.18
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threon; ank,pkinase,UPF0073; 3.16
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cr; IL8; 3.16
 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin,Idl_recep_a,none; 3.16
 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 3.15
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor; none;none; 3.15
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 3.15
 410668; BE379794; Hs.159651; hypothetical protein; death,TNFR_c6; TM=Y;SS=M; 3.15
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y;SS=N; 3.15
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface ; none; TM=M;SS=M; 3.15
 407844; AW073716; Hs.8037; ESTs; transmembrane4,none; 3.14
 408634; AW407254; Hs.356216; calmodulin 2 (phosphorylase kinase, del; none,none; 3.14
 423061; AI290473; Hs.44807; ESTs; Integrin_B,Sema,PSI,TIG,none; 3.14
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 3.13
 431236; AV656840; Hs.285115; Interleukin 13 receptor, alpha 1; fn3; TM=Y;SS=M; 3.13
 425394; AA356730; Hs.323949; kangai 1 (suppression of tumorigenicity; transmembrane4,none; 3.13
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIB (25-hy; p450; 3.13
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; lg,Isodh,Ribosomal_L6,F-box; TM=Y;SS=M; 3.13
 429305; AF095727; Hs.287832; myelin protein zero-like 1; lg,transmembrane4; TM=Y;SS=M; 3.12
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase; TM=M;SS=N; 3.12
 417386; AL037228; Hs.301957; D123 gene product; NUDIX_secY,E1_dehydro,transket_pyr; TM=Y;SS=M; 3.11
 419138; U48508; Hs.89631; tyrodine receptor 1 (skeletal); ion_trans,SPRY,RYDR_JTPR,RyR,MIR; TM=Y;SS=N; 3.11
 440008; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-i; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 3.10
 406467; ; Target Exon; ehand,Acytransferase,none; 3.10
 422956; BE545072; Hs.122578; ECT2 protein (Epithelial cell transform; BRCT,RhoGEF; TM=M;SS=N; 3.10
 417771; AA804698; Hs.82547; retinoid acid receptor responder (tazaro; none,none; 3.09
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHO,SET,zf-
 COXC,EGF,ank,notch,WW,FCH,GATase,GMP_synL,C,Occludin,YEATS,metalithio,EB,heme_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT; TM=M;SS=N; 3.09

- 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 3.09
 416636; N32536; Hs.42645; solute carrier family 18 (monocarboxylic; none,none; 3.09
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans; TM=Y;SS=M; 3.09
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M;SS=N; 3.08
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS; TM=Y;SS=M; 3.08
 402233; ; NM_030760; Homo sapiens endothelial diff; 7tm_1; TM=Y;SS=M; 3.07
 430066; A929659; Hs.237825; signal recognition particle 72kD; TPRAIRC, SAICAR_synth; 3.07
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none; TM=M;SS=Y; 3.06
 434263; N34895; Hs.79187; ESTs; Ig; none; 3.05
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none; TM=M;SS=Y; 3.05
 409378; U42387; Hs.54426; pancreatic polypeptide receptor 1; 7tm_1; TM=Y;SS=M; 3.05
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD_DAPIN_CARD; TM=M;SS=N; 3.05
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; fn3; 3.05
 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class IV); mu o; adh_zinc; TM=M;SS=N; 3.05
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3; ank; 3.05
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2; 3.05
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, poly; pkinase, pkinase_C; TM=M;SS=N; 3.04
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4, LIM; TM=M;SS=N; 3.03
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding, THF_DHG_CYH, THF_DHG_CYH, CAP_GLY, AAA, LON, Peptidase_C9, bZIP, M, xan_ur_permease, HCO3_cotransp; TM=M;SS=N; 3.03
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp; TM=M;SS=M; 3.03
 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; none; TM=Y;SS=M; 3.02
 442875; BE523003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra, DUF51, none; 3.02
 436576; AW58213; Hs.77542; ESTs; 7tm_1, Dna; 3.02
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; none; TM=M;SS=N; 3.02
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1, 7tm_2; TM=Y;SS=M; 3.01
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8; TM=M;SS=Y; 3.00
 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, poly; pkinase, pkinase_C; TM=M;SS=N; 3.00
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF; 2.99
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator; none; 2.99
 430696; AA531276; Hs.59509; ESTs; pkinase, PP2C; none; 2.98
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95); ly; Integrin_B, EGF_PSI; TM=Y;SS=M; 2.97
 410026; A912061; Hs.55016; hypothetical protein FLJ21935; none; none; 2.97
 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitte; SNF; TM=Y;SS=N; 2.97
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2; TM=M;SS=N; 2.97
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (; none; none; 2.97
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none, spectrin, SH3, PH, CH; 2.97
 431941; AK000106; Hs.272277; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase, Furin-like, Recep_L_domain; none; 2.96
 441389; AF134838; Hs.7835; endocytic receptor (macrophage mannose r; fn2, lectin_c; TM=Y;SS=M; 2.95
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF, sugar_tr; none; 2.94
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1, none; 2.94
 402558; ; C1000201.g|204416|gb|AA02627.1| (L0519; none; TM=Y;SS=M; 2.94
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death, TNFR_c6; TM=Y;SS=M; 2.94
 442080; AW444761; Hs.72901; ESTs; ank; 2.94
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M;SS=N; 2.93
 444809; BE207568; Hs.208219; oculoplasmin; transmembrane4; TM=Y;SS=N; 2.93
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none; TM=Y;SS=M; 2.93
 416110; Z42262; Hs.322844; hypothetical protein DKFZp554A176; Sema, PSI, TIG, Integrin_B; TM=Y;SS=M; 2.93
 453768; BE382670; Hs.198511; Homo sapiens mRNA; cDNA DKFZp7611177 (fr, arl, G-alpha; none; 2.92
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian; Furin-like, pkinase, Recep_L_domain; TM=M;SS=M; 2.92
 421429; AW014922; Hs.104305; death effector filament-forming Ced-4 li; LRR, PAAD_DAPIN, AAA, CARD, NB-ARC; NA; NA; 2.92
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 2.91
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3; TM=M;SS=N; 2.91
 422127; AW504286; Hs.112049; SET binding factor 1; dDENN, DENN, GRAM, PH; 2.91
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran, ABC_membrane; TM=Y;SS=M; 2.90
 430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1, pro_isomerase; 2.90
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin; TM=M;SS=N; 2.89
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae, pkinase, POLO_box, IRNA-syn1_b, dynamin, dynamin_2, GED, bZIP, M; 2.89
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none; none; 2.89
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone H; none; none; 2.89
 417018; M16038; Hs.80887; v-src-1 Yamaguchi sarcoma viral related; SH2, SH3, pkinase; TM=M;SS=N; 2.89
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, s; IRK; TM=Y;SS=N; 2.89
 405556; ; homeodomain-interacting protein kinase 3; trypsin; TM=M;SS=N; 2.89
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF, zf-C3HC4, IIR, zf-RanBP; TM=M;SS=N; 2.89
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 2.88
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A); NDK, PH, Oxysterol_BP; 2.88
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin, fn2; TM=Y;SS=M; 2.88
 414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase; TM=Y;SS=M; 2.87
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2; none; 2.86
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high aff; SDF; TM=Y;SS=M; 2.86
 458039; AA835884; Hs.130685; leukotriene b4 receptor (chemokine recep; CIDE-N; none; 2.86
 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f; DSPc; none; 2.86
 425802; Y14838; ; chemokine-like receptor 1; 7tm_1, none; 2.86
 403112; ; Target Exon; ethand, C2, PH, PI-PLC-Y, PI-PLC-X; 2.86
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y;SS=N; 2.85
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for IMAGE; 447; none; none; 2.84
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none; none; 2.84
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90, HATPase_c, zf-C2H2, PHD; none; 2.83
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none; none; 2.83
 446947; AF146747; Hs.232165; polycythemia rubra vera 1; cell surface; none; TM=M;SS=M; 2.83
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD, BNR; TM=Y;SS=M; 2.82
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head, IQ, zf-MYND; TM=M;SS=M; 2.82
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y;SS=M; 2.82

- 459707; AA631362; Hs.120866; gb:np86b01.s1 NCI_CGAP_Thy1 Homo sapiens; 7tm_1:none; 2.82
 422699; BE410590; Hs.119257; ens1 sequence (mammary tumor and squamous; SH3,HS1_rep;TM=M;SS=N; 2.82
 438108; AI471795; Hs.287776; vanilloid receptor-related osmotically a; ank,lon_trans;TM=Y;SS=N; 2.82
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,ln3,Y_phosphatase;TM=M;SS=N; 2.82
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.81
 423598; BE247600; Hs.377968; ESTs; 7tm_1;TM=Y;SS=M; 2.81
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPC; 2.81
 414198; AW505308; Hs.75812; phosphoenolpyruvate carboxykinase 2 (mit; PEPCK; 2.81
 435729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 2.81
 432314; AA533447; Hs.285173; ESTs; Xlink:none; 2.81
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none;TM=Y;SS=M; 2.80
 446985; AL038704; Hs.156827; ESTs, Weakly similar to ALU1_HUMAN ALU S; SAM,SH3,HS1_rep; 2.80
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L;
 aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 2.80
 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;SS=N; 2.80
 426006; R49031; Hs.22627; ESTs; pkinase,TBC; 2.79
 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 2.79
 411185; NM_000169; Hs.69089; galactosidase, alpha; Melibiose; 2.79
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypothetical; ABC_tran,ABC_membrane,Ig,MHC_JI_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 2.78
 44291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 2.78
 421448; AF033850; Hs.104519; phospholipase D2; PH,PLDc,PX;TM=M;SS=N; 2.78
 410226; AI831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;SS=N; 2.78
 433535; AF111108; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT;TM=M;SS=N; 2.78
 442503; AF147078; Hs.375031; p53-responsive gene 5; K_tetra,lon_trans:none; 2.77
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/H; TPR,PDZ,VW,Guanylate_kin;TM=M;SS=N; 2.77
 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;SS=N; 2.77
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 2.77
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain:none; 2.76
 422667; H25642; Hs.132821; ESTs; FMO-like,FMO-like; 2.76
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 2.76
 402316; ; NM_013447;Homo sapiens egf-like module c; 7tm_2,GPS;TM=M;SS=M; 2.75
 425455; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 2.75
 447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), ma; PP2C;TM=M;SS=N; 2.75
 438629; AI187380; Hs.257170; ESTs, Weakly similar to T12515 hypothetical; TNFR_c6:none; 2.75
 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme; HATPase_c:none; 2.74
 408543; N78098; Hs.44289; ESTs; none;TM=M;SS=N; 2.74
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 2.74
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB;TM=M;SS=N; 2.73
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 2.73
 407217; AA477138; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 2.73
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPC,Y_phosphatase;TM=M;SS=N; 2.73
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 2.73
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 2.73
 438022; AW517524; Hs.135201; NOD2 protein; LRR,CARD,GTP_CDC,Viral_helicase1;TM=M;SS=N; 2.72
 420929; AI694143; Hs.326248; programmed cell death 4; MA3;TM=M;SS=N; 2.72
 421155; H87879; Hs.102267; lysyl oxidase; Lysyl_oxidase,Aldose_epim,Epimerase; 2.72
 448564; AL044962; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK; 2.71
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain:none; 2.71
 444533; AF111713; Hs.12284; junctional adhesion molecule 1; Ig;TM=Y;SS=M; 2.71
 412259; AI560292; Hs.279909; protein phosphatase 2 (formerly 2A), reg; WD40;TM=M;SS=N; 2.71
 419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); DSL,EGF,laminin_EGF_vwc,metalathio;TM=M;SS=M; 2.71
 452401; NM_007115; Hs.28352; tumor necrosis factor, alpha-induced pro; Xlink,CUB; 2.71
 458190; BE561793; Hs.21446; KIAA1716 protein; ASC,Galactosyl_T:none; 2.70
 432126; AA865239; Hs.37196; ESTs; 7tm_1;TM=Y;SS=M; 2.70
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 2.70
 424717; H03754; Hs.152213; wingless-type MMTV integration site fam1; wnt:none; 2.70
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;SS=N; 2.70
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 2.70
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none:none; 2.69
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 2.69
 404891; ; Target Exon; none:none; 2.69
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 2.69
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 2.68
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; Ig,kringle,pkinase,Fz;TM=Y;SS=M; 2.68
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor.; Ig,pkinase;TM=Y;SS=N; 2.68
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; Ig,pkinase;TM=Y;SS=M; 2.68
 436856; AI469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 2.68
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp584E2222 (f; SH2,SH3,BTB; 2.67
 450690; AA296696; Hs.333418; FXVD domain-containing lon transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 2.67
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 2.67
 445330; R52656; Hs.21691; ESTs; 7tm_1:none; 2.67
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 2.67
 419754; H52299; Hs.308467; Homo sapiens mRNA; cDNA DKFZp586I0523 (f; none;TM=M;SS=N; 2.67
 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none; 2.67
 445826; BE313754; Hs.13355; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; Ig,bsp_1,ZU5,Nucleoside_tran; 2.66
 446696; AF279265; Hs.298476; solute carrier family 26, member 6; Sulfate_transp,STAS,xan_ur_permease;TM=Y;SS=N; 2.66
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricn_B_Jectin; 2.66
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap_PNP; 2.66
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 2.66
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 2.66
 449030; AI355582; Hs.67100; Homo sapiens mRNA for FLJ00016 protein.; transmembrane4;TM=Y;SS=M; 2.66
 434979; AI953054; Hs.89643; transketolase (Wernicke-Korsakoff syndro; ASC,transketolase,transkeL_pyr,transketolase_C,pkinase; 2.66
 406137; ; NM_000179;Homo sapiens mutS (E. coli) h; MutS_C,PWWP,MutS_N;TM=M;SS=N; 2.66

- 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none; 2.65
 408633; AW953372; Hs.222088; PRO2000 protein; bromodomain,AAA,Sigma54_activat; 2.65
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 2.65
 452682; AA456193; Hs.374574; progesterone membrane binding protein; homeobox;none; 2.65
 401752; ; RAN binding protein 3; SH2,STAT,STAT_bind,STAT_prot,lon_trans,PAC,PAS,Orexin; 2.65
 450747; AI064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rm,zf-RanBP,GAS2; 2.65
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 2.64
 452701; NM_005110; Hs.30332; glutamine-fructose-6-phosphate transamin; GATase_2,SIS;TM=M;SS=N; 2.64
 433933; AI754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none;NA;NA; 2.64
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 2.64
 436469; AK001455; Hs.51198; Down syndrome critical region gene 2; none; 2.64
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanesa;none; 2.64
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;SS=N; 2.64
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin,kinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 2.63
 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 2.63
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_FB_type_C;TM=M;SS=M; 2.63
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 2.63
 425075; AA506324; Hs.1852; acid phosphatase, prostate; acid_phosphat;TM=Y;SS=M; 2.63
 405588; ; NM_000299;Homo sapiens plakophilin 1 (e; Armadillo_seg;TM=M;SS=N; 2.63
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH;none; 2.63
 448243; AW369771; Hs.367688; Integrin, beta 8; Integrin_B;none; 2.63
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisomV,K-box;TM=M;SS=N; 2.63
 412182; AA205588; Hs.73737; Splicing factor, arginine/serine-rich, 4; rm,hormone_rec,zf-C4,sugar_tr; 2.63
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y;SS=N; 2.63
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 2.62
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like; SH2,SAM,Exo_endo_phos; 2.62
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 2.62
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 2.62
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;SS=N; 2.62
 401812; ; sorting nexin 14; AAA,NB-ARC,APS_kinase,cdc48_N,cdc48_2;none; 2.61
 417886; AA214584; ESTs; SPRY,7tm_3,ANF_receptor;none; 2.61
 457670; AF119566; Hs.23449; insulin receptor tyrosine kinase substr; SH3;TM=M;SS=N; 2.61
 428512; AI018187; Hs.375624; Human DNA sequence from clone RP11-243J1; none; 2.61
 425746; J03626; Hs.2057; uridine monophosphate synthetase (orlat; Pribosyltran,OMPdecase;TM=M;SS=N; 2.61
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; Ig,kinase,LRR,LRRNT,LRRCT;none; 2.61
 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24a,SRP54,dENN,DENN,uENN;TM=M;SS=N; 2.60
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M;SS=N; 2.60
 416651; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain;rm;TM=M;SS=N; 2.60
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF; 2.60
 411133; AW819204; ; gb:CM1-ST0283-071299-061-h03 ST0283 Homo; ANF_receptor;none; 2.60
 405602; ; Target Exon; pkinase; 2.60
 400440; X83957; Hs.83870; nebulin; SH3,Nebulin; 2.60
 424848; AI263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin;none; 2.59
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase;TM=M;SS=N; 2.59
 452690; AI536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 2.59
 422753; AJ928995; Hs.1575; small nuclear ribonucleoprotein D3 polyp; Sm; 2.59
 428028; U52112; Hs.182018; Interleukin-1 receptor-associated kinase; death,pkinase;TM=M;SS=N; 2.58
 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rece; 7tm_2,EGF,cadherin,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 2.58
 422785; AJ824114; Hs.289088; heat shock 90kD protein 1, alpha; zf-C2H2;none; 2.58
 416885; U76376; Hs.87247; harakiri, BCL2-interacting protein (cont; none;TM=M;SS=M; 2.58
 452329; N36626; Hs.29106; mitogen-activated protein kinase phosphat; DSPc;TM=M;SS=N; 2.58
 428405; Y00762; Hs.2266; cholinergic receptor, nicotinic, alpha p; Neur_chan_LBD,Neur_chan_membr;TM=Y;SS=M; 2.58
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ; 2.57
 407245; X90568; Hs.172004; Ctin; fn3,Ig,SGXSG,pkinase;TM=M;SS=N; 2.57
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=M; 2.57
 401751; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,lon_trans,PAC,PAS;none; 2.57
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 2.57
 422282; AF019225; Hs.114309; apolipoprotein L; MoA_ExbB;TM=Y;SS=M; 2.57
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; lipoxigenase,PLAT,lipoxygenase,PLAT; 2.57
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 2.57
 401218; ; eukaryotic translation elongation factor; ion_trans;TM=Y;SS=N; 2.57
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc;TM=M;SS=N; 2.57
 444743; AA045648; Hs.301957; nudix (nucleoside diphosphate linked moi; NUDIX,secY,E1_dehydrog,transkeL_pyr;TM=Y;SS=M; 2.56
 429782; NM_005754; Hs.220589; Ras-GTPase-activating protein SH3-domain; rm,NTF2;TM=M;SS=N; 2.56
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 2.56
 456602; AA411607; Hs.118964; ESTs, Weakly similar to KIAA1150 protein; none,pkinase; 2.56
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 2.56
 441699; AW511126; Hs.127572; ESTs; none,Aa_trans; 2.56
 447912; AW576549; Hs.165728; ESTs, Weakly similar to I38022 hypotheti; none,GSPHx,ABC_tran; 2.56
 442945; AI024849; Hs.131853; ESTs; pkinase;none; 2.56
 453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase ; pkinase;TM=M;SS=N; 2.56
 451477; AI798425; Hs.42710; ESTs; SH3;none; 2.56
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Coenzyme A sy; HMG_CoA_synt; 2.55
 413529; U11874; Hs.846; Interleukin 8 receptor, beta; 7tm_1;TM=Y;SS=N; 2.55
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-recept; Y_phosphatase,DSPc;TM=M;SS=M; 2.55
 401321; ; receptor tyrosine kinase-like orphan rec; none;TM=M;SS=N; 2.55
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; none;none; 2.55
 401057; ; eukaryotic translation elongation factor; ion_trans,IQ;TM=Y;SS=N; 2.55
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 2.55
 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, m; Y_phosphatase;TM=M;SS=N; 2.54
 424539; LQ2911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK; pkinase,Activin_rec;TM=M;SS=M; 2.54
 459060; H89244; Hs.303627; heterogeneous nuclear ribonucleoprotein ; rm,pkinase;TM=M;SS=N; 2.54
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 2.54

- 425966; NM_001761; Hs.1973; cyclin F; cyclin_F-box; cyclin_C; TM=M; SS=N; 2.54
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 2.54
 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7m_1; none; 2.54
 457255; AL133011; Hs.263920; Homo sapiens mRNA: cDNA DKFZp434P201 (fr, none, none; 2.54
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 2.53
 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2, PID, zif-C2H2, SCAN, AMP-binding, KRAB; TM=M; SS=N; 2.53
 414570; Y00285; Hs.76473; Insulin-like growth factor 2 receptor; fn2, CMR; TM=M; SS=M; 2.53
 444838; AV651680; Hs.208558; ESTs; Integrin_A, FG-GAP; none; 2.53
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR, SH2, SH3, pkinase; TM=Y; SS=M; 2.53
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none, none; 2.53
 400702; ; Target Exon; lig_chan, SBP_bac_3, ANF_receptor; TM=Y; SS=M; 2.53
 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm, pkinase; TM=M; SS=N; 2.53
 442643; U82756; Hs.374973; PRP4/STK/WD splicing factor; WD40; 2.52
 452050; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2); ABC_tran, IRK, SWIB; 2.52
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin; none; 2.52
 428975; NM_004672; Hs.194649; mitogen-activated protein kinase kinase; pkinase; 2.52
 407608; AF28218; Hs.380063; ATPase, Na⁺ transporting, beta 3 polypep; none, none; 2.51
 414482; S57498; Hs.76252; endothelin receptor type A; 7m_1; TM=Y; SS=M; 2.51
 410293; AK000047; Hs.81960; hypothetical protein; K_tetra; TM=M; SS=N; 2.51
 429663; M68874; Hs.211587; phosphatase A2, group IVA (cytosolic, ; C2, PLA2_B; TM=M; SS=N; 2.51
 425424; NM_004954; Hs.157199; ELK1 motif kinase; pkinase, UBA, KA1; TM=M; SS=N; 2.51
 457013; AA037145; Hs.172865; cleavage stimulation factor, 3' pre-RNA; WD40; TM=M; SS=N; 2.51
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I78885 serin; adh_short, Bcl-2, BH4; none; 2.51
 405429; ; Target Exon; Y_phosphatase; none; 2.51
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase, RIO1; TM=M; SS=N; 2.51
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (ma; ank; 2.50
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin; TM=M; SS=M; 2.50
 414419; F06829; Hs.76090; tumor necrosis factor, alpha-induced pro; K_tetra; TM=M; SS=N; 2.50
 405369; ; NM_005569; Homo sapiens LIM domain kinase; pkinase, LIM, PDZ; 2.50
 418216; AA662240; Hs.283099; AF15q14 protein; Hemagglutinin, squash; TM=Y; SS=N; 2.50
 404321; ; C7001741; gl[2496629]sp[063932]MPK2_MOUSE; none, none; 2.50
 430900; U91939; Hs.248123; G protein-coupled receptor 25; 7m_1; TM=Y; SS=M; 2.49
 440861; BE244115; Hs.7482; KIAA0682 gene product; rrm, Guanylate_kin; TM=M; SS=N; 2.49
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; lg; TM=Y; SS=N; 2.49
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase, Activin_rec, pkinase, Activin_rec; 2.49
 417034; NM_006183; Hs.80962; neurotensin; none; 2.49
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none, none; 2.49
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase; TM=M; SS=N; 2.49
 418255; AW135405; Hs.37251; ESTs; pkinase; none; 2.49
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 2.44
 417791; AW965339; Hs.44269; ESTs; none, fer2, FAD_binding_5, Ald_Xan_dh_C, fer2_2, Ald_Xan_dh_C2, CO_deh_flav_C; 2.44
 453941; U93917; Hs.36820; Bloom syndrome; DEAD, helicase_C, HRDC; TM=M; SS=N; 2.41
 417849; AW291587; Hs.82733; nidogen 2; EGF, Id_recep_L_b, thyroglobulin_1; TM=M; SS=M; 2.39
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; 2.32
 428513; BE220806; Hs.184697; plexin C1; PSI; none; 2.31
 426761; AJ015709; Hs.172089; PORIMIN Pro-oncogene receptor inducing me; none; TM=Y; SS=M; 2.31
 427585; O31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q, Collagen; 2.28
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; SS=N; 2.28
 452461; N78223; Hs.108108; transcription factor; zif-C3HC4, ubiquitin, PHD, YDG_SRA; TM=M; SS=N; 2.26
 429547; AW009166; Hs.99376; FGENSESH predicted novel secreted protein; none, none; 2.15
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; SNF2_N, helicase_C; TM=M; SS=N; 2.15
 401486; ; C4000647; gl[4758508]ref[NP_004253.1] at; none; TM=Y; SS=M; 2.15
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA; TM=M; SS=N; 2.14
 424399; AJ905687; Hs.348419; AJ905687-IL-BT095-190199-019 BT095 Homo ; none; TM=M; SS=M; 2.14
 423761; NM_006194; Hs.132676; paired box gene 9; PAX; TM=M; SS=N; 2.13
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858 3 U1 sm; none, none; 2.13
 439318; AW837046; Hs.6527; G protein-coupled receptor 58; 7m_2, CytC_asm, GPS; TM=Y; SS=M; 2.03
 445019; AJ205540; Hs.281295; ESTs; none, none; 2.00
 443211; AI128388; Hs.143655; ESTs; none, none; 1.98
 449448; D60730; Hs.57471; ESTs; none, none; 1.92
 435243; AW292886; Hs.348932; hypothetical protein dJ434O14.3; IRF; none; 1.85
 406360; ; Target Exon; WD40; TM=M; SS=N; 1.84
 411388; X72925; Hs.69752; desmocollin 1; cadherin; TM=Y; SS=N; 1.84
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz, Frizzled, 7m_2; TM=Y; SS=M; 1.79
 419183; U06669; Hs.89663; cytochrome P450, subfamily XXIV (vitamin; p450; 1.78
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5; TM=Y; SS=M; 1.77
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; Ribosomal_L4; TM=M; SS=N; 1.76
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA sequence; none, none; 1.73
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 1.62
 437915; AJ637993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoc; none, none; 1.58
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz, NTR; 1.50
 434377; AW137148; Hs.306593; intron of periostin (OSF-2os); Fasciclin; none; 1.47
 451592; AJ805416; Hs.213897; ESTs; none, none; 1.47
 404927; ; Target Exon; Galactosyl_T; TM=M; SS=Y; 1.28
 421552; AF026892; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 1.27
 427335; AA448542; Hs.278444; G antigen 7B; none; 1.25
 431808; M30703; Hs.270833; amphiregulin (schwannoma-derived growth ; EGF; TM=Y; SS=M; 1.24
 447993; AW139525; Hs.170362; ESTs; none, none; 1.21
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_HUMAN G ANT; none; TM=M; SS=N; 1.18
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); cadherin; TM=Y; SS=M; 1.14
 438274; AJ918906; Hs.55080; ESTs; PAX; none; 1.14
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin_id_recep_L_a; none; 1.10
 413268; AL039079; Hs.75256; regulator of G-protein signalling 1; RGS; TM=M; SS=N; 1.07

429921; AAS26911; Hs.82772; collagen, type XI, alpha 1; Collagen, COL11, TSPN, laminin, G, CorA; 1.00
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; ZOG-Fell_Oxy; TM=M; SS=N; 1.00

TABLE 25B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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406685	0_0	M18728
418669	12789_14	AA229762 AA230035
425802	8884_3	AA122298 AA360788
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
411133	1070995_1	AW819203 AW819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AW819207 AW819220 AW819208 AW819238
AW819198	AW819234	

TABLE 25C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
405932	7767812	Minus	123525-123713
406467	9795551	Plus	182212-182958
402233	7690102	Plus	90281-91477
402558	9863760	Plus	19047-19145,21133-21293,33968-34069
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
403112	8980973	Minus	113051-113195
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
404891	7328392	Plus	84974-85125
406137	9166422	Minus	30487-31058
401752	9828651	Plus	144600-144794
405588	5002511	Plus	46180-46366
401812	7407975	Minus	55084-55391
405602	4753260	Plus	44647-44778
401751	9828651	Plus	139165-139322
401218	9929301	Minus	40793-41031
401321	9863631	Minus	104278-104748
401057	8117645	Plus	158309-159238
400702	8118856	Minus	11457-11585,26311-26536,27902-28067,3204
405429	7321905	Minus	51577-51723
405369	2078469	Minus	34183-34357,35686-35751
404321	9665209	Minus	76594-77805
401486	7341783	Plus	32585-32758,36281-36540,40791-40933,4401
406360	9256107	Minus	7513-7673
404927	7342002	Plus	68690-69563

TABLE 26A: 834 GENES UP-REGULATED IN EWING'S SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 26A lists about 834 genes up-regulated in Ewing's sarcoma compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 1.5. The "average" kidney cancer level was set to the 75th percentile amongst Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UniGeneID: UniGene number
UniGene Title: UniGene gene title
R1: Ratio of Ewing sarcoma to normal tissue

Pkey	ExAccn	UniGeneID	UniGene Title	R1
101447	M21305		gb:Human alpha satellite and satellite 3	38.4
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	34.2
110278	AF061573	Hs.19492	protocadherin 8	32.2
121362	AF050147	Hs.97932	chondromodulin I precursor	30.3
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	26.3

	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	24.4
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidyseri	23.4
	104659	AW969769	Hs.105201	ESTs	20.2
5	106533	AL134708	Hs.145998	ESTs	16.9
	124006	AI147155	Hs.270016	ESTs	15.0
	110728	AA737106	Hs.32250	ESTs, Moderately similar to 178885 serin	14.8
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	14.6
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	14.5
10	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	13.7
	121231	AA814948	Hs.95343	ESTs, Weakly similar to ALUC_HUMAN IIII	12.3
	129526	S69681	Hs.177582	surfactant, pulmonary-associated protein	12.1
	119791	AA554907	Hs.58291	ESTs	11.7
	116301	AW969705	Hs.293332	ESTs	11.2
	123308	C14187	Hs.103538	ESTs	10.9
15	127742	AW293496	Hs.180138	ESTs	10.8
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	10.7
	127489	AA650250	Hs.272076	ESTs	10.6
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.6
20	101063	D54745	Hs.80247	cholecystokinin	10.6
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	10.5
	100299	D49493	Hs.2171	growth differentiation factor 10	10.1
	127987	AI022103	Hs.124511	ESTs	10.1
	131313	R96290	Hs.336629	ribosomal protein L44	9.2
25	126799	AW753865	Hs.74376	cilfactomedin related ER localized protei	8.5
	125847	AW161885	Hs.249034	ESTs	7.0
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	6.9
	114837	BE244930	Hs.166895	ESTs	6.6
	123049	BE047680	Hs.211869	clcktopf (Xenopus laevis) homolog 2	6.6
30	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.5
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous r	6.5
	125186	AA610620	Hs.181244	major histocompatibility complex, class	6.4
	118644	AA443241	Hs.336629	ribosomal protein L44	6.3
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	6.3
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	6.1
	113003	AW292315	Hs.7215	ESTs	5.8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.7
	101050	AU077324	Hs.1832	neuropeptide Y	5.7
	118790	AW161357	Hs.101174	microtubule-associated protein tau	5.5
40	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	5.1
	132315	AF091086	Hs.44563	hypothetical protein	5.0
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	4.9
	126077	M78772	Hs.210836	ESTs	4.7
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	4.6
45	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	4.5
	123619	AA602964		gb:nc97c02.s1 NCL_CGAP_Pr2 Homo sapiens	4.4
	128361	AW172570	Hs.130246	ESTs	4.3
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	4.3
	100020				4.2
50	125556	AB033064	Hs.334806	KIAA1238 protein	4.2
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	4.0
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.0
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp781G02121 (3.9
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	3.9
55	129012	R81936	Hs.336629	ribosomal protein L44	3.9
	125447	AI582222	Hs.128686	ESTs	3.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	3.6
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	3.6
	128391	AW188326	Hs.170652	ESTs	3.5
60	123829	AF251237	Hs.112208	XAGE-1 protein	3.4
	123949	AA621665	Hs.208957	EST	3.4
	126872	AW450979		gb:Ut-H-813-ata-e-12-0-UI.s1 NCL_CGAP_Su	3.4
	101266	L36645	Hs.73964	EphA4	3.3
	121309	AA293834	Hs.97312	ESTs	3.3
65	130637	AA356764	Hs.17109	Integral membrane protein 2A	3.2
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	3.2
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	3.2
	107599	AW684072	Hs.60136	ESTs	3.2
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.2
70	131688	AI935413	Hs.30692	p21 (CDKN1A)-activated kinase 2	3.1
	120147	AI917116	Hs.155376	hemoglobin, beta	3.1
	110343	AW136703	Hs.17268	ESTs	3.1
	127664	AA806164	Hs.116502	ESTs	3.0
	103076	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	3.0
75	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.0
	125558	R59305		gb:yh16c10.r1 Soares_infant_brain_1NIB H	3.0
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.9
	133421	AF134160	Hs.7327	claudin 1	2.8
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.8
80	113577	AI300699	Hs.278937	PRO0470 protein	2.8
	118397	BE139479	Hs.161492	ESTs	2.8
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
	127262	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	2.8

5	106472	AJ207162	Hs.3815	slathmin-like protein RB3	2.7
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	2.7
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	2.7
	126600	AA699949	Hs.191385	ESTs	2.7
	120325	AA195651	Hs.104106	ESTs	2.7
10	127256	AJ738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN	2.7
	117357	N24829		gb:yc98h12.s1 Soares melanocyte 2NbHM Ho	2.7
	126735	M69113	Hs.226795	glutathione S-transferase pi	2.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	2.7
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (2.6
15	129706	AA443241	Hs.336629	ribosomal protein L44	2.6
	107731	AA016086	Hs.272106	ESTs, Weakly similar to I38022 hypothe	2.6
	128283	AI076570	Hs.134053	ESTs	2.6
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	2.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
20	105577	AW852257	Hs.171391	C-terminal binding protein 2	2.6
	126301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	2.6
	130262	D63216	Hs.153684	frizzled-related protein	2.6
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.6
	102479	NM_001991	Hs.194669	enhancer of zeste (Drosophila) homolog 1	2.6
25	128531	H03721	Hs.2953	ribosomal protein S15a	2.6
	126165	AJ741816	Hs.125897	ESTs	2.6
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	2.5
	118967	AI668670	Hs.216756	ESTs	2.5
	120830	AI568170	Hs.96886	ESTs	2.5
30	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.5
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	2.5
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	2.5
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
35	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.5
	126693	C05723		gb:C05723 Human pancreatic islet Homo sa	2.5
	126021	AA775894	Hs.187516	ESTs	2.5
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.5
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
40	125743	H17151		gb:ym37a05.r1 Soares infant brain 1N1B H	2.5
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	2.5
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	2.4
	123110	AA486256	Hs.193510	EST	2.4
	113283	T66813	Hs.12947	EST	2.4
45	107711	W96141	Hs.220687	ESTs	2.4
	128992	H04150	Hs.107708	ESTs	2.4
	106111	AW875398	Hs.6451	PRO0659 protein	2.4
	129948	AI537182	Hs.263988	ESTs	2.4
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.4
50	116728	F13687	Hs.227976	EST	2.4
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	2.4
	124971	T23800	Hs.151001	hypothetical protein FLJ14728	2.4
	131019	V28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory s	2.4
55	111795	AI435437	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.4
	119127	AA708035	Hs.12248	ESTs	2.4
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	2.4
	111898	R38944	Hs.183475	Homo sapiens clone Z5061 mRNA sequence	2.4
	131916	AA025976	Hs.34569	ESTs	2.4
60	130850	AB040922	Hs.20237	DKFZP566C134 protein	2.4
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.4
	126722	N66148	Hs.11125	HSPC033 protein	2.4
	123720	AA609734	Hs.112755	EST	2.4
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
65	131136	AB033099	Hs.23413	KIAA1273 protein	2.4
	129001	AA443323	Hs.107812	BPOZ protein	2.4
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.4
	107593	AI093688	Hs.60051	ESTs	2.4
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
70	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.4
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.4
	128367	AW811791	Hs.150742	ESTs	2.4
	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	2.4
	112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	2.3
75	114721	D61939	Hs.103822	ESTs	2.3
	127768	AW085002	Hs.156187	ESTs	2.3
	127706	AI174238	Hs.186982	ESTs	2.3
	126029	AA704253	Hs.169359	ESTs	2.3
	124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.3
80	117265	AA451966	Hs.43005	RAB9-like protein	2.3
	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	2.3
	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.3
	127252	AI049545	Hs.94	OnaJ (Hsp40) homolog, subfamily A, membe	2.3
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	2.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.3
	109252	BE440157	Hs.85944	ESTs	2.3
	127889	AJ147408	Hs.144941	ESTs	2.3

	121292	AA401807		gb:zv65f11.s1 Soares_t0tal_fetus_Nb2HF8_	2.3
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	2.3
	132985	AL045579	Hs.62113	KIAA0717 protein	2.3
5	125174	W51835	Hs.231082	EST	2.3
	125401	AI204637	Hs.337585	ESTs, Highly similar to KIAA0350 [H.sapi]	2.3
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.3
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.3
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	2.3
10	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.3
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	2.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361.1 HSPC	2.3
	101086	AA382524	Hs.250959	histatin 1	2.3
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	2.3
	126879	D90391	Hs.1265	branched chain keto acid dehydrogenase E	2.3
15	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.3
	124691	R05835	Hs.110153	ESTs	2.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	2.3
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	2.2
20	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.2
	129248	W04606	Hs.171637	hypothetical protein MGC2628	2.2
	100780	BE561958	Hs.302063	Immunoglobulin heavy constant mu	2.2
	135416	BE281018	Hs.99969	fusion, derived from t(12;16) malignant	2.2
	129928	A1338993	Hs.134535	ESTs	2.2
25	103319	X83492	Hs.82359	tumor necrosis factor receptor superfamily	2.2
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.2
	120734	AA299948		gb:EST12544 Uterus tumor I Homo sapiens	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128963	J03890	Hs.1074	surfactant, pulmonary-associated protein	2.2
30	108451	AA079195		gb:zm92h12.s1 Stralagene ovarian cancer	2.2
	134364	AI803516	Hs.272891	hippocalcin-like protein 4	2.2
	127248	AA364195		gb:EST75015 Pineal gland II Homo sapiens	2.2
	125761	R68351		gb:yh99b03.r1 Soares placenta Nb2HP Homo	2.2
	101358	M10058	Hs.12056	asialoglycoprotein receptor 1	2.2
35	101613	M24283	Hs.168383	Interleukin adhesion molecule 1 (CD54)	2.2
	107121	AB015427	Hs.250493	zinc finger protein 219	2.2
	118751	N74210	Hs.50454	ESTs	2.2
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.2
40	126581	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 f1s, clone MA	2.2
	127634	AA633469	Hs.193283	ESTs, Weakly similar to unnamed protein	2.2
	130765	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.2
	132867	AF226667	Hs.58553	CTP synthase II	2.2
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	2.2
45	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26550 DNA-bindi	2.2
	125549	R20215		gb:ygl8b09.r1 Soares infant brain 1NB H	2.2
	128059	AA972446	Hs.145096	ESTs	2.2
	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.2
	125722	H29796	Hs.268622	ESTs	2.2
50	106383	AA447453	Hs.27850	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	2.2
	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.2
	128179	AW293689	Hs.127116	ESTs	2.2
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	2.2
	126952	R12014	Hs.20976	ESTs	2.2
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.2
55	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.2
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothet	2.2
	108743	AI580150	Hs.71074	ESTs	2.2
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	2.2
	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	2.2
60	109929	AA773187	Hs.294027	ESTs	2.2
	129059	AW069534	Hs.279583	CGI-81 protein	2.2
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 f1s, clone PL	2.2
	116962	H79677		gb:yu78g10.s1 Soares fetal liver spleen	2.2
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	2.2
65	106711	BE390125	Hs.143187	hypothetical protein	2.2
	135191	X16886	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.2
	125822	H03162	Hs.268768	ESTs	2.2
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	2.2
	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36299 prolina-r	2.2
70	126250	AL050391	Hs.321247	Homo sapiens mRNA; cDNA DKFZp586A181 (fr	2.2
	103392	X94563		gb:H.sapiens dbi/acbp gene exon 1 & 2	2.2
	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	2.2
	100253	D38024	Hs.157425	double homeobox, 2	2.2
	130743	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.2
75	125466	R08234	Hs.180461	ESTs	2.2
	122682	AA984531	Hs.159293	ESTs	2.2
	133347	BE257758	Hs.71475	acid cluster protein 33	2.2
	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.2
	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2
80	131163	AA099524	Hs.23754	ESTs	2.2
	109592	AI198059	Hs.26370	ESTs	2.2
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.1
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 f1s, clone C	2.1
	128434	AI190914	Hs.143880	ESTs	2.1

5	103163	AU077018	Hs.3235	keratin 4	2.1
	112379	AK001713	Hs.17860	hypothetical protein FLJ10851	2.1
	127507	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.1
	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
	126153	H85692	Hs.40730	ESTs	2.1
10	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	2.1
	100554	M95923		gb:Human 12-lipoxygenase mRNA, partial c	2.1
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.1
	132664	AJ740461	Hs.54542	ESTs	2.1
	114620	AA642974		gb:nr60h01.s1 NCL_CGAP_Lym3 Homo sapiens	2.1
15	115348	AA281562	Hs.292100	ESTs	2.1
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	133160	N54968	Hs.66309	hypothetical protein MGC11061	2.1
	124656	AW297702	Hs.102915	ESTs	2.1
	133576	M19650	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiester	2.1
20	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothet	2.1
	126505	AA282881	Hs.190057	ESTs	2.1
	118865	AA736405	Hs.54530	ESTs	2.1
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.1
25	133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	2.1
	112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.1
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.1
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	2.1
	134889	AL157518	Hs.90421	PRO2463 protein	2.1
30	128869	AA768242	Hs.80618	hypothetical protein	2.1
	129179	AW969025	Hs.109154	ESTs	2.1
	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.1
	101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferase	2.1
	129726	H15474	Hs.132898	fatty acid desaturase 1	2.1
35	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	126271	AL250773	Hs.270012	ESTs	2.1
	116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ca	2.1
	128468	T23625	Hs.150580	putative translation initiation factor	2.1
	116031	AA452239	Hs.103329	KIAA0970 protein	2.1
40	130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	2.1
	121897	AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.1
	123808	AA620552		gb:aa58g11.s1 Stratagene lung carcinoma	2.1
	122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.1
	127841	AW136558	Hs.125246	ESTs	2.1
45	100023				2.1
	113002	BE243513	Hs.7212	hypothetical protein PP1044	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC16040	2.1
	113697	T97183	Hs.17992	Homo sapiens mRNA; cDNA DKFZp434J1726 (f	2.1
	128033	AI248705	Hs.149321	ESTs	2.1
50	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.1
	112370	AF052095	Hs.167344	Homo sapiens clone 23911 mRNA sequence	2.1
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	2.1
	113226	AI821008	Hs.10697	ESTs	2.1
	117997	N52090	Hs.47420	EST	2.1
55	116996	H83935	Hs.40535	ESTs	2.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.1
	122591	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.1
	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia	2.1
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.1
60	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1
	127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.1
	128352	AW137413	Hs.169942	ESTs	2.1
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.0
	128275	AI218235	Hs.131240	ESTs	2.0
65	125976	AA436760		gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_	2.0
	120820	AA347417	Hs.96869	EST	2.0
	134937	AI251449	Hs.171939	ESTs	2.0
	129602	AI282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	2.0
	129535	AA397972	Hs.169965	chimerin (chimaerin) 1	2.0
70	106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.0
	128538	R44214	Hs.101189	ESTs	2.0
	105593	AA279341	Hs.174151	aldehyde oxidase 1	2.0
	105788	AB009598	Hs.23965	solute carrier family 22 (organic anion	2.0
	128148	AA918175	Hs.126637	ESTs	2.0
75	125982	R98091		gb:yr30e11.r1 Soares fetal liver spleen	2.0
	125746	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	127835	AA748762	Hs.163113	ESTs, Weakly similar to I38022 hypothet	2.0
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	2.0
	124282	AA018408	Hs.110287	ESTs	2.0
80	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 Integrin	2.0
	100221	D28383		gb:Human mRNA for ATP synthase B chain,	2.0
	126053	H64450		gb:yu62d01.r1 Weizmann Olfactory Epithel	2.0
	100944	L07518	Hs.159593	mucin 6, gastric	2.0
	125581	AI272848	Hs.75309	eukaryotic translation elongation factor	2.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.0
	114612	AI124557	Hs.95456	ESTs	2.0
	130453	U80735	Hs.173854	PAX transcription activation domain inte	2.0

	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.0
	114419	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse 1	2.0
	126283	N40359	Hs.271896	ESTs	2.0
5	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.0
	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0
	127717	F12209	Hs.173380	CK2 interacting protein 1; HQ0024c prote	2.0
	126893	AJ252060	Hs.26320	TRABID protein	2.0
	105798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
10	103760	AA642973	Hs.183842	ubiquitin B	2.0
	118922	AW206193	Hs.91065	hypothetical protein DKFZp761B2423	2.0
	133195	AI434760	Hs.279949	KIAA1007 protein	2.0
	133424	AA350994	Hs.20281	KIAA1700	2.0
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.0
	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	2.0
15	125599	H13295	Hs.106135	ESTs	2.0
	114459	AW445217	Hs.103362	ESTs	2.0
	128478	AA708205	Hs.100343	ESTs	2.0
	127271	H96820		gb:yy99b03.r1 Soares melanocyte 2NbHM Ho	2.0
20	111122	N63753	Hs.16492	DKFZP564G2022 protein	2.0
	130695	T97205	Hs.17998	ESTs, Weakly similar to 2109260A B cell	2.0
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	2.0
	119244	AW407564	Hs.275865	ribosomal protein S18	2.0
	127603	AI016798	Hs.9925	hypothetical protein FLJ20772	2.0
25	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	128115	AI435590	Hs.130168	ESTs	2.0
	117639	AA377165	Hs.44833	ESTs	2.0
	127033	AF169301	Hs.9098	sulfate transporter 1	2.0
	112411	R43090	Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	2.0
30	114601	AA075566		gb:zm88f06.a1 Stratagene ovarian cancer	2.0
	127573	AA594196	Hs.269464	ESTs, Weakly similar to S65657 alpha-1C-	2.0
	125500	AW952654	Hs.244624	ESTs	2.0
	119416	T97186		gb:ye50h09.s1 Soares fetal liver spleen	2.0
	115467	AJ366784	Hs.48820	TATA box binding protein (TBP)-associate	2.0
35	128902	AA036637	Hs.107052	ESTs	2.0
	127684	AA668631	Hs.32556	KIAA0379 protein	2.0
	126288	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	2.0
	122059	AA431737	Hs.98749	EST, Moderately similar to T42671 hypoth	2.0
	125486	AI023895	Hs.190587	ESTs	2.0
40	128895	AW467000	Hs.106985	ESTs	2.0
	105301	AW352357	Hs.7457	MAGE1 protein	2.0
	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	121387	AA405854		gb:zu66g08.s1 Soares_testis_NHT Homo sap	2.0
	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	2.0
45	126860	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.0
	102907	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.0
	127804	AA740634	Hs.292084	ESTs	2.0
	130566	R85474	Hs.16073	ESTs	1.9
	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.9
50	124119	AA040123	Hs.248953	solute carrier family 27 (fatty acid tra	1.9
	132490	NM_001290	Hs.4980	LIM domain binding 2	1.9
	125494	AU077029	Hs.177643	antigen identified by monoclonal antibod	1.9
	100237	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	1.9
	127687	AW772383	Hs.300635	ESTs	1.9
55	103136	AF087917	Hs.247936	olfactory receptor, family 1, subfamily	1.9
	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	126208	N22588	Hs.288548	Homo sapiens cDNA FLJ12368 fis, clone MA	1.9
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	1.9
	128660	AA011597	Hs.177398	ESTs	1.9
60	118049	N53145		gb:yy55f09.s1 Soares fetal liver spleen	1.9
	134624	AF035119	Hs.8700	deleted in liver cancer 1	1.9
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.9
	126414	AJ363157	Hs.24756	hepatocyte growth factor-regulated tyros	1.9
	120861	AA350394	Hs.95952	ESTs	1.9
65	124669	AJ571594	Hs.102943	hypothetical protein MGC12916	1.9
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-II	1.9
	103891	NM_007212	Hs.124186	ring finger protein 2	1.9
	128727	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.9
	126831	AI929107	Hs.79933	cyclin I	1.9
70	125360	AW898892	Hs.189741	ESTs	1.9
	124276	H83465		gb:ys91a11.s1 Soares retina N2b5HR Homo	1.9
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
	126647	AK000283	Hs.270502	hypothetical protein FLJ20276	1.9
	125957	H41694		gb:yo06b06.r1 Soares adult brain N2b5HB5	1.9
75	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	1.9
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.9
	130945	U20582	Hs.2149	actin like protein	1.9
	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13992 fis, clone Y7	1.9
	103558	BE616547	Hs.2785	keratin 17	1.9
80	126982	AA211419		gb:zn55g05.s1 Stratagene muscle 937209 H	1.9
	125613	AA765957	Hs.21077	KIAA0532 protein	1.9
	129601	AB032964	Hs.115726	KIAA1138 protein	1.9
	126007	H51097	Hs.143261	ESTs	1.9
	123627	AA908619	Hs.112668	ESTs	1.9

	111587	AI125867	Hs.20734	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLJ22237	1.9
	128897	AW979134	Hs.10700	hypothetical protein	1.9
5	109891	H04757	Hs.323176	ESTs	1.9
	127704	AA679609		gb:ag72c02.s1 Gessler Wilms tumor Homo s	1.9
	129340	H75334	Hs.11050	F-box only protein 9	1.9
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	1.9
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	1.9
10	127136	R36277	Hs.7773	Homo sapiens ubiquitin conjugating enzym	1.9
	110636	H72868	Hs.19110	ESTs	1.9
	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	1.9
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.9
	130829	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	1.9
15	125768	AI557486	Hs.119122	ribosomal protein L13a	1.9
	123613	AA609158	Hs.291166	EST	1.9
	127506	T61039	Hs.252574	ribosomal protein L10a	1.9
	123546	AA608817	Hs.112597	EST	1.9
	126516	R95872	Hs.117572	chemokine binding protein 2	1.9
20	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9
	127426	AA854756	Hs.124076	ESTs	1.9
	112339	R56570	Hs.50547	ESTs	1.9
	129101	NM_013403	Hs.108665	zinedin	1.9
	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	1.9
25	118103	AA401733	Hs.184134	ESTs	1.9
	125752	AW136622	Hs.206673	ESTs	1.9
	102926	W28363	Hs.239752	nuclear receptor subfamily 2, group F, m	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
30	127329	AW160551	Hs.124021	soggy-1 gene	1.8
	126559	T16245		gb:NIB1005R Normalized Infant brain, Ben	1.8
	127297	AW629485	Hs.140720	GSK-3 binding protein FRAT2	1.8
	127640	AI557486	Hs.119122	ribosomal protein L13a	1.8
	103409	NM_004454	Hs.43697	els variant gene 5 (els-related molecule	1.8
35	127964	F06298		gb:HSC13F081 normalized Infant brain cDN	1.8
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	1.8
	128193	AJ224442	Hs.155020	putative methyltransferase	1.8
	115173	BE612940	Hs.88252	ESTs	1.8
	125532	AJ734146	Hs.271800	ESTs, Weakly similar to alternatively sp	1.8
40	126541	AJ271671	Hs.7854	zinc/iron regulated transporter-like	1.8
	127309	AI669765	Hs.133184	ESTs	1.8
	129062	AA452970	Hs.155218	E1B-55kDa-associated protein 5	1.8
	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	1.8
	127775	AA128808	Hs.179902	transporter-like protein	1.8
45	126994	AA455265	Hs.86686	ESTs, Moderately similar to I54374 gene	1.8
	130734	AW137091	Hs.18624	KIAA1052 protein	1.8
	114461	AA531187	Hs.126705	ESTs	1.8
	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	1.8
50	127389	T65126	Hs.12743	camitine O-octanoyltransferase	1.8
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	1.8
	107736	AA016239	Hs.60715	ESTs	1.8
	125669	R51308	Hs.333256	ESTs, Weakly similar to ALU8_HUMAN ALU	1.8
	100370	D79989	Hs.164884	KIAA0167 gene product	1.8
	113479	AI023133	Hs.10739	ESTs	1.8
55	105165	BE280787	Hs.16079	hypothetical protein FLJ10233	1.8
	120802	AA808018	Hs.109302	ESTs	1.8
	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	1.8
60	134212	AA654353	Hs.17719	EBP50-PDZ Interactor of 64 kD	1.8
	104204	AK001691	Hs.57655	hypothetical protein FLJ10829	1.8
	127464	AW971875	Hs.292071	ESTs	1.8
	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	1.8
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.8
	132380	AW373665	Hs.46853	ESTs	1.8
65	120087	AF186780	Hs.79219	RaiGDS-like gene; KIAA0959 protein	1.8
	116356	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	1.8
	125499	H10543		gb:ym04c06.r1 Soares Infant brain 1NIB H	1.8
	128846	AA730767	Hs.285753	SCG10-like-protein	1.8
	123669	AA620924	Hs.112923	EST	1.8
70	108889	AA135722	Hs.61481	ESTs	1.8
	126528	Z24895		gb:HSB87F122 STRATAGENE Human skeletal m	1.8
	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	130004	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	1.8
	130847	AJ672483	Hs.20220	lipase protein	1.8
75	111620	R14853	Hs.307478	EST, Weakly similar to I39058 hypotheti	1.8
	131971	BE567100	Hs.154938	hypothetical protein MDS025	1.8
	121360	AA405635	Hs.96854	ESTs, Weakly similar to DYLX_HUMAN CYTOP	1.8
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	1.8
80	124687	AA833902	Hs.270745	ESTs	1.8
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	1.8
	126730	AA442429		gb:zv70g02.r1 Soares fetal_fetus_Nb2HF8_	1.8
	127916	AJ239950	Hs.294111	ESTs, Moderately similar to B34087 hypo	1.8
	128408	AJ183407	Hs.143704	EST	1.8
	128440	AW090340	Hs.14337	Homo sapiens cDNA FLJ14407 fis, clone HE	1.8

	123783	AA610112		gb:af19g05.s1 Soares_total_fetus_Nb2HF8_	1.8
	109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.8
	107242	AB020672	Hs.175411	KIAA0865 protein	1.8
5	132804	AI805943	Hs.326067	hypothetical protein MGC5178	1.8
	125387	AJ243669	Hs.8127	KIAA0144 gene product	1.8
	121578	AA398791	Hs.178185	ESTs	1.8
	132944	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	1.8
	126295	AI281459	Hs.270114	ESTs	1.8
10	133335	BE251012	Hs.263812	nuclear distribution gene C (Ankylans)	1.8
	129879	AK001696	Hs.13109	Ran binding protein 11	1.7
	125175	W52355	Hs.303030	EST	1.7
	126919	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	1.7
	127773	AA725863	Hs.120508	ESTs	1.7
15	126495	AB029021	Hs.137732	KIAA1098 protein	1.7
	126948	AW968535	Hs.14328	hypothetical protein FLJ20071	1.7
	126671	C03105	Hs.285847	CG-19 protein	1.7
	115428	AA284112	Hs.94680	ESTs, Weakly similar to I78885 serine/t	1.7
	128232	AI830319	Hs.334641	hypothetical protein DKFZp434i1916	1.7
20	126082	H81188	Hs.269571	ESTs	1.7
	120467	AW292562	Hs.187628	ESTs	1.7
	124041	AW590171	Hs.101413	ESTs	1.7
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.7
25	123951	AB012922	Hs.173043	metastasis-associated 1-like 1	1.7
	126449	AF223944	Hs.325443	breast cell glutaminase	1.7
	124554	N65961		gb:za27d03.s1 Soares fetal liver spleen	1.7
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.7
	126780	R12421	Hs.5811	chromosome 21 open reading frame 59	1.7
	125661	AA491830	Hs.25689	ESTs	1.7
30	125888	H18298		gb:yn48b09.r1 Soares adult brain N2b5HB5	1.7
	127245	AA323958		gb:EST26810 Cerebellum II Homo sapiens c	1.7
	111223	AA852773	Hs.334838	KIAA1866 protein	1.7
	115611	R44789	Hs.33191	Homo sapiens, Similar to transmembrane r	1.7
	124846	R59977	Hs.158196	transcriptional adaptor 3 (ADA3, yeast	1.7
35	100397	D84424	Hs.57697	hyaluronan synthase 1	1.7
	127180	T27097	Hs.22790	ESTs	1.7
	102598	BE250742	Hs.106673	eukaryotic translation initiation factor	1.7
	134076	AF086215		gb:Homo sapiens full length Insert cDNA	1.7
	115659	W99382	Hs.283709	lipopolysaccharide specific response-7 p	1.7
40	125555	R19382	Hs.117869	ESTs	1.7
	126382	AI136886	Hs.143243	ESTs	1.7
	127710	AA682867	Hs.191901	ESTs	1.7
	125445	AI452722	Hs.7709	WW domain binding protein 1	1.7
	129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE:3873720, mRNA	1.7
45	119898	R93325	Hs.58690	ESTs	1.7
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	1.7
	133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.7
	119726	AF086289	Hs.234766	skin-specific protein	1.7
	125198	W69474	Hs.323140	ESTs	1.7
50	121414	AW291477	Hs.188763	testis expressed sequence 13A	1.7
	112542	AI458867	Hs.24276	ESTs	1.7
	101368	M13058	Hs.73952	proline-rich protein HaeIII subfamily 2	1.7
	125820	AA730136	Hs.75561	teratocarcinoma-derived growth factor 1	1.7
	128091	AA056483	Hs.301463	Human Chromosome 16 BAC clone CIT987SK-A	1.7
55	132609	U20165	Hs.53250	bone morphogenetic protein receptor, typ	1.7
	119447	W31714	Hs.122656	ESTs, Highly similar to formin 2-like pr	1.7
	113875	T81034	Hs.14841	ESTs	1.7
	113701	T97301	Hs.18026	ESTs	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
60	127133	AA280740	Hs.292072	ESTs, Moderately similar to A46010 X-link	1.7
	113316	T70318	Hs.268581	ESTs	1.7
	123316	AI290561	Hs.155361	ESTs	1.7
	122638	AL137476	Hs.123609	Homo sapiens mRNA; cDNA DKFZp434i0623 (f	1.7
	105053	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.7
65	103305	X82279		gb:Hsapiens Fas, Apo-1 gene (promoter a	1.7
	110384	H45282	Hs.268798	ESTs	1.7
	115626	AW630870	Hs.86674	ESTs, Weakly similar to hypothetical pro	1.7
	126905	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	1.7
	130820	AL353934	Hs.288798	hypothetical protein FLJ21012	1.7
70	112394	AK000373	Hs.8358	hypothetical protein FLJ20366	1.7
	129589	AW504292	Hs.11517	ESTs	1.7
	126446	NM_015670	Hs.118926	centrin/SUMO-specific protease 3	1.7
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	1.7
	120287	AF219946	Hs.102237	tubby super-family protein	1.7
75	129991	R28388	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
	123912	AA621283	Hs.332855	EST	1.7
	102071	AL120051	Hs.144700	ephrin-B1	1.7
	121046	AB033083	Hs.97377	KIAA1257 protein	1.7
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.7
80	104268	AL043864	Hs.70604	ATPase, Class II, type 9A	1.7
	111598	R11505	Hs.268912	ESTs	1.7
	128109	AW269421	Hs.128093	ESTs	1.7
	125435	R08480	Hs.272138	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7
	133104	AI091195	Hs.65029	growth arrest-specific 1	1.7

	126826	AA099764		gb:zn61112.r1 Stratagene muscle 937209 H	1.7
	106483	NM_006548	Hs.30299	IGF-II mRNA-binding protein 2	1.7
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	1.7
5	115904	AI167560	Hs.61297	ESTs	1.7
	125514	AB040912	Hs.191098	hypothetical protein FLJ11598	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	133179	U81599	Hs.66731	homeo box B13	1.7
	115167	AA749209	Hs.43728	hypothetical protein	1.7
10	118036	AA71862	Hs.195008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.7
	124540	N63232		gb:yz39a12.s1 Morton Fetal Cochlea Homo	1.7
	126183	BE018708	Hs.81972	SHC (Src homology 2 domain-containing) l	1.7
	127897	AA773681		gb:al77b12.r1 Soares_NhHMPu_S1 Homo sapi	1.7
	126680	F07097	Hs.133865	transmembrane 6 superfamily member 1	1.7
15	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.7
	130605	BE514362	Hs.306024	FK506-binding protein 3 (25kD)	1.7
	127541	AA573449	Hs.171515	ESTs	1.7
	127392	AI816736	Hs.14896	DHHC1 protein	1.7
	106879	AI190785	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	1.7
20	128303	AI096444	Hs.7187	hypothetical protein FLJ10707	1.7
	128469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.7
	125766	BE174587	Hs.289721	growth arrest specific transcript 5	1.7
	132332	AW978906	Hs.45005	hypothetical protein FLJ12960	1.6
	127142	AW452942	Hs.130393	ESTs	1.6
25	128416	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.6
	103790	AL122044	Hs.331633	hypothetical protein DKFZp566N034	1.6
	134578	AL110193	Hs.224137	hypothetical protein	1.6
	110023	AW294701	Hs.31040	ESTs	1.6
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.6
30	111483	R06569	Hs.269534	ESTs	1.6
	127363	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	1.6
	126231	AA991766	Hs.300793	ESTs	1.6
	106181	AI803651	Hs.191608	ESTs	1.6
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	1.6
35	119929	W88464	Hs.304825	ESTs	1.6
	132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.6
	127155	AA284993		gb:zz23e10.r1 Soares ovary tumor NbHOT H	1.6
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.6
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.6
40	131330	D13969	Hs.184669	zinc finger protein 144 (Me1-18)	1.6
	129445	W52452	Hs.29797	ribosomal protein L10	1.6
	113427	T85105	Hs.15471	ESTs	1.6
	106124	H93368	Hs.7587	Homo sapiens cDNA: FLJ21962 fis, clone H	1.6
	128135	AA954381	Hs.269721	ESTs, Moderately similar to ALU1_HUMAN	1.6
45	111460	R02728	Hs.117331	ESTs	1.6
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	1.6
	134118	BE336680	Hs.182877	KIAA0116 protein	1.6
	111570	AF059203	Hs.20580	sterol O-acyltransferase 2	1.6
	113511	T89578	Hs.189740	ESTs	1.6
50	113286	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	1.6
	109875	H03260	Hs.30385	ESTs	1.6
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.6
	105564	BE616694	Hs.288042	hypothetical protein FLJ14299	1.6
55	128063	AI377750	Hs.167177	ESTs	1.6
	109779	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.6
	125334	T86569	Hs.182118	ESTs	1.6
	127208	AW816490	Hs.337508	ESTs	1.6
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidyseri	1.6
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.6
60	114062	AI560984	Hs.27283	ESTs	1.6
	122550	AA451859	Hs.99253	ESTs	1.6
	113413	R08872	Hs.186512	ESTs	1.6
	127019	AI929355	Hs.286128	hypothetical protein FLJ23329	1.6
	105251	R12607	Hs.35101	proline-rich Gla (G-carboxyglutamic acid	1.6
65	112670	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	1.6
	114913	AI435199	Hs.58940	ESTs, Weakly similar to I38022 hypotheti	1.6
	126604	AI023299	Hs.269806	ESTs	1.6
	125324	R07785		gb:yl15c06.r1 Soares fetal liver spleen	1.6
	121438	AW445024	Hs.139389	ESTs	1.6
70	127289	AI041014	Hs.220752	ESTs, Weakly similar to unnamed protein	1.6
	126935	AI198535	Hs.89463	potassium large conductance calcium-acti	1.6
	132430	AW973652	Hs.283105	ESTs	1.6
	133541	H75334	Hs.11050	F-box only protein 9	1.6
	102612	U65402	Hs.248124	G protein-coupled receptor 31	1.6
75	120228	AI192528	Hs.164537	ESTs	1.6
	122652	AA454641		gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	103456	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	1.6
	105355	AL031447	Hs.26938	Homo sapiens, clone IMAGE:4053044, mRNA,	1.6
	108043	AA042873	Hs.160412	ESTs	1.6
80	128695	NM_003478	Hs.101299	cullin 5	1.6
	127984	AA846377	Hs.193706	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.6
	124405	AA228137	Hs.25005	hypothetical protein MGC3329	1.6
	103934	BE278111	Hs.134200	DKFZP564C186 protein	1.6
	124195	H83034		gb:yq48e07.r1 Soares fetal liver spleen	1.6

5	110938	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT	1.6
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.6
	121226	AA364109	Hs.177990	ESTs	1.6
	120415	AA235810		gb:z41a03.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	123864	AA620882		gb:af95g01.s1 Soares_testis_NHT Homo sap	1.6
10	125045	AI114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	1.6
	133425	AA444390	Hs.155482	hydroxyacyl glutathione hydrolase	1.6
	126578	AF151861	Hs.107528	androgen induced protein	1.6
	102406	U43177		(NONE)	1.6
	114126	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	1.6
15	125233	W85713	Hs.110092	ESTs	1.6
	109635	F04296	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.6
	125675	BE294972	Hs.55406	Homo sapiens cDNA FLJ13549 fis, clone PL	1.6
	129707	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKFZp566L203 (fr	1.6
	127569	AI765107	Hs.274422	hypothetical protein FLJ20550	1.6
20	113302	T66919	Hs.268575	ESTs	1.6
	119705	AI984203	Hs.57874	ESTs	1.6
	127226	AL036559	Hs.3463	ribosomal protein S23	1.6
	123489	AA599708		gb:ag11a10.s1 Gessler Wilms tumor Homo s	1.6
	107468	AA740979	Hs.91389	ESTs	1.6
25	115916	AI052731	Hs.91910	ESTs	1.6
	127815	AA743490	Hs.255015	ESTs	1.6
	100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.6
	125568	AW615396	Hs.105613	ESTs	1.6
	105260	N81201	Hs.31755	ESTs	1.6
30	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	1.6
	111275	N70970	Hs.35006	ESTs	1.6
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.6
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.6
	124770	AA984414	Hs.120429	ESTs	1.6
35	117936	AI382904	Hs.47213	ESTs	1.6
	134385	M14660	Hs.169274	ESTs, Highly similar to IFT2_HUMAN INTER	1.6
	108367	AW410478	Hs.104019	transforming, acidic coiled-coil contain	1.6
	131143	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	1.6
	105441	N28522	Hs.8935	quinolinate phosphoribosyltransferase (n	1.6
40	128215	AA973310		gb:op91e06.s1 Soares_NFL_T_GBC_S1 Homo s	1.6
	127344	AI003929	Hs.80624	hypothetical protein MGC2560	1.6
	126478	BE541249	Hs.108697	ESTs	1.6
	122053	AI637498	Hs.98745	ESTs	1.5
	111760	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	1.5
45	112401	R51279	Hs.237536	ESTs, Weakly similar to AF151067 1 HSPC2	1.5
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.5
	125575	H14983		gb:ym19h09.r1 Soares Infant brain 1NIB H	1.5
	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.5
	108935	AA147848	Hs.67991	hypothetical protein DKFZp434G0522	1.5
50	121221	AI140708	Hs.97461	ESTs	1.5
	120091	AW024672	Hs.59558	EST	1.5
	107375	BE011845	Hs.251064	high-mobility group (nonhistone chromoso	1.5
	125803	AW876115	Hs.29852	ESTs	1.5
	115132	AA811762	Hs.71433	ESTs	1.5
55	113346	AF143876	Hs.14318	Homo sapiens clone IMAGE:113399 mRNA seq	1.5
	107357	U63973	Hs.103501	rhodopsin kinase	1.5
	125443	BE251057	Hs.177592	ribosomal protein, large, P1	1.5
	133803	M24461	Hs.76305	surfactant, pulmonary-associated protein	1.5
	113378	T80738	Hs.14757	ESTs	1.5
60	105540	BE391690	Hs.9265	hypothetical protein FLJ20917	1.5
	127446	F13008		gb:HSC3HE011 normalized Infant brain cDN	1.5
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	1.5
	127585	AA604144	Hs.190632	ESTs	1.5
	125824	Z45258	Hs.286013	short coiled-coil protein	1.5
65	127606	AA621135	Hs.136552	ESTs	1.5
	125585	AW298113	Hs.92909	SON DNA binding protein	1.5
	107757	BE621721	Hs.280792	hypothetical protein FLJ12387 similar to	1.5
	109978	H09356	Hs.22528	ESTs	1.5
	132297	BE272446	Hs.265317	hypothetical protein MGC2562	1.5
70	115784	AW402151	Hs.54673	tumor necrosis factor (ligand) superfam1	1.5
	127880	W39735	Hs.73818	ubiquinol-cytochrome c reductase hinge p	1.5
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.5
	102868	X02419	Hs.77274	plasminogen activator, urokinase	1.5
	133457	J04948	Hs.333509	alkaline phosphatase, placental-like 2	1.5
75	130339	AA435746		gb:z179e03.s1 Soares_testis_NHT Homo sap	1.5
	125444	N28476	Hs.159161	Rho GDP dissociation inhibitor (GDI) ctp	1.5
	123470	AW303285	Hs.303632	Human DNA sequence from clone RP11-110H4	1.5
	100025				1.5
	127063	AI276526	Hs.331564	Homo sapiens mRNA: cDNA DKFZp434H1215 (f	1.5
80	127945	AA815031	Hs.123598	ESTs	1.5
	111557	R09510	Hs.20373	EST	1.5
	116009	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	1.5
	119858	W01370	Hs.46824	ESTs	1.5
	106509	AI042309	Hs.64552	hypothetical protein MGC15563	1.5
	124124	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HE	1.5
	126713	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	1.5
	126475	AW959075	Hs.238797	ESTs, Moderately similar to t38022 hypot	1.5

	126851	R40611	Hs.137565	ESTs	1.5
	104820	AW182768	Hs.22520	ESTs	1.5
	127235	AU17309	Hs.225583	ESTs, Weakly similar to 2004399A chromos	1.5
5	126552	AF168711	Hs.159397	x 010 protein	1.5
	127523	AA617637		gb:np34h12.s1 NCI_CGAP_Lu1 Homo sapiens	1.5
	131692	BE559681	Hs.30736	KIAA0124 protein	1.5
	112974	AL353965	Hs.101174	microtubule-associated protein tau	1.5
	118921	N91914	Hs.54751	ESTs	1.5
10	100676	X02761	Hs.287820	fibronectin 1	1.5
	127721	T59578	Hs.188440	ESTs, Weakly similar to ALUF_HUMAN IIII	1.5
	115254	AA279024	Hs.269316	ESTs, Weakly similar to S65657 alpha-1C	1.5
	128173	AJ457242	Hs.127024	ESTs	1.5
	126846	AA663527	Hs.116910	ESTs	1.5
15	125294	R40025	Hs.106551	ESTs	1.5
	127494	AW978730	Hs.291956	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.5
	134191	W26632	Hs.7979	KIAA0736 gene product	1.5
	107394	AA864798	Hs.186180	Homo sapiens cDNA: FLJ23038 fls, clone L	1.5
	131562	NM_003512	Hs.28777	H2A histone family, member L	1.5
20	127310	AW450671	Hs.189284	ESTs	1.5
	122359	AA523486		gb:nl57111.s1 NCI_CGAP_Pr12 Homo sapiens	1.5
	100524	M80902	Hs.183704	ubiquitin C	1.5
	128422	T77794		gb:y20d09.r1 Soares fetal liver spleen	1.5
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.5
25	126784	T81887	Hs.108854	HSPC163 protein	1.5
	123343	AJ761902	Hs.99597	ESTs	1.5
	105458	AW954377	Hs.26412	ring finger protein 26	1.5
	112266	AJ652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.5
	127622	AA628222	Hs.97883	ESTs	1.5
30	113659	R06545	Hs.189781	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.5
	116892	AJ573283	Hs.38458	ESTs	1.5
	126995	NM_014351	Hs.189810	sulfotransferase family 4A, member 1	1.5
	111657	R07364	Hs.288667	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	100243	AB028125	Hs.77854	regucalcin (senescence marker protein)-30	1.5
35	116153	AF107203	Hs.57937	ataxin 2-binding protein 1	1.5
	108892	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	1.5
	113294	AJ037922	Hs.11000	leptin receptor overlapping transcript-I	1.5
	126691	W03046	Hs.283664	aspartate beta-hydroxylase	1.5
	106979	AW015227	Hs.289053	hypothetical protein FLJ14733	1.5
40	125546	H09950		gb:ym01d12.r1 Soares infant brain 1N1B H	1.5
	113990	AJ497945	Hs.83097	hypothetical protein FLJ22955	1.5
	129295	U63127	Hs.110121	SEC7 homolog	1.5
	125431	AW851639	Hs.75584	polymyositis/scleroderma autoantigen 2 (1.5
	112558	AK001621	Hs.15921	hypothetical protein FLJ10759	1.5
45	122046	AJ560456	Hs.107319	ESTs	1.5
	122472	AA448509	Hs.128652	ESTs	1.5
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1.5
	131714	AA842831	Hs.31016	putative DNA binding protein	1.5
	101233	AL135173	Hs.878	sorbitol dehydrogenase	1.5
50	109501	AF047437	Hs.90436	sperm associated antigen 7	1.5
	126984	AA213820	Hs.255533	ESTs, Weakly similar to S11998 finger pr	1.5
	125765	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly	1.5
	127693	AA676727		gb:zj68b11.s1 Soares_fetal_liver_spleen_	1.5
	128453	X02761	Hs.287820	fibronectin 1	1.5
55	119418	T97590	Hs.221711	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr	1.5
	116708	F10528	Hs.70001	ESTs, Moderately similar to JC6169 nucl	1.5
	122420	AA446971		gb:zw85f11.s1 Soares_total_fetus_Nb2HF8_	1.5
	100238	L24959	Hs.348	calcium/calmodulin-dependent protein kin	1.5
60	109710	D20044	Hs.12929	hypothetical protein FLJ20721	1.5
	105704	AJ282341	Hs.75431	fibrinogen, gamma polypeptide	1.5
	112712	R91060	Hs.330761	ESTs	1.5
	100098	AF003743		gb:Homo sapiens delayed rectifier potass	1.5
	114122	R46128	Hs.12751	ESTs	1.5
65	132397	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	1.5
	107881	AJ568350	Hs.61273	hypothetical protein MGC2650	1.5
	106302	AA398859	Hs.18397	hypothetical protein FLJ23221	1.5
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.5
	104957	AJ359009	Hs.10026	mitochondrial ribosomal protein L17	1.5
70	102909	NM_006269	Hs.2693	glioma-associated oncogene homolog (zinc	1.5
	125559	BE297488	Hs.279877	cell division protein FtsJ	1.5
	109634	H17063	Hs.183646	ESTs	1.5
	116607	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.5
	127175	R11937		gb:yf54b08.r1 Soares infant brain 1N1B H	1.5
75	110617	W93231	Hs.285901	Homo sapiens, clone IMAGE:3948563, mRNA,	1.5
	125988	W27648		gb:37e10 Human retina cDNA randomly prim	1.5
	115093	AJ241932	Hs.3542	hypothetical protein FLJ11273	1.5
	121207	AA705799	Hs.183714	ESTs	1.5
	112652	BE269599	Hs.235782	solute carrier family 21 (organic anion	1.5
80	125213	AB014554	Hs.109299	protein tyrosine phosphatase, receptor t	1.5
	125912	AW867467	Hs.278712	eukaryotic translation initiation factor	1.5
	133046	R96881	Hs.63609	HpaII liny fragments locus 9C	1.5
	122791	AL122055	Hs.129836	KIAA1028 protein	1.5

Table 268

5	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
10	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
10	108451	13766_27	AA079195 AA084955 AA126308 AA084956
	124195	2606_3	H83034 H52379
	123619	371681_1	AA602964 AA609200
15	125165	1852047_1	W45350 W45406
	125324	1692163_1	R07785 T85948 T86972
	126053	1601238_1	H64450 H64464
20	126086	1606216_1	H75681 H70975
	126098	1629789_1	M79088 N88221
	125464	168460_1	N71807 AA203399
25	125499	1562851_1	H10543 R11878
	126127	1205826_1	N95428 W24040 AW751366 H81987
	125546	356478_1	H09950 R18413 AA570553 AW973425
30	125549	1702179_1	R20215 R18767
	125558	1703083_1	R59305 R19748
	125575	1566885_1	H14983 R21554
35	125743	5025_5	H17151 H11956
	125761	1744008_1	R68351 R68364
	126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017
40	127155	200358_1	AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
	127175	1695805_1	AA284993 AA478122 AA477923
	126528	1276201_1	R11937 Z45532
45	125957	1583542_1	Z24895 AW891336 R01294
	125976	296453_1	H41694 H45213
	125982	1766315_1	AA436760 AW237453 BE327496 N47347 N56957
50	125988	1365728_1	R98091 W92898
	127245	226662_1	W27648 R99193 BE090398
	127248	227560_1	AA323958 AA370268
55	127262	231725_1	AA364195 AA325029 AW962050
	126659	1541209_1	AA828125 AA834883 AA330555
	126693	87363_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
60	127315	37938_1	C05723 AA018342
	126730	297653_1	AF116622 AJ114507 AA640834 AA377999
	103898	187213_3	AA442429 T19477
65	127446	16001_2	AA248884
	126826	127356_1	F13008 T75435
	126872	142698_1	AA099764 AA112950
70	128132	177108_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073, BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	127523	351071_1	BE011368 BE011362 BE011215 BE011365 BE011363
	126982	171753_1	AA225832 AJ820970 AJ820952 AA226472 AJ732140 AJ732059 AA226307
75	128215	530345_1	AA225500
	127704	405690_1	AA617637 AA554983
	127705	966283_2	AA211419 AA211566
80	128422	1811283_1	AA973310
	127897	446527_1	AA679609 AA694592
	120734	208882_1	AJ003322 AJ003324
85	100098	25117_13	T77794 T85681
	114620	32062_8	AA773681 AA773857
	122652	100842	AA299948 AA299949
90	123808	123864	AF003743
	118049	102408	AA642974 AA084223
	116962	134076	26401_30 AA454641
95	125888	127271	tigr_H74398 U05597
	127271	321389_1	genbank_AA610112
	113119	104799	genbank_T74884
100	127693	790317_1	genbank_AA620552
	120415	122359	genbank_AA620882
	122359	122420	genbank_N53145
105	124540	124554	entrez_U43177
	117357	103305	genbank_H79677
	103305	103305	AF086215 W02702 AA284288 W25655
110	124554	117357	H18298 H46830
	117357	103305	H96820 H79463
	103305	103305	genbank_T47910 T47910
115	124554	117357	genbank_AA029703 AA029703
	117357	103305	AA676727 AA704704
	103305	103305	genbank_AA235810 AA235810
120	124554	117357	F08298 R18057
	117357	103305	681003_1 AA523486 AW026780 AJ821660 AA443898
	103305	103305	genbank_AA446971
125	124554	117357	genbank_H83465
	117357	103305	entrez_M21305
	103305	103305	genbank_N63232
130	124554	117357	genbank_N65961
	117357	103305	genbank_N24829
	103305	103305	entrez_X82279

103392	entrez_X94563
119416	genbank_T97186
105225	genbank_AA211777
121292	genbank_AA401807
112853	genbank_T02843
121387	genbank_AA405854
114601	genbank_AA075566
100221	entrez_D28383
130339	genbank_AA435746
100554	ligr_HT2241
123423	genbank_AA598484
123474	genbank_AA599209
123489	genbank_AA599708

TABLE 27A: ABOUT 895 GENES UP-REGULATED IN COMBINED LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 27A lists about 895 genes that are upregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with the normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of fibrosis to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title R1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L 56.0
424917	AJ636208	Hs.95901	Homo sapiens cDNA: FLJ23049 fis, clone L 26.5
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitter 25.5
457200	U33749	Hs.197764	thyroid transcription factor 1 22.2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein 21.1
429272	W25140	Hs.110667	ESTs 19.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial 19.1
442006	AW975183	Hs.292663	ESTs 18.8
445885	AJ734009	Hs.127699	KIAA1603 protein 18.0
440452	AJ925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY 17.8
422426	W79117	Hs.58559	ESTs, Weakly similar to rholekin [M.musc 17.4
444929	AJ685841	Hs.161354	ESTs 16.5
440807	AW269421	Hs.128093	ESTs 16.3
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence 14.2
446967	AJ699529	Hs.156781	ESTs 13.3
417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep 12.3
437119	AJ379921	Hs.177043	ESTs 12.3
451103	R52804	Hs.25956	DKFZP564D208 protein 11.5
443450	N66045	Hs.133529	ESTs 11.4
411880	AW872477		gbchm30103.x1 NCL_CGAP_Thy4 Homo sapiens 11.3
432519	AJ221311	Hs.130704	ESTs 11.3
414142	AW368397	Hs.150042	ESTs 11.0
433283	BE041135	Hs.175622	ESTs 10.1
441082	AW444804	Hs.202655	ESTs 10.1
452039	AJ922988	Hs.172510	ESTs 10.0
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein 9.9
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H 9.8
412372	R65998	Hs.118615	ESTs 9.8
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily 9.7
431007	AF039564	Hs.248211	retinoblastoma-binding protein 9 9.4
443709	AJ082692	Hs.134662	ESTs 9.3
448232	AJ281848	Hs.165547	ESTs 9.2
448253	H25899	Hs.201591	ESTs 9.2
432133	AB033088	Hs.272567	KIAA1262 protein 9.1
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (tr 9.0
431353	AA828032	Hs.189076	ESTs 8.8
450050	AJ681268	Hs.257883	ESTs 8.8
458194	AW383618	Hs.265459	ESTs, Moderately similar to ALJ2_HUMAN A 8.8
414968	C16096	Hs.297777	ESTs 8.7
425664	AJ006276	Hs.159003	transient receptor potential channel 6 8.7
408562	AJ436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein, 8.6
453672	U73531	Hs.34526	G protein-coupled receptor 8.5
429420	AK001679	Hs.202289	hypothetical protein FLJ10376 8.5
421478	AJ683243	Hs.97258	ESTs 8.4
404916			ESTs 8.4
444396	T65213	Hs.4257	ESTs 8.3
442275	AW449467	Hs.54795	ESTs 8.3
437479	R61866	Hs.101277	ESTs 8.2
432203	AA305746	Hs.49	macrophage scavenger receptor 1 8.2
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein 7.9
406747	AJ925153	Hs.217493	annexin A2 7.8

5	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	7.7
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	7.6
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	7.5
	421155	H87879	Hs.102267	lysyl oxidase	7.5
	446917	AI347863	Hs.155672	ESTs	7.5
10	422798	R92347	Hs.34574	ESTs	7.4
	426830	AA385751	Hs.160392	ESTs	7.4
	437157	BE048860	Hs.120655	ESTs	7.4
	433231	AB040926	Hs.143552	KIAA1493 protein	7.3
	451561	N52812	Hs.177403	ESTs	7.1
15	430656	AA482900	Hs.162080	ESTs	7.1
	448206	BE622585	Hs.3731	ESTs	7.1
	420209	AA256444	Hs.32295	Homo sapiens cDNA FLJ12604 fis, clone NT	7.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	6.9
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.9
20	409718	D86640	Hs.55045	src homology three (SH3) and cysteine ri	6.8
	443324	R44013	Hs.164225	ESTs	6.8
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	6.8
	427356	AW023482	Hs.97849	ESTs	6.7
	418735	N48769	Hs.44609	ESTs	6.7
25	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	6.6
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.6
	430099	AW194988	Hs.20537	Homo sapiens cDNA FLJ13942 fis, clone Y7	6.6
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	6.5
	428508	BE252383	Hs.184668	SBBI31 protein	6.5
30	438202	AW169287	Hs.22568	ESTs	6.5
	441233	AA972965	Hs.135568	ESTs	6.4
	433384	AI021992	Hs.124244	ESTs	6.3
	427043	AA397679	Hs.298460	ESTs	6.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	6.3
35	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	433365	AF026944	Hs.293797	ESTs	6.3
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.2
	431337	N48107	Hs.292593	ESTs	6.1
40	434819	AA650099	Hs.291541	ESTs	6.0
	458219	H22195	Hs.31874	ESTs	6.0
	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fasclclin	5.9
	435933	AA805520	Hs.192075	ESTs	5.9
	436954	AA740151	Hs.130425	ESTs	5.9
45	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	5.8
	449108	AI140683	Hs.98328	ESTs	5.8
	410334	AW979261	Hs.291993	ESTs	5.7
	447112	H17800	Hs.7154	ESTs	5.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serin	5.7
50	449208	AW263635	Hs.48643	ESTs	5.7
	445657	AW612141	Hs.279575	ESTs	5.7
	421554	AW137676	Hs.97775	ESTs, Weakly similar to Testis-specific	5.7
	435299	AI745458	Hs.122614	ESTs, Weakly similar to apoptotic protea	5.6
	416769	AI339257	Hs.115436	ESTs	5.6
55	433527	AW235613	Hs.133020	ESTs	5.6
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (cal	5.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.5
	411514	AW850178	Hs.18995	KIAA1304 protein	5.5
	424084	AI940575	Hs.20914	Homo sapiens cDNA: FLJ23056 fis, clone L	5.5
60	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.4
	429710	AI337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	5.4
	432113	AA935065	Hs.152385	ESTs	5.4
	447997	H00656	Hs.29792	ESTs	5.4
	449328	AI962493	Hs.197647	ESTs	5.3
65	416575	W02414	Hs.38383	ESTs	5.3
	432009	AL137424		gb:Homo sapiens mRNA: cDNA DKFZp761G2123	5.3
	434088	AF116677	Hs.249270	hypothetical protein PRO1965	5.3
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	5.2
	414299	AA142989	Hs.71730	ESTs	5.2
70	431041	AA490967	Hs.105276	ESTs	5.2
	448104	AI674818	Hs.178391	ribosomal protein L44	5.2
	445279	R41900	Hs.22245	ESTs	5.1
	408978	AL133817	Hs.49421	Homo sapiens mRNA: cDNA DKFZp434M0728 (f	5.1
	415094	D59513		gb:HUM042H108 Clontech human fetal brain	5.1
75	428244	AI584123	Hs.42500	ADP-ribosylation factor-like 5	5.1
	452784	BE463857	Hs.151258	Homo sapiens cDNA: FLJ21062 fis, clone C	5.1
	455431	AW938484	Hs.80738	slatophorin (gpL115, leukostatin, CD43)	5.1
	449416	AI651016	Hs.246311	ESTs	5.1
	421659	NM_014459	Hs.106511	protocadherin 17	5.1
80	407638	AJ404672	Hs.288693	Homo sapiens cDNA FLJ11567 fis, clone HE	5.0
	446164	AW273539	Hs.199329	Homo sapiens cDNA: FLJ23577 fis, clone L	5.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	5.0
	446608	N75217	Hs.257846	ESTs	4.9
	419807	R77402		gb:yl75f11.s1 Soares placenta Nb2HP Homo	4.9
	447164	AF026941	Hs.17518	Homo sapiens cgl5 mRNA, partial sequence	4.9
	442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	4.9
	429496	AA453800	Hs.192793	ESTs	4.8

	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor I	4.8
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	4.8
	425509	AF079363	Hs.158213	sperm associated antigen 6	4.8
5	424717	H03754	Hs.152213	wingless-type MMTV Integration site fam1	4.8
	436061	AJ248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	4.8
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	4.7
	453382	AA709285	Hs.5997	Homo sapiens cDNA FLJ13078 fis, clone NT	4.7
	447033	AJ357412	Hs.157601	ESTs	4.7
10	417235	AA810278	Hs.24250	ESTs	4.7
	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	4.7
	427652	AJ673025	Hs.43874	ESTs	4.7
	431255	AA497043	Hs.115685	ESTs	4.7
	441143	AJ027604	Hs.159650	ESTs	4.7
15	452293	AJ871833		gb:wm51h09.x1 NCL_CGAP_U12 Homo sapiens	4.7
	443903	AJ220547	Hs.135223	ESTs	4.7
	422352	AA766296	Hs.99200	ESTs	4.7
	424105	AJ142336	Hs.43977	ESTs	4.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	4.6
20	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.6
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.6
	425804	BE501698	Hs.258189	ESTs	4.6
	435347	AW014873	Hs.116963	ESTs	4.6
	446002	AJ346468	Hs.145789	ESTs	4.6
25	452883	X80031	Hs.150318	ESTs	4.8
	442176	AA983764	Hs.128910	ESTs	4.6
	443253	AJ041212	Hs.132117	ESTs	4.5
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.5
	439920	H05430	Hs.144455	ESTs	4.5
30	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.5
	434424	AJ811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L	4.4
	408625	AW243323	Hs.266785	ESTs	4.4
	449299	AA299919		gb:EST12592 Uterus tumor I Homo sapiens	4.4
	450656	AA010539	Hs.18912	ESTs	4.4
35	433815	AJ696602	Hs.112757	ESTs	4.4
	416879	H98899	Hs.42599	ESTs	4.3
	432182	AW607789	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.3
	445386	AA22005	Hs.160380	ESTs	4.3
	450478	AW451709	Hs.271200	ESTs	4.3
40	453080	AA23056	Hs.23921	Homo sapiens cDNA FLJ12482 fis, clone NT	4.3
	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	4.3
	443257	AJ34040	Hs.11614	Homo sapiens cDNA: FLJ23555 fis, clone L	4.3
	453921	AJ824009	Hs.44577	ESTs	4.3
	419721	NM_001650	Hs.288550	aquaporin 4	4.2
45	432316	AW973235	Hs.293697	ESTs	4.2
	435202	AJ971313	Hs.170204	KIAA0551 protein	4.2
	440320	AA879294		gb:bmw86e09.a1 NCL_CGAP_Pr12 Homo sapiens	4.2
	438796	W67821	Hs.109590	genethonin 1	4.2
	400269				4.2
50	447724	AW298375	Hs.24477	ESTs	4.1
	446509	AF169693	Hs.132892	protocadherin 20	4.1
	451620	AW449888	Hs.257224	ESTs	4.1
	451963	AJ825440	Hs.224952	ESTs	4.1
	458408	AJ288348	Hs.23450	mRNA for FLJ00023 protein	4.1
55	425895	AJ269484	Hs.161427	zinc finger protein 215	4.1
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	4.1
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	4.0
	415929	AA724373	Hs.295306	ESTs, Highly similar to unnamed protein	4.0
	426625	T78300	Hs.171409	serologically defined colon cancer antig	4.0
60	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	4.0
	437138	AJ935622	Hs.271245	ESTs	4.0
	455024	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo	4.0
	436246	AW450963	Hs.119991	ESTs	4.0
	416030	H15261	Hs.21948	ESTs	4.0
65	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	3.9
	445122	AW241632	Hs.147377	Homo sapiens cDNA: FLJ23598 fis, clone L	3.9
	414812	X72755	Hs.77387	monokine induced by gamma interferon	3.9
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	3.9
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.9
70	429208	AA447990	Hs.190478	ESTs	3.9
	442957	AJ949952	Hs.49397	ESTs	3.9
	444050	AW138295	Hs.135024	ESTs	3.9
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.9
	451024	AA442176		gb:zw63b08.r1 Soares_tota_fetus_Nb2HF8_	3.9
75	442832	AW206560	Hs.253569	ESTs	3.9
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	3.9
	451895	T93573	Hs.16970	ESTs	3.9
	442353	BE379594	Hs.49136	ESTs	3.8
	421464	AA291553	Hs.190086	ESTs	3.8
80	404043				3.8
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	3.8
	410008	AA079552		gb:czm20h12.s1 Stratogene pancreas (93720	3.8
	410247	AF181721	Hs.61345	RU2S	3.8
	417461	R38403	Hs.13305	ESTs	3.8

	423609	AA328348	Hs.218289	ESTs	3.8
	440444	AA885221	Hs.156984	ESTs	3.8
	446254	BE179829	Hs.179852	Homo sapiens cDNA FLJ12832 fis, clone NT	3.8
5	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (tr	3.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	3.8
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	3.8
	444271	AW452569	Hs.149804	ESTs	3.8
	434217	AW014795	Hs.23349	ESTs	3.8
	452571	W31518	Hs.34665	ESTs	3.7
10	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	3.7
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.7
	431322	AW970522		gb:EST382704 MAGE resequences, MAGK Homo	3.7
	445034	AW293376	Hs.160323	ESTs	3.7
	438842	AA827176	Hs.124316	ESTs	3.7
15	424906	AJ566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	415025	AW207091	Hs.72307	ESTs	3.7
	420313	AB023230	Hs.96427	KIAA1013 protein	3.7
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.7
	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.7
20	434636	AA083764	Hs.241334	ESTs	3.7
	435747	AJ079519	Hs.134398	ESTs	3.7
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.s	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fam1	3.7
	410060	NM_001448	Hs.58367	glypican 4	3.7
25	426116	AA868729	Hs.144694	ESTs	3.7
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	3.7
	414259	W44633	Hs.25044	Homo sapiens cDNA: FLJ23131 fis, clone L	3.7
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.6
	431889	AA521277	Hs.124946	ESTs	3.6
30	430414	AW365665	Hs.120388	ESTs	3.6
	433426	H69125	Hs.133525	ESTs	3.6
	421764	AJ681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.6
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	3.6
	455235	AW875951		gb:CM1-PT0013-131299-067-f09 PT0013 Homo	3.6
35	408399	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	3.6
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.6
	436982	AB018305	Hs.5378	spodrin 1, (f-spondin) extracellular mat	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	3.6
	432837	AA310693	Hs.279512	HSPC072 protein	3.6
40	452166	AJ948607	Hs.264680	ESTs	3.5
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234 Homo	3.5
	420362	U97934	Hs.97206	huntingtin interacting protein 1	3.5
	424202	BE350295	Hs.15032	ESTs, Weakly similar to RAN binding prot	3.5
45	410658	AW105231	Hs.192035	ESTs	3.5
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	419503	AA243642	Hs.137422	ESTs	3.5
	439479	AJ734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.5
50	424268	AA397653	Hs.144339	Human DNA sequence from clone 495O10 on	3.5
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.5
	450715	AJ264484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.5
	428927	AA441837	Hs.90250	ESTs	3.5
	422544	AB018259	Hs.118140	KIAA0716 gene product	3.4
55	431207	AA495925	Hs.9394	ESTs	3.4
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13558 fis, clone PL	3.4
	441484	AA935481	Hs.58972	ESTs	3.4
	425916	NM_005786	Hs.162200	wortensin 2	3.4
	401793				3.4
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.4
60	438038	AJ732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	3.4
	439619	AW975998	Hs.58595	ESTs	3.4
	446577	AB040933	Hs.15420	KIAA1500 protein	3.4
	450445	AW974636	Hs.194563	ESTs	3.4
65	459482	AA625339	Hs.237052	EST, Weakly similar to ALU1_HUMAN ALU SU	3.4
	445495	BE622641	Hs.38489	ESTs	3.4
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	3.4
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.4
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	3.3
	419235	AW470411	Hs.288433	neurotrophin	3.3
70	429703	T93154	Hs.28705	ESTs	3.3
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.3
	406182				3.3
	417307	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	3.3
	430140	AW296771	Hs.221999	ESTs	3.3
75	436111	AJ803082	Hs.157212	ESTs	3.3
	449729	R72032	Hs.29235	ESTs	3.3
	457620	AA602711		gb:np03h06.s1 NCL_CGAP_Pr2 Homo sapiens	3.3
	428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	3.3
80	406554				3.3
	451381	BE241831		gb:TCAAP2E0011 Pediatric acute myelogeno	3.3
	443113	AJ040686	Hs.132908	ESTs	3.3
	421470	R27496	Hs.1378	annexin A3	3.3
	446428	AW082270	Hs.210617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3

	435031	AI632091	Hs.116877	ESTs	3.3
	413136	BE066941		gb:PMO-BT0340-091299-002-a11 BT0340 Homo	3.2
	429228	AI553633	Hs.104985	ESTs	3.2
	420252	AW270404	Hs.193161	ESTs	3.2
5	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.2
	444339	T96555	Hs.31562	ESTs	3.2
	434164	AW207019	Hs.148135	ESTs	3.2
	404599				3.2
	426920	AA393351	Hs.132121	ESTs	3.2
10	453736	AL118674	Hs.34871	KIAA0569 gene product	3.2
	408923	H73881	Hs.255436	ESTs	3.2
	430919	AA489041	Hs.295448	ESTs	3.2
	431622	AW979271	Hs.293184	ESTs	3.2
	433584	AW295399		gb:U1-H-B12-ahv-h-03-0-ULs1 NCI_CGAP_Su	3.2
15	437073	AI885608	Hs.94122	ESTs	3.2
	438394	BE379623	Hs.27693	CGI-124 protein	3.2
	446242	N65336	Hs.7360	ESTs	3.2
	452542	AW812256		gb:RCO-ST0174-191099-031-a07 ST0174 Homo	3.2
20	454009	AW015927	Hs.233071	ESTs	3.2
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN AL	3.2
	415652	T79213	Hs.272073	ESTs	3.2
	453931	AL121278	Hs.25144	ESTs	3.2
	439382	BE247684	Hs.103070	ESTs	3.2
	420077	AW512260	Hs.87767	ESTs	3.2
25	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.2
	446745	AW118189	Hs.158400	ESTs	3.1
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	3.1
	450320	AW291775	Hs.213793	ESTs	3.1
30	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.1
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	451110	AI955040	Hs.301584	ESTs	3.1
	431745	AW972448	Hs.163425	ESTs	3.1
	410781	AI375672	Hs.165028	ESTs	3.1
35	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
	444330	AI597655	Hs.49265	ESTs	3.1
	408761	AA057264	Hs.238936	ESTs	3.1
	409026	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	3.1
	432055	AW972359	Hs.293334	ESTs	3.1
40	432441	AW292425	Hs.163484	ESTs	3.1
	408045	AW138959	Hs.245123	ESTs	3.1
	427191	BE221825	Hs.97691	ESTs	3.1
	416965	N26223	Hs.160436	ESTs	3.1
	441594	ALD41080	Hs.208765	ESTs	3.1
45	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	3.0
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.0
	438323	AI985394	Hs.123369	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	424296	AI631874	Hs.169391	ESTs	3.0
50	450522	AI696839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.0
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.0
	417991	AA731452	Hs.190008	ESTs	3.0
	422589	AA312735	Hs.179725	ESTs	3.0
	437583	AA761190	Hs.244627	ESTs	3.0
55	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.0
	449494	AW237014	Hs.288650	aquaporin 4	3.0
	444188	AI393165	Hs.19175	ESTs	3.0
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.0
	410811	AW805687	Hs.300648	ESTs	3.0
	450584	AA040403	Hs.60371	ESTs	3.0
60	428043	T92248	Hs.2240	uteroglobin	3.0
	436120	AI248193	Hs.119860	ESTs	3.0
	442324	R63578	Hs.28426	ESTs	2.9
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	2.9
65	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.9
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	2.9
	408427	AW194270	Hs.177236	ESTs	2.9
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to U4/U6 small nucl	2.9
	408938	AA059013	Hs.22607	ESTs	2.9
70	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	2.9
	422022	AA302420	Hs.200442	ESTs	2.9
	426890	AA393167	Hs.41294	ESTs	2.9
	427374	AI150033	Hs.143686	ESTs	2.9
75	434208	T92641	Hs.127648	hypothetical protein PRO2176	2.9
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	2.9
	451229	AW967707	Hs.48473	ESTs	2.9
	415511	AI732617	Hs.182362	ESTs	2.9
	408776	AA057365	Hs.63356	ESTs	2.9
	421110	AJ250717	Hs.1355	calthepsin E	2.9
80	453636	R67837	Hs.169872	ESTs	2.9
	436578	AI091435	Hs.134859	ESTs	2.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 EZIG5	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to dJ202121.4 [H.sa	2.8

5	408171	AA301228	Hs.43299	Homo sapiens cDNA FLJ12690 fis, clone NT	2.8
	445189	AJ936450	Hs.147482	ESTs	2.8
	419150	T29618	Hs.89540	TEK tyrosine kinase, endothelial (venous	2.8
	427457	AW779105	Hs.164682	ESTs, Weakly similar to ORF2 consensus s	2.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	2.8
10	446932	AA961459	Hs.125644	ESTs	2.8
	439140	W85737	Hs.290830	ESTs	2.8
	405041				2.8
	421306	AA806207	Hs.125889	ESTs	2.8
	427514	AA640773	Hs.209224	ESTs	2.8
15	427939	T92459	Hs.16886	ESTs	2.8
	429127	AA749382	Hs.107233	ESTs	2.8
	429590	AJ219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	2.8
	433163	R40468	Hs.163582	ESTs	2.8
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone H	2.8
20	448015	AJ458065	Hs.23196	ESTs	2.8
	456761	D59899	Hs.127842	CGI-142	2.8
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	2.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	2.8
25	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.8
	433515	AA595800	Hs.190246	ESTs	2.8
	424450	AL137526	Hs.147472	dynein Intermediate chain 2	2.8
	438122	AJ620270	Hs.129837	ESTs	2.8
	424086	AJ351010	Hs.102267	lysyl oxidase	2.8
30	438885	AJ886558	Hs.184987	ESTs	2.8
	412903	BE007967	Hs.155795	ESTs	2.8
	454111	AW081681	Hs.269064	ESTs	2.8
	439398	AA284267	Hs.221504	ESTs	2.8
	445802	AW901804	Hs.23984	hypothetical protein FLJ20147	2.8
35	434812	AA649860	Hs.189496	ESTs	2.8
	432583	AW023624	Hs.162282	ESTs	2.8
	428104	AA421350	Hs.191604	ESTs	2.8
	408217	AJ433201	Hs.279860	hypothetical protein FLJ20030	2.8
	438016	AJ949638	Hs.109150	SH3-domain binding protein 5 (BTK-associ	2.8
40	436396	AJ683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.7
	430887	N66801	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	416185	AW975881	Hs.291995	ESTs	2.7
	408613	AW242086	Hs.253967	ESTs	2.7
45	442510	AF150179	Hs.249890	ESTs	2.7
	433293	AF007835	Hs.32417	ESTs	2.7
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.7
	404488				2.7
	408936	AL138043	Hs.293549	ESTs	2.7
50	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, clone C	2.7
	436738	AW102613	Hs.152913	ESTs	2.7
	451797	AW663858	Hs.56120	ESTs	2.7
	452163	AJ863140		gb:tz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.7
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.7
55	459366	AA129703		gb:zn92b05.r1 Stratagene lung carcinoma	2.7
	431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	2.7
	430733	AW975920	Hs.283361	ESTs	2.7
	453652	AW009540	Hs.28369	ESTs	2.7
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	2.7
60	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.7
	408729	AA195764	Hs.72639	ESTs	2.7
	450726	AW204600	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.7
	447720	AL038765	Hs.161304	ESTs	2.7
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	2.7
65	442074	C17511	Hs.128430	ESTs	2.7
	424115	AA335497	Hs.293965	ESTs	2.7
	417728	AW138437	Hs.24790	KIAA1573 protein	2.7
	433803	AJ823593	Hs.27688	ESTs	2.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	2.7
70	424310	AA338648	Hs.50334	ESTs	2.6
	438504	AW665281	Hs.224625	ESTs	2.6
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (I	2.6
	430417	AA461045	Hs.50701	ESTs	2.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	2.6
75	422505	AL120862	Hs.124165	ESTs	2.6
	457285	AJ038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-tyr	2.6
	428667	AJ375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.6
80	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.6
	403903				2.6
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.6
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	2.6
	435043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.6
	436645	AW023424	Hs.156520	ESTs	2.6
	408380	AF123050	Hs.44532	diubiquitin	2.6
	402629				2.6

	406594			2.6	
	415122	D60708	Hs.22245	ESTs	2.6
	416747	AW876523	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT	2.6
	420159	A1572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
5	444361	W76027	Hs.23920	Homo sapiens cDNA FLJ13124 fis, clone NT	2.6
	446609	BE395090	Hs.15535	Human gene from PAC 886K2, chromosome 1	2.6
	449260	AA741180	Hs.29879	ESTs	2.6
	452311	AW304029	Hs.252744	ESTs	2.6
	413802	AW964490	Hs.32241	ESTs	2.6
10	417318	AW953937	Hs.12891	ESTs	2.6
	440028	AW473675	Hs.125843	ESTs	2.6
	437960	A1669586	Hs.222194	ESTs	2.6
	433687	AA743991		gb:ny57g01.s1 NCL_CGAP_Pr18 Homo sapiens	2.6
	430573	AA744550	Hs.136345	ESTs	2.6
15	439737	A1751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.6
	453204	R10799	Hs.191990	ESTs	2.6
	436751	AA732217	Hs.294054	ESTs	2.6
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	2.6
20	431120	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens	2.5
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	2.5
	438458	AW975186	Hs.162875	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	446063	A1720140	Hs.151079	ESTs	2.5
	430499	AW969408	Hs.231991	ESTs	2.5
	450496	AW449251	Hs.257131	ESTs	2.5
25	441330	A1692984	Hs.129354	ESTs	2.5
	424433	H04607	Hs.9218	ESTs	2.5
	434677	AW444575	Hs.130834	ESTs	2.5
	445779	A1253104	Hs.189267	ESTs	2.5
	444649	AW207523	Hs.197628	ESTs	2.5
30	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	2.5
	432222	A1204995		gb:an03c03.x1 Stratagene schizo brain S1	2.5
	404288				2.5
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	2.5
35	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	2.5
	410095	AW589638	Hs.258947	ESTs	2.5
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298	2.5
	418343	AA216372	Hs.159501	ESTs	2.5
40	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.5
	428637	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	2.5
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	2.5
	432507	BE391093		gb:60128604ZF1 NIH_MGC_44 Homo sapiens c	2.5
	433858	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT	2.5
45	438651	H64500	Hs.123646	ESTs	2.5
	443830	A1142095	Hs.143273	ESTs	2.5
	446800	A1341635	Hs.156486	ESTs	2.5
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN A	2.5
	451343	AW975057	Hs.293353	ESTs	2.5
50	451539	AA059467	Hs.218933	ESTs	2.5
	452412	AA029608	Hs.61373	ESTs	2.5
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	2.5
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.5
	424943	AU077260	Hs.153924	death-associated protein kinase 1	2.5
55	440106	AA854968	Hs.127699	KIAA1603 protein	2.5
	458429	AV648559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	2.5
	415261	T40928	Hs.8346	ESTs	2.5
	420026	A1831190	Hs.166676	ESTs	2.5
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	2.5
60	458722	AA741545	Hs.282832	ESTs	2.5
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	2.5
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.5
	433644	AW342028	Hs.256112	ESTs	2.5
	419172	AW338625	Hs.22120	ESTs	2.5
65	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular testi	2.5
	443348	AW873696	Hs.57572	ESTs	2.5
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.5
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.5
	448030	N30714	Hs.20161	HDCME31P protein	2.5
70	417203	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE	2.5
	449275	AW450848	Hs.205457	KIAA1620 protein	2.4
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.4
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	2.4
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.4
75	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
	453142	AA033648	Hs.7473	ESTs	2.4
	425657	T89839	Hs.119471	ESTs	2.4
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone H	2.4
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	2.4
80	458332	A1000341	Hs.220491	ESTs	2.4
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	2.4
	459644				2.4
	429125	AA446854	Hs.271004	ESTs	2.4
	448337	AW206453	Hs.3782	ESTs	2.4

	427778	AA412323	Hs.105323	ESTs	2.4
	425371	D49441	Hs.155981	mesothelin	2.4
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.4
5	447610	AW296286	Hs.255534	ESTs	2.4
	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.4
	440817	AI341423	Hs.270165	ESTs	2.4
	420020	BE295866	Hs.94382	adenosine kinase	2.4
10	435395	AA729235	Hs.117907	ESTs	2.4
	424144	AA454033	Hs.41644	Homo sapiens cDNA: FLJ23003 fis, clone L	2.4
	405494				2.4
	458145	AI239457	Hs.130794	ESTs	2.4
	408547	AA574291	Hs.57837	ESTs	2.4
15	408941	AI452459	Hs.165221	ESTs	2.4
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276 Homo	2.4
	417137	U46265	Hs.81281	hypothetical protein	2.4
	418950	T78517	Hs.13941	ESTs	2.4
	420756	AA411800	Hs.189900	ESTs	2.4
20	428316	AI860775	Hs.98508	ESTs	2.4
	432896	NM_014097	Hs.279778	PRO1693 protein	2.4
	436148	BE005252		gb:CM1-BN0116-030400-171-g02 BN0116 Homo	2.4
	436284	AA708016	Hs.190389	ESTs	2.4
	437327	AL353942		gb:Homo sapiens mRNA; cDNA DKFZp761L2312	2.4
25	442611	BE077155	Hs.177537	ESTs	2.4
	456062	AI866286	Hs.71962	ESTs	2.4
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.4
	401335				2.4
30	428771	AB028992	Hs.193143	KIAA1069 protein	2.4
	419140	AI982647	Hs.215725	ESTs	2.4
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.4
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.4
	407339	AA777542	Hs.132670	ESTs	2.4
35	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	2.4
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	2.4
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.4
	452561	AI692181	Hs.49169	KIAA1634 protein	2.4
	427878	C05766	Hs.181022	CGI-07 protein	2.4
	419752	AA249573	Hs.152618	ESTs	2.4
40	430073	U86136	Hs.232070	telomerase-associated protein 1	2.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	2.4
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.3
	407905	AW103655	Hs.252905	ESTs	2.3
45	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.3
	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	2.3
	453049	BE537217	Hs.30343	ESTs	2.3
	438568	R98865	Hs.11135	major histocompatibility complex, class	2.3
	453445	AL036532	Hs.91453	ESTs	2.3
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.3
50	446346	AI290205		gb:q179g06.x1 Soares_NhHMPu_S1 Homo sapi	2.3
	441974	AI583782	Hs.128245	ESTs	2.3
	444805	AB007899	Hs.12017	KIAA0439 protein; homolog of yeast ubiq	2.3
	424027	AW337575	Hs.201591	ESTs	2.3
	419606	AW294795	Hs.198529	ESTs, Weakly similar to similar to acyl-	2.3
55	428613	AB037749	Hs.186928	KIAA1328 protein	2.3
	434340	AI193043	Hs.128585	ESTs	2.3
	450297	AW901347	Hs.38592	Homo sapiens cDNA: FLJ23342 fis, clone H	2.3
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.3
	433650	AA603472	Hs.28456	ESTs	2.3
60	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	2.3
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PL	2.3
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo	2.3
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.3
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	2.3
65	400610				2.3
	402222				2.3
	407162	N63855	Hs.142834	zinc finger protein	2.3
	415250	F02614	Hs.27319	ESTs	2.3
70	421751	AW813731	Hs.159153	ESTs	2.3
	428552	AW274560	Hs.129520	ESTs	2.3
	432658	AW973769	Hs.162319	ESTs	2.3
	434742	AA648302	Hs.291695	ESTs	2.3
	436586	AI308862	Hs.167028	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
75	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [R.norvegicu	2.3
	443160	AI467915	Hs.36053	ESTs	2.3
	448764	AI568607	Hs.182112	ESTs	2.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	2.3
	439810	AL109710	Hs.85568	EST	2.3
80	413714	AI560944	Hs.71428	ESTs	2.3
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	2.3
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	2.3
	438670	AI275803	Hs.123428	ESTs	2.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.3

	459702			2.3	
	414888	AL039185	Hs.77558	thyroid hormone receptor Interactor 7	2.3
	438474	AW865818	Hs.6232	KIAA0764 gene product	2.3
5	453037	AA045175	Hs.177552	ESTs	2.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	2.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	2.3
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	2.3
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	2.3
10	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.3
	406506				2.3
	448330	AL036449	Hs.207163	ESTs	2.3
	409719	AI769160	Hs.108681	ESTs	2.3
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.3
15	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.3
	427961	AW293165	Hs.143134	ESTs	2.3
	447357	AI375922	Hs.159367	ESTs	2.3
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	2.3
	453716	AA037675	Hs.152675	ESTs	2.3
20	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	407949	W21874	Hs.247057	ESTs	2.2
	427972	AA854870	Hs.181304	putative gene product	2.2
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, clone H	2.2
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	2.2
25	424238	AA337401	Hs.137635	ESTs	2.2
	452930	AW195285	Hs.194097	ESTs	2.2
	424527	AW138558	Hs.267158	ESTs	2.2
	453095	AW295660	Hs.252756	ESTs	2.2
	449161	N53431	Hs.47647	ESTs, Weakly similar to KIAA0423 [H.sapi	2.2
30	429586	T73510	Hs.209153	angiotensin-like 3	2.2
	423782	AI472209	Hs.288369	ESTs	2.2
	458124	AW005548	Hs.124590	ESTs	2.2
	450109	AI539295	Hs.17967	ESTs	2.2
	421461	AW291023	Hs.97255	ESTs	2.2
35	412222	AA528283	Hs.292737	ESTs	2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	441736	AW292779	Hs.169799	ESTs	2.2
	401049				2.2
	440727	AI073991	Hs.134268	ESTs	2.2
40	419751	AW195581	Hs.93121	KIAA0761 protein	2.2
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.2
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.2
	410292	AA843087	Hs.124194	ESTs	2.2
45	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	2.2
	449695	AA164569	Hs.34550	ESTs	2.2
	429399	AA452244	Hs.16727	ESTs	2.2
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.2
50	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	2.2
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.2
	445268	AI218358	Hs.175048	ESTs	2.2
	402481				2.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.2
55	416521	H60929	Hs.44197	hypothetical protein DKFZp564D0462	2.2
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
	421211	AA284966	Hs.266308	ESTs, Weakly similar to AF216312 1 type	2.2
	427541	AI798983	Hs.97961	ESTs	2.2
60	432013	AI796879	Hs.162102	ESTs	2.2
	436461	AW511956	Hs.293261	ESTs	2.2
	438002	AI560246	Hs.201648	ESTs, Weakly similar to ZN42_HUMAN ZINC	2.2
	440312	AW814597	Hs.72475	ESTs	2.2
	440479	AA886461	Hs.208161	ESTs	2.2
65	441178	W90789	Hs.153976	ESTs	2.2
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.2
	443314	AW771701	Hs.54646	ESTs	2.2
	422165	AL041199	Hs.1481	histidine decarboxylase	2.2
	450696	AI654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	2.2
70	432974	BE348793		gb:ht70g02.x1 NCL_CGAP_Lu24 Homo sapiens	2.2
	404200				2.2
	435990	AI015862	Hs.131793	ESTs	2.2
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	451558	NM_001089	Hs.26530	ATP-binding cassette, sub-family A (ABC1	2.2
75	416642	T96118	Hs.226313	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	406672	M26041	Hs.198253	major histocompatibility complex, class	2.2
	417819	AI253112	Hs.133540	ESTs	2.2
	417355	D13168	Hs.82002	endothelin receptor type B	2.2
	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.2
80	404274				2.2
	415086	AI597963	Hs.118726	ESTs	2.2
	418210	R54575	Hs.13337	ESTs, Weakly similar to unnamed protein	2.2
	419220	AA811938	Hs.291759	ESTs	2.2
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.2

	451050	AW937420	Hs.69662	ESTs	2.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	2.2
	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.2
5	412925	AI089319	Hs.179243	ESTs	2.2
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.2
	410976	R36207	Hs.25092	ESTs	2.2
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.2
	449677	AA002071		gb:zh85d01.s1 Soares fetal liver spleen	2.2
10	449321	AA001150	Hs.132937	ESTs	2.2
	418557	BE140602	Hs.246645	ESTs	2.2
	416320	H47887	Hs.34024	ESTs	2.2
	426384	AI472078		gb:ij85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.2
	414140	AA281279	Hs.23317	ESTs	2.2
15	419520	AB009303	Hs.297790	Human clone 23734 mRNA sequence	2.2
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	2.2
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	2.2
	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	2.1
	407366	AF026942		gb:Homo sapiens clg33 mRNA, partial sequ	2.1
20	410048	W76467	Hs.274550	proline oxidase homolog	2.1
	400880				2.1
	418092	R45154	Hs.106604	ESTs	2.1
	428780	AI478578	Hs.50636	ESTs	2.1
	431067	AW574823	Hs.200413	ESTs	2.1
25	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	2.1
	412104	AW205197	Hs.240951	ESTs	2.1
	422819	AL122084	Hs.121073	hypothetical protein FLJ10466	2.1
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	2.1
	424806	AA382523	Hs.105689	ESTs	2.1
30	434445	AI349306	Hs.11782	ESTs	2.1
	442994	AI026718	Hs.16954	ESTs	2.1
	410371	AA084482	Hs.115850	ESTs	2.1
	450232	BE300815	Hs.201326	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1
35	430899	BE018217	Hs.183528	ESTs, Weakly similar to Bem46-like prote	2.1
	431814	BE256242	Hs.270847	delta-tubulin	2.1
	417543	AA203620	Hs.110153	ESTs, Weakly similar to BCGF_HUMAN B-CEL	2.1
	444542	AI161293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.1
	404593				2.1
40	434803	AW974640		gb:EST386744 MAGE resequences, MAGM Homo	2.1
	451623	H77818	Hs.268991	ESTs	2.1
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	2.1
	402046				2.1
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.1
45	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	2.1
	401987				2.1
	423119	AA322201	Hs.131976	EST	2.1
	427112	Z32887	Hs.290951	ESTs	2.1
	414464	AI870175	Hs.13957	ESTs	2.1
50	447829	AI433029	Hs.164104	ESTs	2.1
	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 fis, clone HE	2.1
	405472				2.1
	413621	AI808648	Hs.184156	ESTs	2.1
	432212	AW137742	Hs.293451	ESTs	2.1
55	404289				2.1
	415362	F06735		gb:HSC1JB091 normalized Infant brain cDN	2.1
	427739	AW196755	Hs.98105	ESTs	2.1
	427772	AA412289	Hs.98123	ESTs	2.1
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.1
60	434335	AA630107	Hs.213220	ESTs	2.1
	436052	AI021983	Hs.271432	ESTs	2.1
	442773	AB037722	Hs.8707	Homo sapiens mRNA; cDNA DKFZp434N1131 (f	2.1
	446799	AW978373	Hs.49221	ESTs, Weakly similar to zinc finger prot	2.1
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.1
65	455673	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	2.1
	458624	AI362790	Hs.181801	ESTs	2.1
	405095				2.1
	447207	AA442233	Hs.17731	hypothetical protein FLJ12692	2.1
	433589	AA886530	Hs.186912	ESTs	2.1
70	438398	AA806526	Hs.130277	ESTs	2.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 fis, clone H	2.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.1
	431087	H12723	Hs.290791	ESTs	2.1
	409064	AA062954	Hs.141883	ESTs	2.1
75	427558	D49493	Hs.2171	growth differentiation factor 10	2.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	2.1
	438118	AW753311	Hs.259415	ESTs	2.1
	427621	BE621182	Hs.179882	Homo sapiens cDNA FLJ12437 fis, clone NT	2.1
	452114	N22687	Hs.8236	ESTs	2.1
80	448782	AL060295	Hs.301550	KIAA0758 protein	2.1
	403937				2.1
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	2.1
	452416	AA026115	Hs.114777	ESTs	2.1
	451609	AL046019	Hs.209276	ESTs	2.1

5	435934	R19382	Hs.117869	ESTs	2.1
	445158	AJ92108	Hs.127206	ESTs	2.1
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.1
	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen	2.1
	443949	AW827419	Hs.235070	ESTs	2.1
10	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.1
	438676	AA813745	Hs.123446	ESTs	2.1
	405848				2.1
	416940	N75620	Hs.43157	ESTs	2.1
15	442381	AJ185136	Hs.48650	ESTs	2.1
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586f1823 (f	2.1
	435252	AJ539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	2.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.1
20	439425	AF086244	Hs.114659	ESTs	2.1
	421168	AF182277	Hs.1360	cytochrome P450, subfamily IIB (phenobar	2.1
	449611	AJ970394	Hs.197075	ESTs	2.1
	404548				2.1
	416734	H81213	Hs.14825	ESTs	2.1
25	435865	AA883552	Hs.16810	ESTs	2.1
	439072	AF085930	Hs.269123	ESTs	2.1
	447482	AB033059	Hs.18705	KIAA1233 protein	2.1
	457292	AJ921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	2.1
	444974	AJ203500	Hs.151612	ESTs	2.1
30	456034	AW450979		gb:U1-H-B13-ata-a-12-0-U1.s1 NCL_CGAP_Su	2.1
	430634	AJ860651	Hs.26685	ESTs	2.1
	426782	R14614	Hs.191254	ESTs	2.0
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.0
	445326	AJ220072	Hs.165893	ESTs	2.0
35	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.0
	409994	D68864	Hs.57735	acetyl LDL receptor, SREC	2.0
	443268	AJ800271	Hs.129445	hypothetical protein FLJ12496	2.0
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.0
	417321	N68722	Hs.191368	ESTs	2.0
40	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.0
	404323				2.0
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	421047	AW514772	Hs.104473	ESTs	2.0
	425497	AA524596	Hs.188844	ESTs	2.0
45	444623	AJ183829	Hs.202111	ESTs	2.0
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.0
	433563	AJ732637	Hs.277901	ESTs	2.0
	406485				2.0
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.0
50	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.0
	425465	L18964	Hs.1904	protein kinase C, iota	2.0
	449424	AW448937	Hs.197030	ESTs	2.0
	427940	AA417812	Hs.38775	ESTs	2.0
	411502	AW946605	Hs.250154	Homo sapiens cDNA FLJ12973 fis, clone NT	2.0
55	411365	M76477	Hs.278242	tubulin, alpha, ubiquitous	2.0
	412369	H80456	Hs.285243	Homo sapiens cDNA: FLJ22029 fis, clone H	2.0
	452959	AJ933416	Hs.188674	ESTs	2.0
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.0
	428775	AA434579	Hs.143691	ESTs	2.0
60	420000	AB036063	Hs.180726	Homo sapiens cDNA FLJ13543 fis, clone PL	2.0
	408321	AW405882	Hs.44205	cortistatin	2.0
	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	2.0
	411050	AW814902		gb:MR1-ST0205-120400-022-f08 ST0205 Homo	2.0
	452453	AJ902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.0
65	428978	AA442784	Hs.125445	ESTs	2.0
	458562	N34128	Hs.145268	ESTs	2.0
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.0
	403760				2.0
	424368	AB037766	Hs.146085	KIAA1345 protein	2.0
70	421229	AJ056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	2.0
	436304	AA339622	Hs.108887	ESTs	2.0
	453498	BE181412	Hs.23245	Homo sapiens cDNA FLJ11767 fis, clone HE	2.0
	439018	AW300887	Hs.26638	ESTs, Weakly similar to unnamed protein	2.0
	453280	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (fr	2.0
75	420193	AJ460080	Hs.202869	ESTs	2.0
	444610	AJ174783		gb:HA2501 Human fetal liver cDNA library	2.0
	401575				2.0
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.0
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.0
80	410763	AF279145	Hs.8966	tumor endothelial marker 8	2.0
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	2.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.0
	405963				2.0
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.0
	420831	AA280824	Hs.190035	ESTs	2.0
	424152	AL133591	Hs.301405	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.0
	424641	AB001106	Hs.151413	glla maturation factor, beta	2.0

5	427616	AI698684	Hs.98028	ESTs	2.0
	435115	AI821726	Hs.116603	ESTs	2.0
	437636	AA764781	Hs.291844	ESTs	2.0
	438295	AI394151	Hs.37932	ESTs	2.0
	439430	AF124250	Hs.5554	breast cancer anti-estrogen resistance 3	2.0
	445388	AI925280	Hs.236842	EST	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.0
10	449623	C00719	Hs.120440	ESTs	2.0
	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	2.0
	456613	R19992	Hs.106620	Homo sapiens clone 23950 mRNA sequence	2.0
	457233	AI355009	Hs.221698	ESTs	2.0
	457384	AA501760	Hs.18075	chromosome 9 open reading frame 3	2.0
15	457471	AW971364		gb:EST383453 MAGE resequences, MAGL Homo	2.0

TABLE 27B

20	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
25	409457	1132521_1	AW818081 AW392887 AW514700 AW392881
	409519	113722_1	AA075368 AA075369
	410008	116812_1	AA079552 BE142525 BE142527
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
	411050	1230330_1	AW814902 BE156656 BE156667 BE156590 BE156441 BE156447
30	411880	1263110_1	AW872477 BE088101 T05990
	411905	1265181_1	BE265067 BE264978 AW875420
	412303	1288130_1	AW936336 AW936339
	413136	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925
	413499	1373910_1	BE144884 H97942
35	413875	1396766_1	BE176776 H85072
	415094	1522103_1	D59513 D59515 D80174 D59514
	415362	1534980_1	F06735 R55896 R12110 H08697
	416624	1604694_1	H69044 T47567 H75691 T50292
	418378	174656_1	AW962081 AA218925 AA354237
40	419546	185766_1	AA244199 AA244272 H57440
	419807	188252_1	R77402 AA262462 AA250988 R06794
	420637	195241_1	AW976153 AA278945 AA747691
	422429	216469_1	AA310527 AW962295 Z4865 H06641
	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
45	426384	266211_1	AI472078 AA377209 AA865807
	428637	293660_1	AW979268 AA878419 AA431342 AA431628
	430153	313709_1	AW968128 AA468102 AA468165
	430844	324570_1	T94960 AA487679 T95013
	431120	328264_1	AA492588 AA492498 AA492571
50	431169	328799_1	AW971240 AA493843 AA493723
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	432009	34025_1	AL137424 BE007148 T52277
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
	432507	348711_1	BE391093 AA551334 BE389643
55	432779	354024_1	AW979241 AA565006 AA847102
	432803	354267_1	AA565398 AW894072 H97930
	432869	355475_1	AW974094 AA569074 AA602574
	432974	356950_1	BE348793 AA573118 N79366
	433492	367934_1	AW605849 AW262898 N41060 AA594852
60	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
	433687	373061_1	AA743991 AA604852 AW272737
	434803	393471_1	AW974640 AA649516 N76626
	436148	41500_1	BE005252 AK000786
	437327	43610_1	AL353942 AW994305
65	438909	45684_1	AF085839 R69137 AW188788 R69254
	440320	491930_1	AA879294 N67538 AA74541
	444314	600667_1	AI140497 AW749625 AW749626 AW749844
	444610	612257_1	AI174783 R83569 R12271
	446346	673545_1	AI290205 AW235762 AI651268
70	447197	711623_1	R36075 AI366546 R36167
	448404	761515_1	BE089973 AI498612 AW805032
	449299	80436_1	AA299919 AW957012 AA001107 T83831 BE156389
	449540	80945_2	AA001713 H63836
75	449677	81270_1	AA002071 AA002232 T99209
	450522	837264_1	AI698839 AI909260 AI909259
	451024	85565_1	AA442176 AA259181
	451381	867770_1	BE241831 AW249135 BE548847 AW250245
	452163	902067_1	AI863140 W80703 R43474
	452293	909195_1	AI871833
80	452453	918300_1	AI902519 AI902518 AI902516
	452542	921410_1	AW812258 AW812257 AI906423 AI906422
	452771	930983_1	T05477 T07655 AI917711
	454359	1130674_1	N71277 AW390764

5	454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	455024	1249196_1	AW851309 AW850888 AW851419 AW851412 AW851299
	455226	1262534_1	AW902103 AW869012 AW869139
	455235	1265634_1	AW875951 AW875950 AW875936 AW875948 AW875939 AW875957
	455673	1349656_1	BE065939 BE066079 BE065956
10	455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	457471	340916_1	BE011368 BE011362 BE011215 BE011365 BE011363
	457620	371514_1	AW971364 AA525021 AA570759
	458154	491768_1	AA502711 BE078290
15	459267	966605_1	AW818379 AA888282 AA879046 AA879195
			AJ003631 AJ003650 AJ003651

TABLE 27C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source: 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400610	9887671	Minus	117606-117928,124040-124147
400880	9931121	Plus	29235-29336,36363-36580
401049	7232177	Plus	149157-150692
401335	9884881	Plus	15736-16352
401575	7229804	Minus	76253-76364
401793	7263888	Minus	102945-103083
401987	4406829	Minus	72893-73021,76938-77049
402046	8072415	Plus	166394-166556,168167-168395
402222	9958106	Plus	3261-3834,3939-4269
402481	9797406	Plus	87891-88991
402629	9931216	Plus	33641-33775,34182-34372,36003-36084,40343-40612
403760	7712202	Minus	45910-46260,47563-47824
403903	7710671	Minus	101165-102597
403937	7711761	Minus	12609-12773
404043	9558573	Plus	29042-29135,46597-46699
404200	6010176	Minus	7066-7210
404274	9885189	Plus	104127-104318
404288	2769644	Plus	3512-3691
404289	2769644	Plus	15049-15286,30267-30457
404323	9719753	Minus	31913-32219
404488	8113286	Minus	64835-64994
404548	8570305	Minus	83896-84162
404593	9944086	Minus	74922-75788
404599	8705107	Plus	110443-110733
404916	7341826	Plus	91057-91188
405041	7547195	Plus	121230-121714
405095	8072599	Plus	138877-139066
405472	8439781	Plus	106297-106447,108462-108596
405494	8050952	Minus	70284-70518
405848	7651809	Minus	28135-28244
405963	8247788	Plus	4056-4699
406182	5923650	Minus	28256-28935
406485	7711305	Plus	125036-125422
406506	7711374	Minus	6843-8077
406554	7711566	Plus	106956-107121
406594	8248611	Minus	35543-35845

TABLE 28A: ABOUT 796 GENES DOWN-REGULATED IN LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 28A lists of about 796 genes that are downregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with normal "body map" samples. These were selected from about 69680 probesets on an Affymatrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues sample expression was less than or equal to 0.1. The "average" normal lung tissue level was set to the 75th percentile amongst normal lung tissues. The "average" fibrosis expression level was set to the 95th percentile amongst fibrosis samples. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal lung to fibrosis

Pkey	ExAccn	Unigene ID	Unigene Title	R1
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	18.18
421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	9.39
404518	A1815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	8.30
404795				5.56

	403211				5.46
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	5.43
	400489				5.19
5	425571	AJ007292	Hs.158306	ephrin-A2	5.19
	406357				5.08
	407979	AA046306	Hs.62927	ESTs	5.08
	452378	AA025855	Hs.19597	ESTs	4.78
	408053	AW139474	Hs.246862	ESTs	4.62
10	421770	AA374192	Hs.108124	ribosomal protein L41	4.52
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	4.49
	402386				4.39
	402448				4.37
	448245	AI923551	Hs.170843	ESTs	4.31
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	4.29
	419958	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.24
	447768	X86400	Hs.19520	FXD domain-containing ion transport reg	4.21
	405163				4.19
	437120	AI356125	Hs.157767	ESTs, Weakly similar to human HOXA2 [Hs	4.19
20	409020	AA062549	Hs.21162	ESTs	4.09
	431073	BE254470	Hs.249186	cone-rod homeobox	4.07
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	4.05
	403716				3.99
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.94
25	404348				3.90
	407070	Y10209		gb:H.sapiens mRNA for CD30L protein	3.82
	412919	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.81
	402409				3.80
	456150	Z42308		gb:HSC0FB121 normalized infant brain cDN	3.79
30	427030	AA397600	Hs.97531	ESTs	3.76
	426328	AW631296		gb:hh83c09.y1 NCI_CGAP_GU1 Homo sapiens	3.74
	429307	AU076592	Hs.198951	jun B proto-oncogene	3.71
	400172				3.70
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	3.68
35	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-r	3.68
	446850	R71245	Hs.174303	ESTs	3.67
	405147				3.64
	406821	AA977896	Hs.128873	ESTs, Highly similar to ALFA_HUMAN FRUCT	3.57
	402762				3.55
40	401496				3.50
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	3.50
	402911				3.49
	425330	D25216	Hs.155650	KIAA0014 gene product	3.49
	438004	AA774984	Hs.220649	ESTs, Weakly similar to FCE2 MOUSE LOW A	3.46
45	448185	AI633040	Hs.172730	ESTs	3.46
	433367	AA584930	Hs.269451	ESTs, Weakly similar to XAP-5-like prote	3.43
	416596	H67669	Hs.38564	ESTs	3.41
	400545				3.39
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB5	3.37
50	426507	AA380285		gb:EST93491 Supt cells Homo sapiens cDNA	3.35
	403479				3.34
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	3.34
	401919				3.33
	449031	AI867502	Hs.271462	ESTs	3.33
55	400116				3.31
	401590				3.29
	401007				3.28
	404610	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.25
	408641	AW245207	Hs.5555	Homo sapiens cDNA FLJ13170 fis, clone NT	3.25
60	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma vtru	3.23
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	3.23
	433232	AI658621	Hs.127769	ESTs	3.23
	457937	AW976930	Hs.128760	ESTs	3.23
	406101				3.18
65	407080	Z38133	Hs.113973	myosin, heavy polypeptide 8, skeletal mu	3.18
	419947	AW298744	Hs.118894	ESTs	3.16
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	3.16
	454019	D31846	Hs.37025	aquaporin 2 (collecting duct)	3.16
	428674	AA431734	Hs.104915	ESTs	3.14
70	402056				3.06
	425182	AF041259	Hs.155040	zinc finger protein 217	3.06
	425393	NM_000218	Hs.156115	potassium voltage-gated channel, KQT-lik	3.06
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.05
	402158				3.03
	404938				3.02
75	403376				3.01
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-ty	3.00
	402423				2.99
	416253	BE250659	Hs.15463	ESTs	2.99
	435265	AA779958	Hs.185932	ESTs	2.99
80	425655	BE614551	Hs.158675	ribosomal protein L14	2.98
	428704	AA432007	Hs.249484	ESTs	2.98
	425439	D38024	Hs.157425	double homeobox, 2	2.97
	445613	BE550889	Hs.158491	ESTs	2.97

	402714			2.96	
	403526			2.96	
	403605			2.95	
5	441852	AB028968	Hs.7989	KIAA1045 protein	2.95
	417629	T76945	Hs.64211	ESTs, Weakly similar to similar to acyl-	2.94
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgr	2.91
	419821	AW587486	Hs.189119	ESTs	2.90
	446993	AI570964	Hs.164257	ESTs	2.89
10	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	2.88
	423379	AI985349	Hs.157492	Homo sapiens cDNA FLJ14079 fis, clone HE	2.88
	440206	AI762232	Hs.46794	ESTs	2.88
	402212	AW502761	Hs.30909	KIAA0430 gene product	2.87
	406059				2.86
15	423548	AF007194	Hs.129782	mucln 3A, intestinal	2.86
	402051				2.85
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	2.85
	455446	AW947749		gb:RC0-MT0005-130300-031-b01 MT0005 Homo	2.85
	442428	BE464988	Hs.298302	ESTs	2.84
20	403247				2.83
	404825				2.83
	459184	L35001	Hs.95669	ESTs	2.83
	402968				2.82
	417575	R00382	Hs.191199	ESTs	2.82
25	404668				2.81
	420619	AF130255	Hs.99430	testis zinc finger protein	2.81
	447241	BE382838	Hs.19322	ESTs	2.80
	448793	AI864581	Hs.215477	ESTs	2.79
	453014	AI937242	Hs.176590	ESTs	2.79
30	446775	AI792836	Hs.232273	ESTs	2.78
	455075	AW854850		gb:QV2-CT0261-201099-011-h03 CT0261 Homo	2.78
	408704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	2.75
	457546	AA568484	Hs.153632	ESTs	2.75
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.74
35	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN A	2.74
	405703				2.73
	408840	AW277132	Hs.254880	ESTs	2.73
	413958	BE277913	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.73
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein,	2.73
40	408702	Z20656	Hs.278432	myosin, heavy polypeptide 6, cardiac mus	2.72
	408664	R56362		gb:yg93c07.r1 Soares infant brain 1N1B H	2.72
	402457				2.71
	403612				2.71
	407049	X72632		(NONE)	2.71
45	415423	AA164743	Hs.187617	Homo sapiens cDNA FLJ13941 fis, clone Y7	2.70
	402862				2.69
	403540				2.69
	431465	AW293178	Hs.180086	ESTs	2.69
50	406563				2.68
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.68
	426220	AI383475	Hs.171697	ESTs, Weakly similar to immunoglobulin s	2.68
	446707	AI591214	Hs.156336	ESTs	2.68
	447557	AW028809	Hs.229570	ESTs	2.68
	413529	U11874	Hs.846	interleukin 8 receptor, beta	2.67
55	403997				2.66
	408704	AA056635	Hs.5366	Homo sapiens cDNA: FLJ21522 fis, clone C	2.66
	407005	U20230		gb:Human guanylt cyclase C gene, partial	2.65
	405075				2.64
	430728	AW968522		gb:EST380598 MAGE resequences, MAGJ Homo	2.64
60	405327				2.63
	409419	BE207219	Hs.20474	ESTs, Highly similar to S17112 Interfero	2.63
	434300	AA740944	Hs.116295	ESTs	2.63
	405895				2.62
	431929	AW294163	Hs.146127	ESTs	2.61
65	405217				2.60
	437569	AA760849	Hs.294052	ESTs	2.60
	419822	AW966864	Hs.255780	ESTs	2.59
	445918	AW014139	Hs.145656	ESTs	2.59
	446149	BE242960	Hs.203181	ESTs	2.59
70	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [Hsa	2.58
	404282				2.53
	409778	AW499705		gb:UL-HF-BR0p-ajk-b-05-0-UL.r1 NIH_MGC_5	2.53
	445353	BE561465	Hs.175211	ESTs	2.53
	458764	BE619386		gb:601473204F1 NIH_MGC_68 Homo sapiens c	2.53
75	402195				2.52
	404247				2.52
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.52
	402588				2.50
	432301	U34249	Hs.167075	ring finger protein 9	2.50
80	424958	AA984420	Hs.283659	ESTs	2.49
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo	2.49
	415003	M11437	Hs.77741	kininogen	2.48
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	2.48
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	2.47

5	440424	AI991125	Hs.189109	Homo sapiens cDNA: FLJ21458 fis, clone C	2.47
	402153				2.46
	432152	AK000245	Hs.272790	Homo sapiens cDNA FLJ20238 fis, clone CO	2.46
	454414	R55574	Hs.164675	ESTs	2.45
	401603				2.44
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.44
	408513	AW206468	Hs.103118	ESTs	2.43
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	2.42
	400672				2.41
10	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	2.41
	449748	H23963	Hs.32043	ESTs	2.41
	453756	AW139415	Hs.61906	ESTs	2.41
	400624				2.40
	403125				2.40
15	406118				2.39
	402165				2.38
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.38
	425515	W26609		gb:35f12 Human retina cDNA randomly prim	2.38
	402951				2.37
20	427886	AA417083	Hs.104789	ESTs	2.37
	447173	AW449385	Hs.157294	ESTs	2.37
	448703	BE613942	Hs.170890	Homo sapiens cDNA: FLJ21129 fis, clone C	2.37
	426344	H41821	Hs.169393	transcriptional activator of the c-fos p	2.36
	401840				2.35
25	403731				2.34
	405378				2.34
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.34
	416559	AI039195	Hs.128060	ESTs, Weakly similar to cDNA EST yk481g5	2.34
	438216	Z83952	Hs.252815	ESTs	2.34
30	448427	BE395260		gb:601311130F1 NIH_MGC_44 Homo sapiens c	2.34
	451588	AW072057		gb:ws58g05.x1 NCI_CGAP_Bm25 Homo sapien	2.34
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA	2.33
	451172	AW206465	Hs.207423	ESTs	2.33
	401015				2.32
35	414705	BE464157	Hs.281455	ESTs	2.32
	439894	AA853077		gb:NHTBCae03a05f1 Normal Human Trabecula	2.31
	446305	AW270149	Hs.254515	ESTs, Moderately similar to AF248953 1 g	2.31
	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker pr	2.29
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo s	2.28
40	457197	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	2.28
	457275	AA463422	Hs.209431	ESTs	2.28
	458766	AW183618	Hs.188417	ESTs, Weakly similar to ZnT-3 [H.sapiens	2.28
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	2.27
45	430210	AL157426	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (fr	2.27
	442614	AI269030		gb:qj73c12.x1 NCI_CGAP_Kid3 Homo sapiens	2.27
	402538				2.26
	439891	AL389940	Hs.109968	ESTs	2.26
	440056	BE294828	Hs.13323	hypothetical protein FLJ22059	2.26
	406150				2.25
50	426880	AA453482		gb:zx47a11.r1 Soares_testis_NHT Homo sap	2.25
	447129	AW014123	Hs.161402	ESTs	2.25
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25
	456778	AI458309	Hs.117406	ESTs	2.24
	401728				2.23
55	404139				2.23
	414095	BE293546		gb:601186671F1 NIH_MGC_15 Homo sapiens c	2.23
	432037	AW450592	Hs.300459	ESTs	2.23
	451965	AA021163	Hs.22287	ESTs	2.23
60	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.22
	427586	AA609681	Hs.190592	ESTs	2.22
	454108	AA161071	Hs.71465	squalene epoxidase	2.22
	429749	AI885174	Hs.22293	ESTs	2.21
	434507	AW511138	Hs.256581	ESTs	2.21
	436652	AA724543	Hs.168824	ESTs	2.21
65	437433	R74016	Hs.121681	ESTs	2.21
	401688				2.20
	441748	R14439	Hs.209194	ESTs	2.19
	453072	BE251845	Hs.221516	ESTs, Weakly similar to tetraspan TM4SF	2.19
	400635				2.18
70	417176	AW974475	Hs.143467	ESTs	2.18
	427858	NM_001971	Hs.21	elastase 1, pancreatic	2.18
	454886	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	2.18
	458232	BE217872	Hs.279537	ESTs	2.18
	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB5	2.17
75	423668	Y10148	Hs.131138	neurotensin receptor 2	2.17
	440338	R62431	Hs.12758	ESTs	2.17
	403115				2.16
	409125	R17268	Hs.301560	ESTs	2.16
	426887	AI971975	Hs.212892	ESTs	2.16
80	413811	BE168828		gb:QV1-HT0517-020400-145-f04 HT0517 Homo	2.15
	442962	AI025315	Hs.131615	ESTs	2.15
	403921				2.14
	413140	T06607	Hs.6846	hypothetical protein FLJ13055	2.14

	421996	AW583807	Hs.1460	glucagon	2.14
	436130	AA341497	Hs.31408	ESTs	2.14
	407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	2.13
5	407708	AF019968	Hs.37336	suppressor of variegation 3-9 (Drosophila)	2.13
	442792	AI352340	Hs.131194	ESTs	2.12
	454406	AA213605	Hs.267861	ESTs	2.12
	424648	AA344576		gb:EST50478 Gall bladder 1 Homo sapiens	2.11
	433963	AI218808	Hs.187778	ESTs	2.11
10	400736				2.10
	406343				2.10
	409702	AI752244	Hs.285749	Human DNA from chromosome 19-specific co	2.10
	432092	AF135026		gb:Homo sapiens kallikrein-like protein	2.10
	441915	AI566116	Hs.207066	ESTs, Weakly similar to FOG [Musculus]	2.10
	453147	AA733098	Hs.279909	CGI-05 protein	2.10
15	415604	Z44177	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.08
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.08
	401211	AJ004832	Hs.5038	neuropathy target esterase	2.07
	413808	J00287	Hs.182183	caldesmon 1	2.07
	414433	BE407755	Hs.169100	Homo sapiens cDNA FLJ12529 fis, clone NT	2.07
20	421978	AJ243662	Hs.110196	NICE-1 protein	2.07
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	2.07
	433605	AI378012	Hs.147953	ESTs	2.06
	449383	AW444712	Hs.196573	ESTs	2.06
	455652	BE064675		gb:RC1-BT0313-301299-012-h11 BT0313 Homo	2.05
25	402382				2.04
	407282	AI345597	Hs.254727	ESTs	2.04
	457273	AI167145	Hs.165538	ESTs	2.04
	459073	AW968616	Hs.296234	ESTs, Highly similar to mitogen-activate	2.04
	402394				2.03
30	428875	AW451624	Hs.178202	ESTs	2.03
	456634	AA609911	Hs.109012	ESTs	2.03
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.02
	439281	AA100768	Hs.48485	ESTs	2.02
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.02
35	401122				2.01
	444340	AI143198	Hs.143561	ESTs	2.01
	455104	BE064863		gb:RC1-BT0313-110300-015-06 BT0313 Homo	2.01
	415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	2.00
40	440144	AW082297	Hs.88523	ESTs	2.00
	403183				1.99
	409802	AW500732		gb:UI-HF-BN0-akm-h-07-0-UI.r1 NIH_MGC_50	1.98
	430144	AI732722	Hs.187694	ESTs	1.98
	444580	AI168365	Hs.268663	ESTs	1.98
45	401704				1.97
	401810				1.97
	424473	AK001405	Hs.148584	Homo sapiens cDNA FLJ10543 fis, clone NT	1.97
	438573	AW135084	Hs.299865	ESTs	1.97
	412921	BE009345	Hs.128942	ESTs	1.96
50	422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	1.96
	425352	NM_009939	Hs.1897	proopiomelanocortin (adrenocorticotrophin)	1.96
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	1.95
	414323	NM_014759	Hs.239500	KIAA0273 gene product	1.94
	428119	AW298211	Hs.255737	ESTs	1.94
55	424510	AK001841	Hs.149797	hypothetical protein FLJ10979	1.92
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxylase 1 (sol	1.92
	429785	H82114	Hs.301769	ESTs	1.92
	437344	R90921	Hs.6846	hypothetical protein FLJ13055	1.92
	451819	AI819096	Hs.249260	ESTs	1.92
60	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein	1.92
	422684	AA315933	Hs.120879	ESTs	1.91
	432247	AA531287	Hs.105805	ESTs	1.91
	453820	R77494	Hs.75416	DAZ associated protein 2	1.91
	400675				1.90
65	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	1.90
	407099	M94891	Hs.278423	pregnancy specific beta-1-glycoprotein 4	1.90
	440297	BE560553	Hs.205450	Homo sapiens cDNA: FLJ22570 fis, clone H	1.90
	443104	AA088470	Hs.83135	p53-responsive gene 6	1.90
	444329	W73753	Hs.58330	ESTs	1.90
70	402690				1.89
	432354	AW137262	Hs.192713	ESTs	1.89
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.88
	443322	AI825817	Hs.143272	ESTs	1.88
	458185	AI762757	Hs.129869	ESTs, Weakly similar to AF113685 1 PRO09	1.88
	459072	AI815978	Hs.160427	ESTs	1.88
75	402534				1.87
	409689	AA078492		gb:TP04D11 Chromosome 7 Placental cDNA L	1.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	1.87
	430176	AL161995	Hs.234775	neurturin	1.87
80	430631	AJ003147	Hs.278464	olfactory receptor, family 1, subfamily	1.87
	433114	AA121579		gb:zn77f02.r1 Stratagene NT2 neuronal pr	1.87
	439254	U57352	Hs.6517	amiloride-sensitive cation channel 1, no	1.87
	448461	AW166358	Hs.124979	ESTs	1.87
	450675	AA010662	Hs.188639	ESTs	1.87

	401767			1.86
	449891	N64867	Hs.37848	ESTs
	400527			1.85
	428581	AA430570	Hs.104881	ESTs
5	443647	AV653846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT
	444785	AV651441	Hs.282475	ESTs
	449566	AA001778	Hs.288156	Homo sapiens cDNA: FLJ21819 fis, clone H
	436752	AW298529	Hs.255774	ESTs
10	437405	AA338837	Hs.42547	Homo sapiens cDNA FLJ13975 fis, clone Y7
	449174	T66136	Hs.12880	ESTs
	449887	AW080843	Hs.200275	ESTs
	453261	AA034116	Hs.118494	ESTs
	454243	AW241901	Hs.250683	ESTs
15	459188	AA216382	Hs.30002	SH3-containing protein SH3GLB2
	424334	AA393460		gb:z171e05.r1 Soares_testis_NHT Homo sap
	432150	AK000224	Hs.272789	hypothetical protein FLJ20217
	408123	AW163377		gb:au94e02.y1 Schneider fetal brain 0000
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4
20	442196	AI902646	Hs.31844	Homo sapiens cDNA FLJ12586 fis, clone NT
	421419	M99587	Hs.104134	homeo box (H6 family) 1
	405420			1.78
	405737			1.78
	414016	AA134594	Hs.71528	ESTs
25	415744	AW964850	Hs.278307	ESTs
	420375	AF182077	Hs.97244	glioma tumor suppressor candidate region
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1
	401743			1.77
	405187			1.75
30	442763	AI017037	Hs.131121	ESTs
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain
	413248	T64858	Hs.21433	ESTs
	423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti
35	439999	AA115811	Hs.6838	ras homolog gene family, member E
	440185	AW104546	Hs.270929	ESTs
	450482	AI697844	Hs.221720	ESTs
	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYD
	420476	AW575863	Hs.136232	ESTs
40	428748	AW593206	Hs.98785	ESTs
	431148	AA502653	Hs.28621	ESTs
	447205	BE617015	Hs.11006	ESTs
	455994	BE179190		gb:RC0-HT0613-210300-032-07 HT0613 Homo
	401039			1.73
	403251			1.72
45	409762	AW498884	Hs.257970	ESTs
	440914	AA909552	Hs.143884	ESTs
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f
	409605	AW444477	Hs.258507	ESTs
50	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizl
	445624	AW140103	Hs.78880	livB (bacterial acetolactate synthase)-l
	458619	AA872064	Hs.301218	ESTs, Weakly similar to Unknown gene pro
	401969			1.71
	403327			1.70
	407245	X90568	Hs.172004	titin
55	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil
	436034	AF282693	Hs.150185	Inflammation-related G protein-coupled r
	442682	AI014545	Hs.231027	EST
	458494	AI380906	Hs.158438	ESTs
	404682			1.70
60	407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium
	440362	AA883812	Hs.125508	ESTs
	448866	BE297743	Hs.284203	myogenic factor 3
	402201			1.69
65	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)
	403186			1.68
	409543	AW410200		gb:fh05b12.x1 NIH_MGC_17 Homo sapiens cD
	443672	AA323362	Hs.9667	butyrolactone (gamma), 2-oxoglutarate di
70	450391	AI694522	Hs.202280	ESTs
	408919	AW295352	Hs.251836	ESTs
	416136	H45027	Hs.181770	ESTs
	416885	H97863	Hs.42456	ESTs
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa
	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c
75	429134	AA448953	Hs.99004	ESTs
	445041	T64183	Hs.11398	ESTs
	453240	AI969564	Hs.264249	Homo sapiens cDNA: FLJ22334 fis, clone H
	405243			1.66
	426039	BE265133	Hs.217493	annexin A2
80	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate
	435942	R06285	Hs.191215	ESTs
	448106	AI800470	Hs.171941	ESTs
	408591	AF015224	Hs.46452	mammaglobin 1
				1.64

	410881	AW809157		gb:RC0-ST0118-041099-031-c07_1 ST0118 Ho	1.63
	417743	R14738	Hs.8312	ESTs, Weakly similar to AF170723.1 prote	1.62
	430632	AC004597	Hs.248088	olfactory receptor, family 10, subfamily	1.62
	448651	BE246440	Hs.93728	pre-B-cell leukemia transcription factor	1.62
5	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, c	1.62
	459499	AW402653	Hs.28355	Homo sapiens cDNA: FLJ22402 fis, clone H	1.62
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61
	419113	AJ446585	Hs.21835	ESTs	1.61
	426795	AI810474	Hs.196945	ESTs	1.61
10	426998	BE274360		gb:601121068F1 NIH_MGC_20 Homo sapiens c	1.61
	428407	NM_003963	Hs.184194	transmembrane 4 superfamily member 5	1.61
	444475	C75571		gb:C75571 Human pancreatic islet Homo sa	1.61
	453399	Z70295	Hs.32965	guanylate cyclase activator 2B (uroguany	1.61
	456275	AW976183	Hs.88414	ESTs, Weakly similar to dJ512E2.1 [H.sap	1.61
15	414060	BE246327		gb:TCBAP1E1967 Pediatric pre-B cell acut	1.60
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.60
	428651	AF196478	Hs.188401	annexin A10	1.60
	443853	AI089064	Hs.250644	ESTs	1.60
	407007	U22961		gb:Human mRNA clone with similarity to L	1.59
20	412067	N45697		gb:yy78d01.r1 Soares_multiple_sclerosis_	1.59
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.59
	448619	AI867182	Hs.202255	ESTs	1.59
	403665				1.58
25	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory	1.58
	424286	AA338285	Hs.90744	proteasome (prosome, macropain) 26S subu	1.58
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	1.57
	430218	AW958865	Hs.186703	ESTs	1.57
	431882	NM_001426	Hs.271977	engrailed homolog 1	1.57
	450797	AI761930	Hs.205127	ESTs	1.57
30	455366	AW947563		gb:RC0-MT0004-140300-031-g11 MT0004 Homo	1.57
	408421	AW193734	Hs.253067	ESTs	1.56
	421907	BE018556	Hs.109358	ATPase, Class V, type 10B	1.56
	432742	AA564453	Hs.162339	ESTs	1.56
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	1.56
35	439543	W75935	Hs.146083	ESTs	1.56
	443317	AI051601	Hs.200191	ESTs	1.56
	449097	BE271708	Hs.95110	ESTs, Weakly similar to PIP6_HUMAN 1-PHO	1.56
	457127	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	1.56
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1,	1.55
40	418837	U48263	Hs.89040	preproenkephalin	1.55
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.55
	458475	AI650322	Hs.143249	ESTs	1.55
	402561				1.54
45	411187	AW821291		gb:PMQ-ST0307-241299-002-R03 ST0307 Homo	1.54
	419224	NM_012189	Hs.252716	fibrousheathin II	1.54
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	1.53
	415426	Z41991	Hs.23197	ESTs	1.53
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.53
50	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.53
	428469	AI807459	Hs.98582	ESTs	1.53
	437728	AA766719		gb:aa39c09.s1 NCL_CGAP_GCB1 Homo sapiens	1.53
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.52
	414932	C14577	Hs.194517	ESTs	1.52
55	433500	AF064255	Hs.111401	very long-chain acyl-CoA synthetase homo	1.52
	439688	AW445181	Hs.209637	Homo sapiens cDNA FLJ12921 fis, clone NT	1.52
	453391	AW600302	Hs.232655	ESTs	1.52
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	1.51
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.51
60	443012	AI566813	Hs.132278	ESTs	1.51
	415824	D42039	Hs.78871	mesoderm development candidate 2	1.50
	445152	AI214667	Hs.283597	ESTs	1.50
	455941	BE160011	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1.50
	457889	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.50
65	458503	AL133933	Hs.64310	interleukin 11 receptor, alpha	1.50
	400694				1.49
	420937	AW966719	Hs.1340	collipase, pancreatic	1.49
	426752	X69490	Hs.172004	titin	1.49
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.49
70	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis t	1.49
	444287	AI033077	Hs.10755	dihydropyrimidinase	1.49
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.49
	425747	AI457620	Hs.205360	ESTs	1.48
	432378	AI493046	Hs.146133	ESTs	1.48
	447999	AW138840	Hs.201778	ESTs	1.48
75	453888	AW450670	Hs.252819	ESTs	1.48
	406667	M12523	Hs.75442	albumin	1.47
	418129	X52997	Hs.1144	glycoprotein IX (platelet)	1.47
	426309	AI912555	Hs.157195	peptide YY, 2 (seminalbumin)	1.47
80	426755	BE253469		gb:601108143F1 NIH_MGC_16 Homo sapiens c	1.47
	414258	AA203285	Hs.294141	ESTs, Weakly similar to dJ733D15.1 [H.sa	1.46
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	1.46
	420662	AI345569	Hs.190046	ESTs	1.46
	425011	T51986	Hs.283108	hemoglobin, gamma G	1.46

	443050	AI512788	Hs.132348	ESTs, Weakly similar to diaphanous 1 [H.	1.46
	411074	X50435	Hs.68137	adenylate cyclase activating polypeptide	1.45
	434680	T11738	Hs.127574	ESTs	1.45
	454771	AW819939	Hs.273529	ESTs	1.45
5	415672	N53097	Hs.193579	ESTs	1.44
	418141	AW845738	Hs.171118	Homo sapiens mRNA for FLJ00026 protein,	1.44
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.43
	418197	AA214253		gb:zn58g02.r1 Stratogene muscle 937209 H	1.43
10	431821	AW452256	Hs.271221	hypothetical protein FLJ20064	1.43
	455433	AW939463		gb:QV1-DT0072-310100-056-g02 DT0072 Homo	1.43
	407743	AW814118		gb:MR3-ST0203-151199-011-d09 ST0203 Homo	1.42
	418888	AJ076801	Hs.89438	cadherin 17, LI cadherin (liver-intestin	1.42
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibitor	1.42
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.42
15	452456	BE080763		gb:QV1-BT0631-150200-071-f09 BT0631 Homo	1.42
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.42
	408349	BE546947	Hs.44276	homeo box C10	1.41
	420391	AA456891	Hs.79123	KIAA0084 protein	1.41
	421216	M74587	Hs.102122	insulin-like growth factor binding prote	1.41
20	449329	AW752783		gb:IL3-CT0219-221199-029-F03 CT0219 Homo	1.41
	453615	AA195712	Hs.132696	ESTs	1.41
	417296	L36198	Hs.81884	sulfotransferase family, cytosolic, 2A,	1.40
	420287	AA740907	Hs.88297	ESTs	1.40
25	427583	M82962	Hs.179704	meprin A, alpha (PABA peptide hydrolase)	1.40
	418787	AW296134	Hs.86999	ESTs	1.39
	422072	AB018255	Hs.111138	KIAA0712 gene product	1.39
	425988	BE045897	Hs.274454	ESTs	1.39
	428087	AA100573	Hs.182421	troponin C2, fast	1.39
30	438136	NM_002390	Hs.6088	a disintegrin and metalloproteinase doma	1.39
	455579	BE011320		gb:PM3-BN0218-090500-002-d09 BN0218 Homo	1.39
	402316			ESTs	1.38
	417084	H08370	Hs.33067	ESTs	1.38
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.38
35	433787	AI472951	Hs.173688	ESTs	1.38
	413830	BE263439	Hs.13144	HSPC160 protein	1.37
	423576	NM_000383	Hs.129829	autoimmune regulator (autoimmune polyen	1.37
	401886			chymotrypsinogen B1	1.36
	412688	AW583062	Hs.74502	hypothetical protein FLJ11125	1.34
40	401238			aldo-keto reductase family 1, member B11	1.34
	421511	AA488940	Hs.105216	LIM homeobox protein 1	1.34
	422440	NM_004812	Hs.116724	aquaporin 8	1.34
	425450	U14755	Hs.157449	glutathione peroxidase 2 (gastrointestin	1.34
45	427333	AF067797	Hs.176658	ESTs	1.34
	430937	X53463	Hs.2704	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	1.34
	445204	AW135523	Hs.245853	gb:63E10 Human retina cDNA Tsp5091-cleav	1.34
	452030	AL137578	Hs.27607	gb:CM3-HT0137-150999-011-b05 HT0137 Homo	1.34
	456379	W22206		ESTs	1.33
50	457416	BE142052		ESTs, Weakly similar to LITB_HUMAN LITB	1.33
	415741	AJ902761	Hs.272087	KIAA0599 protein	1.33
	422260	AA315993	Hs.105484	chymotrypsin C (caldecrin)	1.33
	429188	AB011171	Hs.198037	gb:RC3-CT0347-160200-013-d09 CT0347 Homo	1.33
	442776	AW959498	Hs.8709	ESTs, Weakly similar to CGHU2E collagen	1.32
55	454748	AW862014	Hs.300288	KIAA0724 gene product	1.32
	437744	AW290905	Hs.158497	ISL1 transcription factor, LIM/homeodoma	1.32
	451997	AA021351	Hs.505	Homo sapiens cDNA: FLJ23112 fls, clone L	1.31
	452340	NM_002202	Hs.273758	dual specificity phosphatase 9	1.31
	411879	BE145354	Hs.144879		1.30
60	424304	NM_001395			1.30
	401442				1.30
	403942				1.29
	443687	F13040	Hs.182937	peptidylprolyl isomerase A (cyclophilin	1.29
	401624			ESTs, Moderately similar to CRGD_HUMAN G	1.29
65	411885	AA452638	Hs.131057	ESTs	1.29
	418575	AA225313	Hs.222886	ESTs	1.29
	419818	AI657122	Hs.301931	ESTs	1.29
	429845	AB020337	Hs.225943	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	1.29
	447586	AI081980	Hs.285829	solute carrier family 25 (mitochondrial	1.28
	407013	U35837		gb:Human nebulin mRNA, partial cds	1.28
70	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	1.28
	429780	AL137518	Hs.300388	ESTs	1.28
	453539	AW731886	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.eleg	1.28
	400846				1.27
	420257	AA257035	Hs.190042	ESTs	1.27
75	429184	AF095735	Hs.198003	sarcosine dehydrogenase	1.27
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	1.27
	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	1.27
	451139	AW293316	Hs.205558	ESTs	1.27
	431284	AA570148	Hs.126783	Homo sapiens cDNA: FLJ22610 fls, clone H	1.26
80	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	1.26
	406158				1.25
	419548	T73661	Hs.91877	ESTs, Highly similar to THIH_HUMAN THYRO	1.25
	430681	AW939675	Hs.291232	ESTs	1.25
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.25

5	436217	T53925	Hs.107	fibrinogen-like 1	1.25
	440089	AA864468	Hs.135646	ESTs	1.25
	446787	U67167	Hs.315	mucin 2, intestinal/tracheal	1.25
	448207	AW75490	Hs.170577	ESTs	1.25
	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	1.25
10	413271	AA127873	Hs.114949	ESTs	1.24
	422619	AA313322		gb:EST185218 Colon carcinoma (HCC) cell	1.24
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo	1.24
	427530	AA405093	Hs.126519	ESTs	1.24
	437727	AA766707	Hs.153039	ESTs	1.24
15	426435	AI827946	Hs.189118	ESTs	1.23
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	1.22
	407964	AW130334	Hs.281111	ESTs	1.21
	430828	AI763257	Hs.86327	Homo sapiens cDNA: FLJ22431 fis, clone H	1.21
	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	1.21
20	457843	AW138211	Hs.128746	ESTs	1.21
	413242	BE074165		gb:PM3-BT0564-030300-002-e12 BT0564 Homo	1.20
	446057	AI420227	Hs.149358	ESTs	1.20
	447198	D61523	Hs.283435	ESTs	1.20
	449513	AI653232	Hs.195059	EST	1.20
25	415566	F12119		gb:HSC35H091 normalized infant brain cDN	1.19
	423315	R54109	Hs.26096	ESTs	1.19
	455817	BE142384		gb:CM2-HT0144-210999-011-d04 HT0144 Homo	1.19
	459354	BE514778		gb:601317094F1 NIH_MGC_9 Homo sapiens cD	1.19
	408432	AW195262		gb:cn67b05.x1 NCL_CGAP_CML1 Homo sapiens	1.18
30	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.18
	419251	NM_001486	Hs.89771	glucokinase (hexokinase 4) regulatory pr	1.18
	456702	AI684534		gb:wa7210.x1 Soares_NFL_T_GBC_S1 Homo s	1.18
	458009	AI221409	Hs.144983	ESTs	1.18
	410193	AJ132592	Hs.59757	zinc finger protein 281	1.17
35	417779	AA829526	Hs.124977	ESTs	1.17
	435101	AI743156	Hs.131064	ESTs	1.17
	445360	AI798776	Hs.156029	ESTs	1.17
	414160	BE257021		gb:601117426F1 NIH_MGC_16 Homo sapiens c	1.15
	418078	AA521268	Hs.86508	ESTs	1.15
40	425133	NM_002613	Hs.154729	3-phosphoinositide dependent protein kin	1.15
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	1.15
	446377	AW014022	Hs.170953	ESTs	1.15
	420097	AA700127	Hs.190504	ESTs	1.13
	446591	H44186	Hs.15456	PDZ domain containing 1	1.13
45	451477	AI798425	Hs.42710	ESTs	1.13
	459197	BE244587		gb:TCBAP2E0851 Pediatric pre-B cell acut	1.13
	428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	1.12
	431191	AW972118	Hs.100002	HSPC162 protein	1.12
	424403	F05183	Hs.1799	CD1D antigen, d polypeptide	1.11
50	433546	AI075877	Hs.125461	Homo sapiens cDNA FLJ11539 fis, clone HE	1.11
	451179	W05469	Hs.31818	ESTs	1.11
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	1.10
	420774	AA280209	Hs.165270	ESTs	1.10
	428887	AA437009	Hs.98984	ESTs	1.10
55	430582	AI215509	Hs.143964	ESTs	1.10
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	1.10
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.09
	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	1.09
	456387	V28876		gb:5Zh7 Human retina cDNA randomly prime	1.09
60	427965	D00306	Hs.183864	elastase 3B	1.08
	447388	AW630534	Hs.76277	ESTs, Weakly similar to TB2 [H.sapiens]	1.08
	413841	M34276	Hs.75576	plasminogen	1.07
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.07
	433313	W20128	Hs.296039	ESTs	1.07
65	439450	R51613	Hs.125304	ESTs	1.07
	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	1.07
	405161				1.06
	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	1.06
	424294	BE299311		gb:601119256F1 NIH_MGC_17 Homo sapiens c	1.06
70	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.06
	444687	AW972109	Hs.135107	ESTs	1.06
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1.06
	421243	AW873803	Hs.102876	pancreatic lipase	1.05
	444290	AA262496	Hs.29280	ESTs	1.05
75	407984	AW134708	Hs.243569	ESTs	1.04
	439706	AW872527	Hs.59761	ESTs	1.04
	402194				1.03
	427506	AK000134	Hs.179100	hypothetical protein FLJ20127	1.03
	428819	AL135623	Hs.193914	KIAA0575 gene product	1.03
80	434590	T47232		gb:yg64b08.s1 Stratagene ovary (937217)	1.03
	416378	AW044467	Hs.73708	ESTs, Weakly similar to A57291 cytokine	1.02
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	1.02
	443316	AI478463	Hs.18443	ESTs	1.02
	428585	AB007863	Hs.185140	KIAA0403 protein	1.01
80	400440	X83957	Hs.83870	nebulin	1.00
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S.	1.00
	407168	R45175		gb:yg40f01.s1 Soares Infant brain 1N1B H	1.00

	408052	AW501117	Hs.283585	ESTs	1.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.00
5	410234	NM_003837	Hs.61255	fructose-1,6-bisphosphatase 2	1.00
	410319	R23413	Hs.71935	putative zinc finger protein from EUROIM	1.00
	411000	N40449	Hs.201619	ESTs, Weakly similar to SEB4B [H.sapiens	1.00
	412098	AI493054	Hs.158968	ESTs	1.00
	412446	AI768015	Hs.92127	ESTs	1.00
10	412637	AA115097	Hs.261313	ESTs	1.00
	413147	BE067271		gb:PM2-BT0349-161299-001-b05 BT0349 Homo	1.00
	413597	AW302885	Hs.117183	ESTs	1.00
	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	1.00
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	1.00
15	417074	Z49878	Hs.811131	guanidinoacetate N-methyltransferase	1.00
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	1.00
	419768	T72104	Hs.93194	apolipoprotein A-I	1.00
	420182	Z44245	Hs.22999	ESTs	1.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	1.00
20	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.00
	421204	AW081587	Hs.165051	ESTs	1.00
	422189	AF252292	Hs.112933	Tax Interaction protein 40	1.00
	422792	AI951548	Hs.135163	ESTs	1.00
	423371	AU076819	Hs.1650	solute carrier family 26, member 3	1.00
25	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.00
	424922	BE386547	Hs.217112	ESTs, Weakly similar to Similarity to Ye	1.00
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.00
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	1.00
	425983	AK000226	Hs.165619	mucin and cadherin-like	1.00
30	426004	AW600300	Hs.124123	ESTs, Weakly similar to synocollin [R.nor	1.00
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	1.00
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	1.00
	429027	AL022314	Hs.194750	Human DNA sequence from clone 1170K4 on	1.00
	429231	AA813214		gb:aj32a09.s1 Soares_testis_NHT Homo sap	1.00
35	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	1.00
	429930	AI580809	Hs.99569	ESTs	1.00
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1.00
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	1.00
40	431845	AA516469	Hs.270554	ESTs	1.00
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	1.00
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00
	434452	AA634333	Hs.116822	ESTs	1.00
	435499	R89344	Hs.14148	ESTs	1.00
	438433	AB018274	Hs.6214	KIAA0731 protein	1.00
45	442403	AW207724	Hs.129516	ESTs	1.00
	442803	AI675298	Hs.199917	ESTs	1.00
	443266	AI277101	Hs.25890	ESTs, Weakly similar to transducin [H.sa	1.00
	444656	AI277924	Hs.145199	ESTs	1.00
	445573	AI439646	Hs.157494	ESTs, Weakly similar to KIAA0676 protein	1.00
50	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00
	447359	NM_012093	Hs.18268	adenylate kinase 5	1.00
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac mus	1.00
	448657	BE147857	Hs.293841	ESTs, Weakly similar to KIAA0672 protein	1.00
	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	1.00
55	450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	1.00
	450390	N93227	Hs.98403	ESTs	1.00
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	1.00
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	1.00
	452528	AA742457	Hs.291479	ESTs	1.00
60	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	1.00
	453754	AW972580	Hs.172753	ESTs	1.00
	453991	AW014915	Hs.273741	ESTs	1.00
	454517	AW803340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	1.00
	459367	BE148877		gb:CM4-HT0244-111199-040-h12 HT0244 Homo	1.00
65	408021	AW137133	Hs.245867	ESTs	0.99
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	0.99
	437206	AW975934	Hs.283382	ESTs, Weakly similar to Protein sequence	0.99
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	0.98
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	0.98
70	441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.98
	423068	M25629	Hs.123107	kalikrein 1, renal/pancreas/salivary	0.97
	453534	NM_014796	Hs.33187	KIAA0748 gene product	0.97
	457787	AA683268		gb:ac92b04.s1 Stratagene schizo brain S1	0.97
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	0.96
75	422069	AJ010063	Hs.111110	titin-cap (teletthin)	0.96
	425260	L47726	Hs.1870	phenylalanine hydroxylase	0.96
	418406	X73501	Hs.84905	cytokeratin 20	0.95
	425870	AW988536	Hs.190146	ESTs	0.95
	416373	AA195845	Hs.73680	ESTs, Weakly similar to AF198455 1 epith	0.94
80	452243	AL355715	Hs.28555	programmed cell death 9	0.94
	411908	L27943	Hs.72924	cytidine deaminase	0.93
	415067	AI264969	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.93
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	0.93
	450685	L15533	Hs.423	pancreatitis-associated protein	0.92

	427450	AB014526	Hs.178121	KIAA0626 gene product	0.91
	432440	X63597	Hs.2996	sucrase-isomaltase	0.91
	426651	AJ076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.90
5	414910	X12662	Hs.29679	cofactor required for Sp1 transcription	0.89
	423317	AJ272204	Hs.64616	chromosome 12 open reading frame 3	0.89
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fls, clone HE	0.89
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDN	0.89
	452689	F33868	Hs.284176	transferrin	0.89
10	446240	AJ535736	Hs.170165	ESTs	0.88
	449110	H56112	Hs.277053	ESTs	0.88
	453817	AW755253	Hs.61920	ESTs	0.88
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.87
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	0.87
15	445525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fls, clone H	0.87
	453341	AJ758912	Hs.296341	adenylyl cyclase-associated protein 2	0.87
	403740				0.86
	420156	AW449258	Hs.6187	ESTs	0.86
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.86
20	421142	AW503944	Hs.130822	ESTs	0.85
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.85
	419415	AW451692	Hs.192036	ESTs	0.84
	423321	AB013885	Hs.126926	beta-ureidopropionase	0.84
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	0.84
25	433447	U29195	Hs.3261	neuronal pentraxin II	0.84
	403047				0.83
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.81
	407782	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje	0.81
	405232				0.80
30	437776	AA768037	Hs.291671	ESTs	0.80
	415505	R39870	Hs.12548	ESTs	0.79
	444436	N25871	Hs.177337	ESTs	0.78
	409096	AA194412	Hs.50550	sarcomeric muscle protein	0.77
	432134	AI816782	Hs.122583	Homo sapiens cDNA: FLJ21934 fls, clone H	0.76
35	437066	AA743570	Hs.200935	ESTs	0.76
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	0.75
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.73
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	0.71
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	0.71
40	447145	AA761073	Hs.192943	ESTs	0.71
	452103	R42764	Hs.3248	mutS (E. coli) homolog 6	0.71
	410929	H47233	Hs.30643	ESTs	0.70
	400301	X03635	Hs.1657	estrogen receptor 1	0.69
	415702	F28877		gb:HSPD18414 HM3 Homo sapiens cDNA clone	0.67
45	411396	CD4646	Hs.85428	ESTs	0.65
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.65

TABLE 288

Pkey: Unique Ecos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

55	Pkey	CAT number	Accession
	407743	1012151_1	AW814118 AW814257 AW072376
	408123	1040435_1	AW163377 AW160398
	408432	1058667_1	AW195262 R27868 AW811262
60	408664	1073340_1	R56362 AW248096 R07162 R07285
	408922	109017_1	R87388 R84328 AA058916
	409368	112377_1	AA071059 AA085201 AA085020
	409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309
	409689	114833_1	AA078492 AA078333 AA077450 AA077746 AA076896
65	409778	1154206_1	AW499705 AW502537 AW503016
	409802	1155179_1	AW500732 AW504061
	410285	119128_1	AA083609 AA083790 AA112048
	410881	1225682_1	AW809157 AW812181 AW812175 AW812172 AW812161 AW812165
	411187	1235092_1	AW821291 AW821264 AW821287 AW821290 AW821285 AW821280 AW821259
70	412057	1275641_1	N45697 N45540 AW890595
	413147	1350637_1	BE067271 BE067266 BE067286 BE067278 BE067299 BE067285
	413242	1355323_1	BE074165 BE075001 BE075009
	413811	1391117_1	BE168828 BE168830 BE168823 BE168928 BE168820 BE168826
	414060	1413697_1	BE246327 BE244704
75	414095	1416521_1	BE293546 BE249848
	414160	1422273_1	BE257021 BE258316 BE257099
	414580	1463848_1	BE386918 BE408833 BE385437
	415011	151328_1	AW963085 AA159005 AW963073
	415566	1539861_1	F12119 Z45475 T64832
80	415702	1547874_1	F28877 F35687
	417998	171375_1	AW967420 AA210915 AA236991 AA210916
	418197	172864_1	AA214253 AA214259 Z28472 Z28881 Z17828
	418464	1759038_-2	R87580
	418556	1767866_-1	T02850

422619	218670_1	AA313322 BE408282 AA465612 BE073382
422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361 T06241 AA326794 AL138130
		AW407975 AW999277
5	424294	237907_1 BE299311 AA338954 AA338468 AW960907
	424334	238221_1 AA393460 AA338940 AW966277 AA419006
	424548	241947_1 AA344576 AA732430 AA344601
	425515	252721_1 W26609 W27360 AA358818
	426328	264901_1 AW631296 AA375484
10	426507	268382_1 AA380285 AW934727 AW934914
	426755	271382_1 BE253469 BE176417 BE176415 AA384133
	426880	273277_2 AA453482 AF012388
	426998	274259_1 BE274360
	429231	301463_1 AA813214 AI936567 AI743529 AA448279 AA994476 AI807452 AI218180 AA972858
	430728	322706_1 AW968522 AA485112 AA485162 AW968698
15	432092	34124_1 AF135026 AA583908
	433114	35904_1 AA121579 AB005217
	434590	38931_1 T47232 AF147365 T47231
	437237	43506_2 BE513073
20	437728	441520_1 AA766719 AA767041 AW977440
	439894	478738_1 AA853077 AA852175
	442197	535550_1 AW837912 AW837934 AA984475 AW997490
	442614	547073_1 AI269030 AI204085 AI004047
	444475	607874_1 C75571 AI150469 T10778
25	448427	762970_1 BE395520 AW291036 AI500420
	449329	80484_1 AW752783 H38266 AA001166
	451588	87667_1 AW072057 AI225096 AAD18702
	452456	918391_1 BE080763 T96699 BE081135 AI902630 H49182 AI904021 AI902697
	454517	1221063_1 AW803340 AW803280 AW803275 AW803415 AW803343 AW803422
30	454748	1233013_1 AW862014 AW858740 AW858735 AW818542 AW858765 AW862027 AW858775 AW858771 AW858763
	454869	1238137_1 AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164
		AW836002 AW836078 AW836161 AW862135 AW836165 AW836003
	454886	1238987_1 AW837063 AW835882 AW935957
	455075	1252389_1 AW854850 AW854848
35	455104	1253737_1 BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665
		BE064650 BE064691
	455366	1284685_1 AW947563 AW947543 AW947553 AW947549 AW947717 AW902859 AW902927 BE011032
	455433	1290311_1 AW939463 AW939484 AW939480 AW939459 AW939546 AW939593 AW939548 AW939595 AW939106
	455446	1291969_1 AW947749 AW947746 AW947754 AW946636 AW946674
40	455579	1333944_1 BE011320 BE006381 BE006361 BE011180 BE011328 BE011325 BE011157 BE006384 BE006387 BE006385 BE011160 BE011319 BE011346
		BE006370 BE006386 BE011173 BE006389 BE006376 BE006375 BE006364 BE011321 BE006379
	455652	1348736_1 BE064675 BE064761 BE064809 BE064673 BE064672 BE064674
	455817	1371986_1 BE142384 BE142387
	455994	1398737_1 BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
45	456150	1574395_1 Z42308 H23514
	456379	1839113_2 W22206 W22498 W26922
	456387	1842730_1 W28876 W26158
	456702	219191_1 AI684534 BE262411 AA314031 AW752724
	457416	334503_1 BE142052 AW265588 AA506741
50	457787	407235_1 AA683268 BE002903 BE002672
	458764	73207_1 BE619386 AA300687
	459197	924229_1 BE244587 AW936684 AW176490 AI940102 AW844995 AW938670 AI909850 AI909885 AI940079 AI909873

55 TABLE 28C

60 Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
65 400489	8954013	Plus	131475-131652
400527	9796886	Plus	160750-161007
400545	9800107	Minus	124618-124881
400624	7228177	Minus	94097-94756
400635	8567750	Minus	102800-102932,107482-107689
70 400672	8118724	Minus	148067-148503
400675	8118750	Plus	11223-11816
400694	8118802	Plus	94288-94442
400736	8118985	Plus	143447-143851
400846	9188605	Plus	39310-39474
75 401007	8117333	Minus	140821-141050
401015	8117441	Plus	72260-72369
401039	7232177	Plus	6588-6884
401122	8570296	Plus	68258-68444
401238	9954455	Minus	49473-49644
80 401442	8346725	Minus	85674-85910
401496	7381769	Minus	82790-83002
401590	9966320	Minus	33547-33649
401603	7689963	Minus	116659-116780
401624	8575907	Plus	168318-168444,172964-173647

	401688	2347081	Plus	22016-22624
	401704	3097841	Plus	24712-25374
	401728	8134856	Minus	82117-82920
5	401743	2865207	Plus	115475-115640
	401767	9958312	Plus	156823-156921,157364-157554
	401810	7342191	Plus	129053-129476
	401840	7684597	Plus	56283-56439
	401886	7229913	Minus	79215-79393
10	401919	9502466	Plus	67536-67666
	401969	3126777	Plus	44853-45366
	402051	8082020	Minus	19346-19480,20041-20119
	402056	8084234	Plus	207002-207288
	402153	8247879	Minus	122580-122987
15	402158	8516165	Minus	148298-148429,148566-148677
	402165	8569830	Minus	65064-65979
	402194	8576113	Plus	70917-71191
	402195	7689778	Minus	147901-148884
	402201	8576119	Plus	655-951
20	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
	402382	9690314	Minus	155331-155528
	402386	9799769	Plus	22069-22303
	402394	9929690	Plus	33308-33482
	402409	9796255	Minus	8571-10061
25	402423	9796344	Minus	62487-62664
	402448	9796640	Plus	112942-113069,114303-114521
	402457	9796782	Minus	16513-16577,16838-16926
	402534	9801061	Plus	58989-59457
	402538	9801137	Minus	96314-96539
30	402561	9864675	Plus	72967-73163
	402588	9908948	Minus	33027-33183,59060-59198
	402690	8348058	Plus	13368-13998
	402714	8969253	Minus	18811-18886,19105-19328,19525-19764
	402762	9230904	Minus	123298-124035
35	402862	2956660	Minus	18518-18656
	402911	7263904	Plus	142689-142979
	402951	9408717	Plus	73252-73329,73718-73877,76217-76299,78195-78401
	402968	9581763	Minus	58658-58924
	403047	3540153	Minus	59793-59968
40	403115	7331404	Minus	142952-143094,145474-145653,146269-146445,152816-152998
	403125	9180936	Minus	197548-197712
	403183	9838273	Plus	109930-110074
	403186	9838287	Minus	117513-117856
	403211	7630841	Minus	159211-159369
	403247	7656833	Minus	76626-77140
45	403251	7677983	Plus	100391-100652
	403327	8440025	Minus	174311-174451,174587-174705,175523-175592
	403376	9369545	Minus	108698-108830
	403479	7329292	Minus	148369-148533,150678-150809
50	403526	8017144	Plus	55367-55483
	403540	8077057	Minus	56315-56450
	403605	6862654	Plus	91614-91718
	403612	8469060	Minus	94723-94859
	403665	7249278	Plus	69027-69375
55	403716	7239669	Plus	86899-87122
	403731	7543752	Minus	144000-144618
	403740	7630882	Plus	86504-87227
	403921	7711590	Minus	3297-3536
	403942	7711825	Minus	99606-99757
60	403997	7708819	Plus	134427-134593
	404139	9838113	Plus	76707-76891
	404247	7406725	Minus	83949-84214,84312-84415,84499-84677,84878-85114
	404282	2276311	Plus	61503-62205
	404348	7630858	Minus	28895-29062
65	404668	9797204	Minus	11332-11546,12584-12718
	404682	9797231	Minus	40977-41150
	404795	4826439	Plus	147501-147780
	404825	6478944	Plus	210382-210494
	404938	7381808	Minus	165838-165950
70	405075	7770506	Minus	124680-125321
	405147	9438278	Minus	158996-159557
	405161	9966260	Plus	157607-157785
	405163	9966267	Minus	161171-161299
	405187	7229826	Plus	117025-117170,118567-118736
75	405217	7239551	Plus	32646-33138
	405232	7249042	Plus	125904-126063
	405243	7249201	Minus	22312-23197
	405327	6094661	Minus	120550-120750
	405378	6491714	Plus	91139-91440
80	405420	7211837	Minus	13428-13582
	405703	4240388	Minus	15850-16061
	405737	9943984	Minus	104275-104508,104755-104877
	405895	7677903	Minus	66990-67484
	406059	9103984	Minus	13856-14004

5	406101	9124019	Plus	125325-125831
	406118	9143818	Plus	53997-54629
	406150	9886026	Minus	59331-59701
	406158	7144874	Plus	62393-63016,65012-65578
	406343	9255974	Plus	17284-17440,18489-18646,18917-19004,19384-19538
	406357	9256093	Minus	77181-77415
	406563	7711604	Plus	34401-34538

10

TABLE 29A: 2286 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO NORMAL BODY

15 Table 29A lists about 2286 genes that are up regulated in idiopathic pulmonary fibrosis samples as compared with normal "body map" samples. These were selected from about 59580 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis expression level to "average" normal adult tissues sample expression was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

20 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF to normal body tissue

25	Pkey	ExAccn	Unigene ID	Unigene Title	R1
30	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	211.8
	442275	AW449467	Hs.54795	ESTs	189.7
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	134.1
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	130.4
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	116.8
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	92.1
35	406964	M21305		gb:Human alpha satellite and satellite 3	80.7
	443709	AI082692	Hs.134662	ESTs	67.1
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	61.4
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	57.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	54.6
	457200	U33749	Hs.197764	thyroid transcription factor 1	44.9
40	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	42.7
	443324	R44013	Hs.164225	ESTs	39.8
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	27.3
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypotheti	27.1
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	27.1
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	26.9
45	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	22.2
	421659	NM_014459	Hs.106511	protocadherin 17	21.0
	450478	AW451709	Hs.271200	ESTs	20.2
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	19.7
	447033	AJ357412	Hs.157601	ESTs	19.4
	445885	AI734009	Hs.127699	KIAA1603 protein	18.9
50	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	17.9
	432437	W07088	Hs.293685	ESTs	17.8
	424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	17.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	17.2
	440807	AW269421	Hs.128093	ESTs	16.7
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	16.4
55	433365	AF026944	Hs.293797	ESTs	16.4
	445279	R41900	Hs.22245	ESTs	16.4
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	16.4
	405654				16.1
	449328	AI962493	Hs.197647	ESTs	16.1
	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	15.7
60	408826	AF216077	Hs.46376	Homo sapiens clone HB-2 mRNA sequence	15.5
	417728	AW138437	Hs.24780	KIAA1573 protein	15.0
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	14.8
	452039	AI922988	Hs.172510	ESTs	14.4
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	14.3
	421464	AA291553	Hs.190086	ESTs	14.1
65	421554	AW137876	Hs.97775	ESTs	13.8
	431889	AA521277	Hs.124946	ESTs, Weakly similar to A46010 X-linked	13.2
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	13.2
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	12.9
	459702				12.7
	421110	AJ250717	Hs.1355	cathepsin E	12.6
70	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	12.8
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	12.5
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	12.2
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	12.1
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	12.1
	451561	N52812	Hs.177403	ESTs	12.0
75	424086	AI351010	Hs.102257	lysyl oxidase	12.0
	435299	AI745458	Hs.122614	ESTs, Weakly similar to T20593 hypotheti	12.0
	429496	AA453800	Hs.192793	ESTs	11.9

	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
	436081	AJ248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fs, clone C	11.2
5	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	10.9
	421470	R27496	Hs.1378	annexin A3	10.8
	440209	H05049	Hs.22269	neurexin 3	10.8
	428927	AA441837	Hs.90250	ESTs	10.7
	448593	AW004854	Hs.228320	hypothetical protein FLJ23537	10.5
	424717	H03754	Hs.152213	wingless-type MMTV integration site faml	10.4
10	416402	NM_000715	Hs.1012	complement component 4-binding protein,	10.4
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.4
	442176	AA983764	Hs.128910	ESTs	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
	452883	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	10.3
15	417015	M83772	Hs.80876	flavin containing monooxygenase 3	10.3
	422022	AA302420	Hs.200442	ESTs	10.3
	447724	AW298375	Hs.24477	ESTs	10.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	10.0
20	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	9.9
	446232	AJ281848	Hs.194691	retinoic acid induced 3	9.9
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	9.9
	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	9.8
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	9.8
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 (H	9.8
25	407568	AA740964	Hs.62699	ESTs	9.8
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fs, clone L	9.6
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	9.5
	441484	AA935481	Hs.58972	ESTs	9.5
	422426	W79117	Hs.58559	ESTs	9.4
30	406747	AI925153	Hs.217493	annexin A2	9.4
	450050	AI681268	Hs.257883	ESTs	9.4
	431337	N48107	Hs.292593	ESTs	9.3
	408427	AW194270	Hs.177236	ESTs	9.3
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	9.3
35	453636	R67837	Hs.169872	ESTs	9.3
	443450	N66045	Hs.133529	ESTs	9.2
	418735	N48769	Hs.44609	ESTs	9.2
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	9.1
40	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	9.1
	441233	AA972965	Hs.135568	ESTs	9.1
	459587	AA031956		gbzrk15e04.s1 Soares_pregnanUterus_NbH	9.0
	436246	AW450963	Hs.119991	ESTs	9.0
	445189	AI936450	Hs.147482	ESTs	8.9
45	410781	AI375672	Hs.165028	ESTs	8.9
	446868	AV660737	Hs.135100	ESTs	8.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.8
	414988	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	8.8
50	410334	AW979261	Hs.291993	ESTs	8.8
	442510	AF150179	Hs.249890	ESTs	8.8
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	8.7
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	8.7
	444929	AI685841	Hs.161354	ESTs	8.7
55	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	8.6
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	8.6
	412719	AW016610	Hs.129911	ESTs	8.6
	453445	AL036532	Hs.91453	ESTs	8.5
	419261	X07876	Hs.89791	wingless-type MMTV integration site faml	8.5
60	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.5
	433815	AI696602	Hs.112757	ESTs	8.3
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.3
	451103	R52804	Hs.25956	DKFZP564D206 protein	8.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.3
65	424989	AA985520	Hs.23575	ESTs	8.3
	433231	AB040926	Hs.143552	KIAA1493 protein	8.2
	408217	AI433201	Hs.279860	tumor protein, translationally-controlled	8.1
	431808	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	8.1
	436751	AA732217	Hs.294054	ESTs	8.0
70	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLIA	8.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	8.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	7.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	7.8
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	7.8
75	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.7
	421013	M62397	Hs.1345	mutated in colorectal cancers	7.7
	437479	R61866	Hs.101277	ESTs	7.6
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	7.6
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 nbos	7.6
	444396	T65213	Hs.4257	ESTs	7.6
80	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fs, clone H	7.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.6
	445495	BE622641	Hs.36489	ESTs, Weakly similar to I38022 hypotheti	7.6
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	7.6

5	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.5
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5
	416030	H15261	Hs.21948	ESTs	7.5
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp58680220 (f	7.4
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	7.4
10	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	7.3
	432133	AB033088	Hs.272567	KIAA1262 protein	7.3
	447112	H17800	Hs.7154	ESTs	7.3
	446917	AI347863	Hs.156672	ESTs	7.3
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.3
15	431761	AW002846	Hs.105468	hypothetical protein FLJ22690	7.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	7.2
	413499	BE144884		gb:CMO-HT0182-041099-065-e11 HT0182 Homo	7.2
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	7.2
	438122	AI620270	Hs.129837	ESTs, Weakly similar to Z263_HUMAN ZINC	7.2
20	449611	AI970394	Hs.197075	ESTs	7.2
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	7.2
	410060	NM_001448	Hs.58367	glypican 4	7.2
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
	452571	W31518	Hs.34665	ESTs	7.2
25	453736	AL118674	Hs.34871	zinc finger homeobox 1B	7.2
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	7.2
	405494				7.2
	442832	AW206560	Hs.253569	ESTs	7.1
	420193	AI460080	Hs.202869	ESTs	7.1
30	434217	AW014795	Hs.23349	ESTs	7.0
	427356	AW023482	Hs.97849	ESTs	7.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.9
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.9
	442377	AA993807	Hs.167367	ESTs	6.9
35	441143	AI027604	Hs.159650	ESTs	6.9
	445122	AW241632	Hs.147377	hypothetical protein FLJ23598	6.9
	431353	AA828032	Hs.189076	ESTs	6.9
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.8
	426753	T89832	Hs.170278	ESTs	6.8
40	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.8
	451963	AI825440	Hs.224952	ESTs	6.8
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.8
	433426	H69125	Hs.133525	ESTs	6.8
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	6.8
45	415236	R41400		gb:yr94b12.s1 Soares infant brain 1N1B H	6.8
	409031	AA376836	Hs.76728	ESTs	6.7
	427558	O49493	Hs.2171	growth differentiation factor 10	6.7
	437259	AJ377755	Hs.120695	ESTs	6.7
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	6.7
50	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	6.7
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	6.7
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	6.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high effi	6.7
	424750	D29956	Hs.152818	ubiquitin specific protease 8	6.6
55	403574				6.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	6.6
	415025	AW207091	Hs.72307	ESTs	6.5
	448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	6.5
	444271	AW452569	Hs.149804	ESTs	6.5
60	437157	BE048860	Hs.120655	ESTs	6.5
	444050	AW138295	Hs.135024	ESTs	6.5
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	6.5
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	6.5
	424433	H04607	Hs.9218	ESTs	6.4
65	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	6.4
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	6.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	6.4
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	6.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	6.3
70	417246	AI760098	Hs.21411	ESTs	6.3
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	6.3
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	6.3
	438909	AF085639		gb:Homo sapiens full length insert cDNA	6.3
	446002	AI346468	Hs.145789	ESTs	6.3
75	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	6.3
	424202	BE350295	Hs.15032	RAN binding protein 17	6.3
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.2
	415511	AI732617	Hs.182362	ESTs	6.2
80	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.2
	416879	H98899	Hs.42599	ESTs	6.2
	432803	AA565398		gb:rnk41f01.s1 NCI_CGAP_GC2 Homo sapiens	6.2
	442852	BE080429	Hs.15738	ESTs	6.2
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	6.2
	441082	AW444804	Hs.202655	ESTs	6.2
	404599				6.1
	453931	AL121278	Hs.25144	ESTs	6.1

	420252	AW270404	Hs.193161	ESTs	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	456954	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.1
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	419172	AW338625	Hs.22120	ESTs	6.0
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.0
	453037	AA045175	Hs.177552	ESTs	6.0
10	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.0
	431159	AW971240	gb:EST383329	MAGE resequences, MAGL Homo	6.0
	422352	AA766296	Hs.99200	ESTs	5.9
	433527	AW235613	Hs.133020	ESTs	5.9
	420077	AW512260	Hs.87767	ESTs	5.9
15	429703	T93154	Hs.28705	ESTs	5.9
	433098	AW190593	Hs.151143	ESTs	5.9
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	5.9
	449416	AI651016	Hs.246311	ESTs	5.9
	459023	AW968226	Hs.60798	ESTs	5.9
20	450584	AA040403	Hs.60371	ESTs	5.9
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.9
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothetical	5.9
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	5.9
	433479	AW511459	Hs.249972	ESTs	5.8
	443113	AI040686	Hs.132908	ESTs	5.8
25	430414	AW365665	Hs.120388	ESTs	5.8
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	5.8
	435420	AI928513	Hs.59203	ESTs	5.8
	404916				5.8
30	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.8
	448253	H25899	Hs.201591	ESTs	5.8
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.8
	446567	AI699629	Hs.156781	ESTs	5.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	5.7
35	438842	AA827176	Hs.124316	ESTs	5.7
	437260	AA747807	Hs.149500	ESTs	5.7
	410934	AW811114	gb:MR2-ST0131-111199-016-a04	ST0131 Homo	5.7
	428043	T92248	Hs.2240	uteroglobin	5.7
	408045	AW138959	Hs.245123	ESTs	5.7
40	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	5.7
	428508	BE252383	Hs.184668	SBBI31 protein	5.7
	453393	AW956392	Hs.110376	ESTs	5.6
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	5.6
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.6
45	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	5.6
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	404043				5.5
50	415094	D59513	Hs.330778	ESTs	5.5
	453049	BE537217	Hs.30343	ESTs	5.5
	430153	AW968128	Hs.336679	ESTs	5.5
	410811	AW805687	Hs.300648	ESTs	5.5
	443903	AI220547	Hs.135223	ESTs	5.5
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	5.5
55	444471	AB020684	Hs.11217	KIAA0877 protein	5.5
	452542	AW812256	gb:RCO-ST0174-191099-031-a07	ST0174 Homo	5.5
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.5
	432113	AA935065	Hs.152385	ESTs	5.5
	446608	N75217	Hs.257846	ESTs	5.5
60	419945	AW290975	Hs.118923	ESTs	5.5
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	5.4
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	5.4
	439382	BE247684	Hs.103070	ESTs	5.4
	428895	AA437124	Hs.187247	ESTs	5.4
65	446577	AB040933	Hs.15420	KIAA1500 protein	5.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	427778	AA412323	Hs.105323	ESTs	5.4
	437138	AI935622	Hs.271245	ESTs	5.4
	431322	AW970622	gb:EST382704	MAGE resequences, MAGK Homo	5.4
70	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.4
	435202	AI971313	Hs.170204	KIAA0551 protein	5.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	5.3
	434992	AA658501	Hs.283358	ESTs	5.3
	454039	AW079064	Hs.245540	ESTs	5.3
75	456408	AI288348	Hs.23450	mitochondrial ribosomal protein S25	5.3
	406554				5.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1048 (I	5.3
	416769	AI339257	Hs.115436	ESTs, Moderately similar to I54374 gene	5.3
	414299	AA142989	Hs.71730	ESTs	5.3
80	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.3
	459664				5.3
	425509	AF079363	Hs.158213	sperm associated antigen 6	5.3
	401497				5.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	5.2

5	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.2
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypothetical	5.2
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
	400297	AJ127076	Hs.334473	hypothetical protein DKFZp564O1278	5.2
10	404957				5.2
	452771	T05477	Hs.333265	ESTs	5.2
	438885	AJ886558	Hs.184987	ESTs	5.2
	428244	AJ564123	Hs.42500	ADP-ribosylation factor-like 5	5.2
	420481	U50525	Hs.88201	Human BRCA2 region, mRNA sequence CG029	5.2
15	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2
	408729	AA195764	Hs.72639	ESTs	5.1
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	5.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.1
	417154	AJ674701	Hs.21388	ESTs	5.1
20	411869	W20027	Hs.23439	ESTs	5.1
	427043	AA397679	Hs.3991	ESTs	5.1
	445635	AJ769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	429273	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23158 f1s, clone L	5.1
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	5.1
25	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.1
	408677	AJ279892	Hs.46801	sorting nexin 14	5.0
	404097				5.0
	437636	AA764781	Hs.291844	ESTs	5.0
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.0
30	410733	D84284	Hs.66052	CD38 antigen (p45)	6.0
	439140	W85737	Hs.290830	ESTs	5.0
	407366	AF025942		gb:Homo sapiens c1g33 mRNA, partial sequ	5.0
	405547				5.0
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	5.0
35	449168	NM_016206	Hs.23142	colon carcinoma related protein	5.0
	455431	AW938484		gb:CMO-DT0057-290200-253-d06 DT0057 Homo	5.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 f1s, clone PL	5.0
	411149	N68715	Hs.269128	ESTs	5.0
	432441	AW292425	Hs.163484	ESTs	5.0
40	419807	R77402		gb:yl75f11.s1 Soares placenta Nb2HP Homo	5.0
	440615	AJ733055	Hs.130806	ESTs	5.0
	450109	AJ539295	Hs.115740	KIAA0210 gene product	5.0
	449695	AA164569	Hs.34550	ESTs	5.0
	421764	AJ681535	Hs.148135	serine/threonine kinase 33	4.9
45	404593				4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (f	4.9
	419235	AW470411	Hs.288433	neurotrimin	4.9
	436304	AA339622	Hs.108887	ESTs	4.9
50	434613	AJ821826		gb:ns92b10.x5 NCL_CGAP_Pr3 Homo sapiens	4.9
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.9
	415245	N59650	Hs.27252	ESTs	4.9
	428780	AJ478578	Hs.50636	ESTs	4.9
	406333				4.9
55	445034	AW293376	Hs.143659	ESTs	4.8
	440202	AW516211	Hs.125300	ring finger protein 21, Interferon-respo	4.8
	424638	AJ472106	Hs.49303	Homo sapiens cDNA FLJ11663 f1s, clone HE	4.8
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	4.8
	427652	AJ673025	Hs.43874	ESTs, Moderately similar to I54374 gene	4.8
60	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.8
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415261	T40928	Hs.8346	ESTs	4.8
	453543	AA485425	Hs.48919	Homo sapiens cDNA FLJ11508 f1s, clone HE	4.8
65	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 f1s, clone HE	4.8
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	4.8
	441006	AW605267	Hs.7627	CGI-60 protein	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypotheti	4.8
70	453197	AJ916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.8
	439398	AA284287	Hs.221504	ESTs	4.8
	436397	AA715013	Hs.169835	ESTs	4.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
75	425916	NM_006786	Hs.162200	urotensin 2	4.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	4.8
	427457	AW779105	Hs.164682	ESTs	4.7
	451620	AW449888	Hs.257224	ESTs	4.7
	408938	AA059013	Hs.22607	ESTs	4.7
80	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	4.7
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 f1s, clone PL	4.7
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.7
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	435347	AW014873	Hs.116963	ESTs	4.7
	425458	H89317	Hs.182889	ESTs	4.7
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	4.7

	436594	AI419982	Hs.156189	ESTs	4.7
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	4.7
	432731	R31178	Hs.287820	fibronectin 1	4.7
5	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.7
	426320	W47595	Hs.169300	transforming growth factor, beta 2	4.7
	419751	AW195581	Hs.93121	KIAA0761 protein	4.6
	433515	AA595800	Hs.190246	ESTs	4.6
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.6
10	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	4.6
	406992	S82472		gb:beta-pol-DNA polymerase beta (exon a	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	435933	AA805520	Hs.192075	ESTs	4.6
15	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	4.6
	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypotheti	4.6
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapi	4.6
20	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.6
	416258	N45661	Hs.90011	adenylosuccinate synthase	4.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	4.6
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	4.5
	422977	AG631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	4.5
25	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.5
	432015	AL157504	Hs.159115	Homo sapiens mRNA: cDNA DKFZp586O0724 (f	4.5
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	4.5
	409041	AB033025	Hs.50081	KIAA1199 protein	4.5
30	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.5
	452526	W38537	Hs.280740	hypothetical protein MGC3040	4.5
	403271				4.5
	450656	AA010539	Hs.18912	ESTs	4.5
	446096	AI276454		gb:ql71a12.x1 Soares_NhHMPu_S1 Homo sapi	4.5
35	454036	AA374758	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	437960	AI669586	Hs.222194	ESTs	4.5
	440862	H39048	Hs.127432	ESTs	4.5
	410615	AW772721		gb:h195c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.5
	413583	AL120808	Hs.5888	ESTs	4.5
40	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	4.5
	442324	R63578	Hs.28426	ESTs	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
	446509	AF169693	Hs.132892	protocadherin 20	4.4
45	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.4
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.4
	448089	AI467945	Hs.173696	ESTs	4.4
	434387	AB020700	Hs.3830	KIAA0893 protein	4.4
	434757	AI038997	Hs.132921	ESTs	4.4
50	413453	AA129640	Hs.128065	ESTs	4.4
	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	456154	AW816379	Hs.335018	ESTs	4.4
	430417	AA461045	Hs.50701	ESTs	4.4
	434819	AA650099	Hs.291541	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.4
55	438796	W67821	Hs.109590	genethonin 1	4.4
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.4
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.4
	414812	X72755	Hs.77367	monokine Induced by gamma Interferon	4.4
	451895	T93573	Hs.16970	ESTs	4.4
60	435434	AA680387	Hs.187850	ESTs	4.4
	449623	C00719	Hs.120440	EST	4.4
	433563	AI732637	Hs.277901	ESTs	4.3
	444649	AW207523	Hs.197628	ESTs	4.3
	441594	AL041080	Hs.208765	ESTs, Moderately similar to ALU7_HUMAN A	4.3
65	443314	AW771701	Hs.54646	ESTs	4.3
	400292	AA250737	Hs.72472	ESTs	4.3
	427972	AA864870	Hs.181304	putative gene product	4.3
	446932	AA961459	Hs.125644	ESTs	4.3
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.3
70	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.3
	400608				4.3
	411156	AW819939	Hs.273629	ESTs	4.3
	435772	AA700019	Hs.132992	ATP-binding cassette, sub-family G (WHIT	4.3
75	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	4.3
	455511	BE144762		gb:CMO-HT0180-041099-065-b04 HT0180 Homo	4.3
	443257	AI334040	Hs.11614	HSPC065 protein	4.3
	436033	H75391	Hs.255748	ESTs	4.3
	420214	AI146375	Hs.286073	ESTs, Moderately similar to ALU5_HUMAN A	4.3
80	410519	AW612264	Hs.131705	ESTs	4.3
	401189				4.3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3

	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	4.3
	434677	AW444575	Hs.130834	ESTs	4.3
	403310				4.3
5	451830	H18433	Hs.21542	KIAA1035 protein	4.3
	422222	AI699372	Hs.193247	hypothetical protein DKFZp434A171	4.3
	435627	W88774	Hs.118370	ESTs	4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	452166	AI948607	Hs.264680	ESTs	4.3
10	413998	AW103807	Hs.243933	ESTs	4.2
	416642	T96118	Hs.226313	ESTs	4.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	4.2
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypotheti	4.2
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.2
15	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	4.2
	424641	AB001106	Hs.151413	glia maturation factor, beta	4.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
	458771	AW295151	Hs.163612	ESTs	4.2
20	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	4.2
	436645	AW023424	Hs.156520	ESTs	4.2
	426083	AW952712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	4.2
	445268	AI218358	Hs.175048	ESTs	4.2
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.2
25	431917	D16181	Hs.2868	peripheral myelin protein 2	4.2
	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, dal	4.2
	443151	AI827193	Hs.132714	ESTs	4.2
	419255	AA235672	Hs.87491	ESTs	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
30	452561	AI692181	Hs.49169	KIAA1634 protein	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	424268	AA397653	Hs.307438	Human DNA sequence from clone 495010 on	4.2
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	4.2
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	4.2
35	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	4.2
	428771	AB028992	Hs.193143	KIAA1069 protein	4.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	4.1
	417009	AA191719	Hs.314714	ESTs	4.1
	436517	BE080932	Hs.135225	ESTs	4.1
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.1
	414083	AL121282	Hs.257786	ESTs	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	4.1
	441802	AA968636	Hs.127877	ESTs	4.1
45	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.1
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	4.1
	444009	AI380792	Hs.135104	ESTs	4.1
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	4.1
50	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	4.1
	428104	AA421350	Hs.191604	ESTs	4.1
	439648	AW780192	Hs.267596	ESTs	4.1
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.1
55	446364	AB006624	Hs.14912	KIAA0286 protein	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	4.0
	404561				4.0
	401575				4.0
60	419298	AA236115	Hs.120785	ESTs	4.0
	432055	AW972359	Hs.293334	ESTs	4.0
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	4.0
	450320	AW291775	Hs.213793	ESTs	4.0
65	447350	AI375572	Hs.172634	ESTs	4.0
	441974	AI683782	Hs.128245	ESTs	4.0
	453142	AA033648	Hs.7473	ESTs	4.0
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.0
	410292	AA843087	Hs.124194	ESTs	4.0
70	415811	AA450181	Hs.172963	hypothetical protein FLJ14624	4.0
	420218	AW958037	Hs.286	ribosomal protein L4	4.0
	426625	T78300	Hs.300642	serologically defined colon cancer anti	4.0
	417708	N74392	Hs.50495	ESTs	4.0
	451024	AA442176		gb:zw63b08.r1 Soares_tetal_fetus_Nb2HF8_	4.0
75	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	422058	AA862231	Hs.334443	ESTs	4.0
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	4.0
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.0
80	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.0
	453096	AW294631	Hs.11325	ESTs	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
	421002	AF116030	Hs.100932	transcription factor 17	4.0
	445414	AV553692	Hs.146105	ESTs	4.0

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.0
	451353	N21043	Hs.42932	ESTs	4.0
	437075	AA743748	Hs.40758	ESTs	3.9
5	410505	AW752139	Hs.314323	ESTs	3.9
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.9
	426116	AA668729	Hs.144694	ESTs	3.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
10	417718	T86540	Hs.193981	ESTs	3.9
	436772	AW975688	Hs.74170	metallothionein 1E (functional)	3.9
	401045				3.9
	408767	AA057279	Hs.211928	ESTs	3.9
	407303	AA016296	Hs.165200	ESTs, Weakly similar to A56194 thromboxa	3.9
15	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	3.9
	451623	H77818	Hs.268991	ESTs	3.9
	450063	AI681509	Hs.277133	ESTs	3.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.9
	419276	BE165909	Hs.306881	MSTP043 protein	3.9
20	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	422667	H25642	Hs.133471	ESTs	3.9
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.9
	458219	H22195	Hs.31874	ESTs	3.9
25	443613	AI079356		gb:oz39b09.s1 Soares_NhiHMPu_S1 Homo sapi	3.9
	439810	AL109710	Hs.85568	EST	3.9
	436578	AI091435	Hs.134859	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	425087	R62424	Hs.126059	ESTs	3.9
30	454111	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	3.9
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	3.9
	452468	N84635	Hs.29664	hypothetical protein DKFZp564B052	3.9
	424962	NM_012288	Hs.153954	TRAM-like protein	3.9
	435823	R07856	Hs.16355	ESTs	3.9
35	440633	AI140686	Hs.263320	ESTs	3.9
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	3.9
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked mol	3.9
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
	417461	R38403	Hs.13305	ESTs	3.9
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (I	3.8
	419140	AI982647	Hs.215725	ESTs	3.8
	415652	T79213	Hs.272073	ESTs	3.8
	430140	AW296771	Hs.221999	ESTs	3.8
45	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.8
	422165	AL041199	Hs.1481	histidine decarboxylase	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.8
	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.8
50	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.8
	449729	R72032	Hs.29235	ESTs	3.8
	414700	H63202	Hs.38163	ESTs	3.8
	440899	AW449445	Hs.120021	DKFZP434I092 protein	3.8
	438335	AA742697	Hs.62492	ESTs, Weakly similar to B39068 prolina-r	3.8
55	408625	AW243323	Hs.266785	ESTs	3.8
	421987	AI133161	Hs.286131	CGI-101 protein	3.8
	418915	AI474778	Hs.118977	ESTs	3.8
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.8
	428846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	442849	R10099	Hs.269805	ESTs	3.8
60	427191	BE221825	Hs.97691	ESTs	3.8
	407942	AA376608	Hs.5894	hypothetical protein FLJ10305	3.8
	437030	AA742577	Hs.303781	EST	3.8
	427940	AAA17812	Hs.38775	ESTs	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
65	449679	AI823951	Hs.129700	tollold-like 1	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	458663	AV584444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439957	AI453184	Hs.66357	ESTs	3.7
70	446999	AA151520	Hs.334822	hypothetical protein MGC4485	3.7
	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.7
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.7
	418379	AA218940	Hs.137516	fidgetin-like 1	3.7
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068	3.7
75	443584	AI807035	Hs.267245	hypothetical protein FLJ14803	3.7
	416185	AW975861	Hs.47367	KIAA1785 protein	3.7
	417235	AA810278	Hs.24250	ESTs	3.7
	441720	AI346487	Hs.28739	ESTs	3.7
80	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	417355	D13168	Hs.82002	endothelin receptor type B	3.7
	449321	AA001150	Hs.132937	ESTs	3.7
	424806	AA382523	Hs.105689	MSTP031 protein	3.7
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	3.7
	409248	AB033035	Hs.51965	KIAA1209 protein	3.7

	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.7
	420026	AI831190	Hs.166676	ESTs	3.7
5	429419	AB023226	Hs.202276	KIAA1009 protein	3.7
	447410	AI470235	Hs.172698	EST	3.7
	404274				3.7
	416320	H47867	Hs.34024	ESTs	3.7
10	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoletin A;	3.7
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.7
	446025	AW305075	Hs.180948	KIAA0729 protein	3.7
	450458	AA009925		gb:z107e05.r1 Soares_fetal_liver_spleen_	3.7
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor I	3.6
	438257	AW474419	Hs.224794	ESTs	3.6
15	440887	AI799488	Hs.135905	ESTs	3.6
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.6
20	407726	AA435679	Hs.88594	ESTs	3.6
	436026	AI349764	Hs.217081	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	452293	AI871833	Hs.304609	ESTs	3.6
	426330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.6
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.6
25	429208	AA447990	Hs.190478	ESTs	3.6
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	3.6
	404476				3.6
	405848				3.6
30	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	3.6
	437641	AA811452	Hs.291911	ESTs	3.6
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.6
35	446102	AW168067	Hs.252956	ESTs	3.6
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	446453	AV658469	Hs.188546	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
40	452055	AI377431	Hs.141693	hypothetical protein MGC10858	3.6
	440801	AA906366	Hs.190535	ESTs	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	440886	AW511032	Hs.190516	ESTs	3.6
	401049				3.6
45	449424	AW448937	Hs.197030	ESTs	3.6
	418076	R61388	Hs.6724	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	3.6
	438016	AI949638	Hs.336846	EST	3.6
50	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.6
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	3.5
	456536	AW135986	Hs.257859	ESTs	3.5
	428679	AA431765		gb:zw80c03.s1 Soares_tastis_NHT Homo sap	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
55	435344	AA700326	Hs.190599	ESTs	3.5
	445056	AB014530	Hs.12259	KIAA0630 protein	3.5
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.5
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	3.5
60	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	3.5
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.5
	428409	AW117207	Hs.98523	ESTs	3.5
	431087	H12723	Hs.290791	ESTs	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
65	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	437583	AA761190	Hs.244627	ESTs	3.5
	421599	AA293655	Hs.97293	ESTs	3.5
	433687	AA743991		gb:my57g01.s1 NCL_CGAP_Pr18 Homo sapiens	3.5
70	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	3.5
	430499	AW969408	Hs.231991	ESTs	3.5
	451531	AA018311	Hs.114762	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	410658	AW105231	Hs.192035	ESTs	3.5
	427865	AA416931	Hs.126065	ESTs	3.5
75	453390	AA862496	Hs.28482	ESTs	3.5
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	427718	AI798680	Hs.25933	ESTs	3.5
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.5
80	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	442080	AW444761	Hs.44565	ESTs	3.5
	405685	M18728		gb:Human nonspecific crossreacting anti	3.5

	404200			3.5
	417976	BE565892	Hs.83077	Interleukin 18 (Interferon-gamma-inducin
	433285	AW975944	Hs.237396	ESTs
	432868	AW974093	Hs.292775	ESTs
5	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1
	428804	AK000713	Hs.193736	hypothetical protein FLJ20706
	428775	AA434579	Hs.143691	ESTs
	410004	AI298027	Hs.5057	carboxypeptidase D
10	422093	AF151852	Hs.111449	CGI-94 protein
	441736	AW292779	Hs.169799	ESTs
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor
	405970			ESTs
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112
15	459482	AA625339	Hs.237052	EST, Weakly similar to I38022 hypothetic
	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar
	402230			ESTs
20	436120	AI248193	Hs.119860	ESTs
	405336			ESTs
	434374	AA631439		gb:np85d02.s1 NCL_CGAP_Thy1 Homo sapiens
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S
	416057	AI927382	Hs.29857	ESTs
25	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r
	436088	AA704687	Hs.191294	ESTs
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp
	454076	AW204712	Hs.61957	ESTs
	431733	AW298410	Hs.21475	ESTs
30	432974	BE348793	Hs.233331	ESTs
	412576	AA447718	Hs.107057	ESTs
	446142	AI754693	Hs.145958	ESTs
	447432	AW958473	Hs.301957	nucleoside diphosphate linked mol
	433384	AI021992	Hs.124244	ESTs
35	413621	AI808648	Hs.184156	ESTs
	419546	AA244199		gb:nc06c05.s1 NCL_CGAP_Pr1 Homo sapiens
	436111	AI803082	Hs.157212	ESTs
	421236	AI287622	Hs.151956	ESTs
40	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1
	403515			ESTs
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protein
	453375	AI990114	Hs.240091	ESTs
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT
45	412209	AW901458		gb:RCO-NN1012-270300-031-c07 NN1012 Homo
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi
	409642	AW450809	Hs.257347	ESTs
	420092	AA814043	Hs.89045	ESTs
	453365	AA035211	Hs.17404	ESTs
50	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT
	439024	R96696	Hs.35598	ESTs
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedin
	417991	AA731452	Hs.190008	ESTs
	403356			ESTs
55	433650	AA603472	Hs.28456	ESTs
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retrovira
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970
	413714	AI560944	Hs.71428	ESTs
60	430887	N66801	Hs.260287	KIAA1841 protein
	413618	BE154078		gb:PM0-HT0339-200400-010-F04 HT0339 Homo
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr
	436168	AK000883	Hs.301845	Homo sapiens cDNA FLJ10021 fis, clone HE
	405692			ESTs
65	432809	AA565509	Hs.131703	ESTs
	433805	AA705910	Hs.112742	ESTs
	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hergulin
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro
70	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo
	410434	AF051152	Hs.63668	tol-like receptor 2
	416421	AA134008	Hs.79306	eukaryotic translation initiation factor
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l
	444301	AK000136	Hs.10760	asporin (LRR class 1)
75	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl
	458924	BE242158	Hs.24427	DKFZP566O1646 protein
	435934	R19382	Hs.117869	ESTs
	400269			ESTs
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
80	412903	BE007967	Hs.155795	ESTs
	400889			ESTs
	449585	AI655321	Hs.197693	ESTs
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C
	418557	BE140602	Hs.245645	ESTs

5	453204	R10799	Hs.191990	ESTs	3.3
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446545	AI336596	Hs.156294	ESTs	3.3
10	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	3.3
	408761	AA057254	Hs.238936	ESTs, Weakly similar to (define not ava	3.3
	403895				3.2
	414899	AW975433	Hs.36288	ESTs	3.2
15	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.2
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
20	443830	AI142095	Hs.143273	ESTs	3.2
	454982	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_UI2 Homo sapiens	3.2
	417561	AW974345		gb:EST386449 MAGE resequences, MAGM Homo	3.2
	446063	AI720140	Hs.151079	ESTs	3.2
25	423609	AA328348	Hs.218289	ESTs	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.2
	435808	AA702866	Hs.113150	ESTs	3.2
	424001	W67883	Hs.137476	paternally expressed 10	3.2
30	415635	F13168		gb:HSC3JF101 normalized Infant brain cDN	3.2
	418946	AI798841	Hs.164526	ESTs	3.2
	431750	AA514986	Hs.283705	ESTs	3.2
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.2
	428268	AA424957	Hs.294132	ESTs	3.2
35	418878	W20090	Hs.6616	ESTs	3.2
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.2
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	3.2
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.2
	404588				3.2
40	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens	3.2
	407339	AA777542	Hs.132670	ESTs	3.2
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	3.2
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.2
45	419340	AA236590	Hs.87530	ESTs	3.2
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fts, clone CO	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	421187	NM_014721	Hs.102471	KIAA0680 gene product	3.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.2
50	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.2
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.2
	438839	AW297945	Hs.128490	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	427961	AW293165	Hs.143134	ESTs	3.2
55	429228	AI553633	Hs.337139	ESTs	3.2
	431548	AI834273	Hs.9711	novel protein	3.1
	441839	AW975512	Hs.29160	ESTs	3.1
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
60	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	436154	AA764950	Hs.119898	ESTs	3.1
	406752	AI285598		gb:qu49f06.x1 NCI_CGAP_Lym6 Homo sapiens	3.1
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fts, clone HE	3.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
65	435739	BE208022	Hs.127685	KIAA1627 protein	3.1
	451674	AA019104	Hs.175483	Homo sapiens cDNA: FLJ22016 fts, clone H	3.1
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	3.1
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
70	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	3.1
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	3.1
	456551	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.1
75	431814	BE256242	Hs.270847	delta-tubulin	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	436401	AI087958	Hs.29088	ESTs	3.1
	437439	H29796	Hs.269622	ESTs	3.1
	403277				3.1
80	408547	AA574291	Hs.57837	ESTs	3.1
	424131	AA335714	Hs.199665	ESTs	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	3.1
	434636	AA083764	Hs.6101	hypothetical protein MGC3178	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fts, clone NT	3.1
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fts, clone NT	3.1
	407905	AW103655	Hs.252905	ESTs	3.1
	452311	AW304029	Hs.252744	ESTs	3.1

5	434849	AW292765	Hs.8053	ESTs	3.1
	446770	AV660309	Hs.154986	ESTs, Weakly similar to PLLP_HUMAN PLASM	3.1
	424238	AA337401	Hs.137635	ESTs	3.1
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.1
	447829	AI433029	Hs.164104	ESTs	3.1
10	406506				3.1
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.1
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.1
	451229	AW967707	Hs.48473	ESTs	3.1
	401103				3.1
15	433589	AA886530	Hs.188912	ESTs	3.1
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypotheti	3.1
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypotheti	3.1
	404288				3.1
	406195				3.1
20	438202	AW169287	Hs.22588	ESTs	3.1
	425516	BE000707	Hs.29567	ESTs	3.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.1
	422692	AA332376	Hs.24135	transmembrane protein vezatin; hypotheti	3.1
	435414	AW270550	Hs.116957	ESTs	3.1
25	418950	T78517	Hs.13941	ESTs	3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	3.1
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.1
	459371	R20991		gb:yg06h01.r1 Soares infant brain 1N18 H	3.1
30	421823	N40850	Hs.28625	ESTs	3.1
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.1
	452896	AA831508	Hs.32553	ESTs	3.1
	425895	AI269484	Hs.161427	zinc finger protein 215	3.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	3.1
35	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	3.1
	401862				3.1
	444325	AW152618	Hs.16757	ESTs	3.1
	408171	AA301228	Hs.43299	hypothetical protein FLJ12890	3.1
	423949	AI014546	Hs.130912	ESTs	3.1
40	419519	AI198719	Hs.176376	ESTs	3.0
	434683	AW298724	Hs.202639	ESTs	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	415086	AI597963	Hs.118726	ESTs	3.0
	419220	AA811938	Hs.291759	ESTs	3.0
45	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	3.0
	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
50	443253	AI041212	Hs.132117	ESTs	3.0
	444974	AI203500	Hs.151612	ESTs	3.0
	445717	AW664658	Hs.149332	ESTs	3.0
	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
55	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.0
	424406	D54120	Hs.146409	cell division cycle 42 (GTP-binding prot	3.0
	410371	AA084482	Hs.115850	ESTs	3.0
	426384	AI472078	Hs.303662	ESTs	3.0
	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	3.0
60	427050	AA397789	Hs.161803	ESTs	3.0
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	3.0
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	3.0
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	3.0
	455601	AI368680	Hs.816	SRX (sex determining region Y)-box 2	3.0
65	447482	AB033059	Hs.18705	KIAA1233 protein	3.0
	439416	W58294	Hs.56254	ESTs	3.0
	436835	AW104325	Hs.272093	ESTs, Weakly similar to I78885 serine/th	3.0
	419088	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.0
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	3.0
70	415452	F09134	Hs.12839	ESTs	3.0
	427874	AA732367	Hs.98198	ESTs	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	3.0
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	3.0
75	415122	D60708	Hs.22245	ESTs	3.0
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.0
	400227				3.0
	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	3.0
	419503	AA243642	Hs.137422	ESTs	3.0
80	446563	BE326588	Hs.141454	ESTs	3.0
	457285	AI038858	Hs.130522	Kv channel-interacting protein 1	3.0
	434998	AW975157	Hs.26037	ESTs	3.0
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.0
	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	449856	AA203155	Hs.18200	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN A	3.0

	442994	AJ026718	Hs.16954	ESTs	3.0
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	3.0
	421072	AJ215069	Hs.89113	ESTs	3.0
	456273	AF154846	Hs.1148	zinc finger protein	3.0
5	404548				3.0
	426201	AA424158	Hs.205461	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	445413	AA151342	Hs.12677	CGI-147 protein	3.0
	418717	AJ334430	Hs.86984	ESTs	3.0
10	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.0
	407758	D50915	Hs.38365	KIAA0125 gene product	3.0
	431906	AW328038	Hs.37486	ESTs	3.0
	424968	AA349086	Hs.259746	ESTs, Weakly similar to A46010 X-linked	3.0
	431023	AI283133	Hs.297420	ESTs	3.0
15	432596	AJ224741	Hs.278461	matrilin 3	3.0
	452412	AA029608	Hs.61373	ESTs	3.0
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to T2D4_HUMAN TRANS	2.9
	408321	AW405882	Hs.44205	corlatin	2.9
20	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	2.9
	400880				2.9
	417014	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN IIII	2.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.9
	406603				2.9
25	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibitor	2.9
	427878	C05766	Hs.181022	CGI-07 protein	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.9
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.9
30	422634	NM_016010	Hs.118821	CGI-62 protein	2.9
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.9
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.9
	408525	AW206972	Hs.253595	ESTs	2.9
	412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.9
35	432507	BE391093	Hs.324667	ESTs	2.9
	447290	AI476732	Hs.263912	ESTs	2.9
	424188	AW954552	Hs.142634	zinc finger protein	2.9
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
40	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9
45	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	2.9
	444339	T96555	Hs.31562	ESTs	2.9
	446745	AW118189	Hs.156400	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	430573	AA744550	Hs.136345	ESTs	2.9
50	451073	AI758905	Hs.206053	ESTs	2.9
	440575	AA889870	Hs.126006	ESTs	2.9
	402046				2.9
	426882	AA393108	Hs.97365	ESTs	2.9
55	435738	AA699633	Hs.269543	ESTs, Weakly similar to A56194 thromboxa	2.9
	420656	AA279098	Hs.187636	ESTs	2.9
	438323	AI985394	Hs.123369	ESTs	2.9
	453123	AI953718	Hs.221849	ESTs	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
60	431595	AA508196		gb:nh60707.s1 NCL_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	459440	BE048054		gb:tz46c03.y1 NCL_CGAP_Bm52 Homo sapien	2.9
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	2.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	2.9
	456034	AW450979		gb:UL-H-B13-ata-a-12-0-UL.s1 NCL_CGAP_Su	2.9
65	442118	AA976718	Hs.202242	ESTs	2.9
	420727	H75701	Hs.99886	complement component 4-binding protein,	2.9
	433849	BE465884	Hs.280728	ESTs	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	429826	N93266	Hs.40747	ESTs	2.9
70	437913	AI140825	Hs.121623	ESTs	2.9
	441330	AI692984	Hs.129354	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.9
75	444631	AW995395	Hs.84520	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.9
	458186	AA904244	Hs.153205	ESTs	2.9
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.9
	415757	AA830854	Hs.187810	ESTs	2.9
	449299	AA299919	Hs.84561	ESTs	2.9
80	457003	S78234	Hs.172405	cell division cycle 27	2.9
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.9
	424602	AK002055	Hs.151048	hypothetical protein FLJ11193	2.9
	426174	AA547959	Hs.115838	ESTs	2.9

	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	2.9
	429950	AW081608	Hs.105053	ESTs	2.9
	412733	AA984472	Hs.74554	KIAA0080 protein	2.9
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (2.9
5	442555	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypotheti	2.9
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	430447	W17064	Hs.332848	SW/SNF related, matrix associated, acti	2.9
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	2.9
	439737	AJ751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.9
10	406815	AA833930	Hs.288036	IRNA Isopentenylpyrophosphate transferas	2.9
	401094				2.9
	401526				2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
15	418282	AA215535	Hs.98133	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	450006	AI241555	Hs.60171	ESTs	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	2.8
	416623	N74926	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	2.8
20	403329				2.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.8
	419038	AW134924	Hs.190325	ESTs	2.8
	440106	AA864968	Hs.127699	KIAA1603 protein	2.8
	448019	AW947184	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.8
25	431745	AW972448	Hs.163425	ESTs	2.8
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	2.8
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.8
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.8
	441790	AW294909	Hs.132208	ESTs	2.8
30	404443				2.8
	428129	AI244311	Hs.26912	ESTs	2.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.8
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	2.8
	449327	AI638743	Hs.224672	ESTs	2.8
35	400983				2.8
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	2.8
	411213	AA676939	Hs.69285	neuropilin 1	2.8
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.8
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.8
40	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	455092	BE152428		gb:CMD-HT0323-151299-126-b04 HT0323 Homo	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	440192	AA872282	Hs.190596	ESTs	2.8
45	448466	AI522109	Hs.171066	ESTs	2.8
	414869	AA157291	Hs.21479	ubiquitin 1	2.8
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
50	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	2.8
	455512	AW983608		gb:RC3-HN0001-240400-012-c01 HN0001 Homo	2.8
	408380	AF123060	Hs.44532	diubiquitin	2.8
55	435990	AI015862	Hs.131793	ESTs	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	432798	AA565309	Hs.194015	ESTs	2.8
	416288	H51299		gb:yp07c08.s1 Soares breast 3NbHBst Homo	2.8
	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422 2 unkno	2.8
60	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.8
	416940	N75620	Hs.43157	ESTs	2.8
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.8
	438398	AA806526	Hs.130277	ESTs	2.8
	435313	AI769400	Hs.189729	ESTs	2.8
65	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	2.8
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstr	2.8
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.8
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.8
	401323				2.8
70	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.8
	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	2.8
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse l	2.8
	406970	M29994		gb:Human alpha-I spectrin gene, exon 12.	2.8
75	426172	AA371307	Hs.125056	ESTs	2.8
	452114	N22687	Hs.8236	ESTs	2.8
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
80	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.8
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.8
	429881	T80112	Hs.192245	ESTs	2.8
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.8

	409435	AI810721	Hs.95424	ESTs	2.8
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.8
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	2.8
5	444381	BE387335	Hs.283713	ESTs, Weakly similar to S54054 hypotheti	2.8
	412189	R60982	Hs.22581	ESTs	2.8
	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.8
	448330	AL036449	Hs.207163	ESTs	2.8
10	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
	422505	AL120862	Hs.124165	ESTs	2.8
	427752	AA470687	Hs.104772	ESTs	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	433703	AA210863	Hs.3532	nemo-like kinase	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	405621				2.8
15	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.8
	450400	AI694722	Hs.279744	ESTs	2.8
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.8
	418342	BE002723	Hs.226627	leptin receptor	2.8
20	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	439831	AW136488	Hs.25545	ESTs	2.8
25	425661	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	2.8
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	2.8
	418658	AW874263	Hs.32468	ESTs	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	421340	F07783	Hs.1369	decay accelerating factor for complement	2.8
	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.8
30	409241	AF070602	Hs.51649	Homo sapiens clone 24504 mRNA sequence	2.8
	448219	AA228092	Hs.42656	KIAA1681 protein	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
	426471	M22440	Hs.170009	transforming growth factor, alpha	2.8
35	454455	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	401335				2.7
	436577	W84774	Hs.17643	ESTs	2.7
40	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
	421003	T72080	Hs.85667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.7
	436007	AI247716	Hs.232168	ESTs	2.7
45	408874	AW818091	Hs.252730	ESTs	2.7
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	2.7
	435625	H50654	Hs.113999	ESTs	2.7
	435766	R11673	Hs.186498	ESTs	2.7
	410327	T33130	Hs.301746	RAP2A, member of RAS oncogene family	2.7
50	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	429710	AI337113	Hs.146025	hypothetical protein FLJ23594	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.7
	441928	AI370188	Hs.211454	ESTs	2.7
	409721	AW887732	Hs.257861	ESTs	2.7
60	427112	Z32887	Hs.290951	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	432837	AA310693	Hs.87329	HSPC072 protein	2.7
65	438782	AA828380	Hs.126733	ESTs	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	458043	AW979009	Hs.328108	ESTs	2.7
	438171	AW976507	Hs.293515	ESTs	2.7
	452959	AI933416	Hs.189674	ESTs	2.7
70	439556	AI623752	Hs.163603	ESTs	2.7
	446152	AI292036	Hs.150028	ESTs	2.7
	434803	AW974640	Hs.303413	ESTs	2.7
	407771	AL138272	Hs.62713	ESTs	2.7
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.7
75	417543	AA203620	Hs.110153	ESTs	2.7
	401517				2.7
	403677				2.7
	416337	H48713		gb:yq78d02.r1 Soares fetal liver spleen	2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
80	446800	AI341635	Hs.156486	ESTs	2.7
	457906	AW975939	Hs.153290	Homo sapiens cDNA FLJ14318 fis, clone PL	2.7
	452277	AL049013	Hs.28783	KIAA1223 protein	2.7
	416913	AW934714		gb:RC1-DT0001-031299-011-e11 DT0001 Homo	2.7
	416370	N98470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	2.7

5	408715	AA768873	Hs.112250	hypothetical protein FLJ23518	2.7
	410743	AA089474	Hs.272153	ESTs	2.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.7
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.7
	427565	AI287280	Hs.97933	ESTs, Weakly similar to T46370 hypothel	2.7
10	406092				2.7
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	2.7
	438504	AW665281	Hs.224625	ESTs	2.7
	414783	AW069569	Hs.278270	inactive progesterone receptor, 23 kD	2.7
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.7
15	418686	Z36830	Hs.87268	annexin A8	2.7
	413795	AL040178	Hs.142003	ESTs	2.7
	457528	AW973791	Hs.292784	ESTs	2.7
	444230	H95537	Hs.146067	ESTs	2.7
	403760				2.7
20	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.7
	428904	AI312526	Hs.46640	ESTs	2.7
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	2.7
	458638	N78553	Hs.282204	nucleosomal binding protein 1	2.7
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	2.7
25	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.7
	433906	AI167816	Hs.43355	ESTs	2.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.7
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.7
30	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2	2.7
	445158	AI992108	Hs.127206	ESTs	2.7
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.7
	401793				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
35	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	451343	AW975057	Hs.293353	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wil	2.7
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	2.7
40	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypothel	2.7
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	2.7
	451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	2.7
	418269	AA806113	Hs.189025	ESTs	2.7
45	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	441963	AI733307	Hs.128002	ESTs	2.7
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.7
	426902	AI125334	Hs.97408	ESTs	2.7
50	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	445265	AI218295	Hs.144942	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	428613	AB037749	Hs.186928	KIAA1328 protein	2.7
55	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-fin	2.7
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	2.7
	402800				2.7
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.7
	414729	BE466928	Hs.281901	ESTs	2.7
60	453716	AA037675	Hs.152675	ESTs	2.7
	452693	T79153	Hs.48589	zinc finger protein 228	2.7
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	2.7
	443305	AJ050693	Hs.133318	ESTs	2.7
	416709	R99369	Hs.283108	hemoglobin, gamma G	2.7
65	419077	AA233885	Hs.164526	ESTs	2.7
	453878	AW964440	Hs.19025	DC32	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	446817	AI700684	Hs.134166	ESTs	2.7
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	2.6
70	410406	AJ969703	Hs.1466	glycerol kinase	2.6
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.6
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	2.6
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.6
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	2.6
75	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 Integrin	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000690	Hs.158836	hypothetical protein FLJ20583	2.6
	418217	AI910647	Hs.13442	ESTs	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
80	414573	AI821846	Hs.71999	ESTs	2.6
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	2.6
	428483	AI908539	Hs.321444	KIAA0344 gene product	2.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	405059				2.6
	425178	H16097	Hs.161027	ESTs	2.6

	442952	AJ743261	Hs.131860	ESTs	2.6
	428692	AJ372822	Hs.110103	RNA polymerase I transcription factor RR	2.6
	456179	H75490	Hs.271930	ESTs	2.6
5	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	459456	AA486036	Hs.190124	ESTs	2.6
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (I	2.6
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
10	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	438295	AJ394151	Hs.37932	ESTs	2.6
	445550	AJ242754	Hs.137306	ESTs	2.6
	450469	AJ955049	Hs.281326	ESTs	2.6
	458804	AL157625		gb:DKFZp761L2018_r1 761 (synonym: hamy2)	2.6
15	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.6
	429250	H56585	Hs.198308	tryptophan rich basic protein	2.6
	437906	AA771704	Hs.194626	ESTs	2.6
	426775	AA384564	Hs.108829	ESTs	2.6
	443372	AJ792557	Hs.133107	ESTs	2.6
20	453785	AJ368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	425465	L18964	Hs.1904	protein kinase C, iota	2.6
	422746	NM_004484	Hs.119651	glypican 3	2.6
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.6
25	424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	2.6
	414180	AJ863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	2.6
	411402	BE297855	Hs.69855	NRAS-related gene	2.6
	445264	AJ218263	Hs.323472	EST	2.6
	458861	AJ630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.6
30	415227	AW821113	Hs.72402	ESTs	2.6
	435429	AW592035	Hs.254414	ESTs, Weakly similar to 1805195B RNA-bln	2.6
	434445	AJ349306	Hs.11782	ESTs	2.6
	448570	AJ923944	Hs.30913	ESTs	2.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
35	422879	AJ241409	Hs.188092	ESTs	2.6
	409026	AL137554	Hs.49927	protein kinase NYD-SP15	2.6
	425717	X07282	Hs.171495	retinoic acid receptor, beta	2.6
	429127	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
40	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AJ939339	Hs.146883	ESTs	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
	452453	AJ902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.6
45	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interfero	2.6
	430719	AA488988	Hs.293796	ESTs	2.6
	452664	AA033714	Hs.287629	hypothetical protein FLJ14260	2.6
	432095	AW022273	Hs.105769	ESTs	2.6
50	431086	AJ829692	Hs.211561	ESTs	2.6
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	2.6
	423952	AW877787	Hs.136102	KIAA0853 protein	2.6
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	2.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.6
	430933	AW863835		gb:MR3-SN0010-270300-103-h02 SN0010 Homo	2.6
55	420691	AA829433	Hs.275343	ESTs	2.6
	429761	AJ276780	Hs.135173	ESTs	2.6
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
60	436464	AJ016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.6
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	2.6
	438647	AA813118	Hs.163230	ESTs	2.6
	438192	AJ859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.6
65	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.6
	428170	H05530	Hs.12565	ESTs	2.6
	457343	NM_013938	Hs.247862	olfactory receptor, family 12, subfamily	2.6
70	424020	R76946	Hs.39738	ESTs	2.6
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.6
	411965	BE467339	Hs.280115	ESTs	2.6
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.6
	455488	AA102322		gb:z190f03.r1 Stralagene colon (937204)	2.6
75	434340	AJ193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.6
	404285				2.6
	418744	AJ887288	Hs.196379	ESTs, Weakly similar to putative p150 (H	2.6
	454714	AW815098		gb:QV4-ST0212-091199-023-f10 ST0212 Homo	2.6
	429828	AB018494	Hs.225767	IDN3 protein	2.6
80	436387	AA714760	Hs.240075	Homo sapiens cDNA FLJ13234 fis, clone OV	2.6
	448587	AJ539652	Hs.28338	KIAA1546 protein	2.6
	432865	AJ753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160	AJ467915	Hs.36053	ESTs	2.6

	428978	AA442784	Hs.125445	ESTs	2.5
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.5
	453459	BE047032	Hs.257789	ESTs	2.5
5	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.5
	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	2.5
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.5
	458760	AI98631	Hs.111334	fertilin, light polypeptide	2.5
	434131	AI858275	Hs.143659	ESTs	2.5
10	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.5
	417351	T90278	Hs.15049	ESTs	2.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	2.5
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	2.5
15	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	453919	AW959912	Hs.7076	KIAA1705 protein	2.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
20	427491	R43279	Hs.22574	ESTs, Weakly similar to I38022 hypotheti	2.5
	435102	AW899053	Hs.76917	F-box only protein 8	2.5
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.5
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.5
	432887	AI926047	Hs.162859	ESTs	2.5
25	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5
	401078				2.5
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.5
	425201	AA352111		gb:EST60051 Activated T-cells XX Homo sa	2.5
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
30	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	444542	AI161293	Hs.280380	aminopeptidase	2.5
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	2.5
	428497	BE010877	Hs.98584	ESTs	2.5
	457336	AW969657	Hs.291029	ESTs	2.5
35	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	2.5
	423782	AI472209	Hs.323117	ESTs	2.5
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	2.5
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	2.5
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.5
40	417137	U46265	Hs.81281	mitochondrial ribosomal protein S21	2.5
	436787	AA908554	Hs.192756	ESTs	2.5
	440331	AL048412	Hs.202151	ESTs	2.5
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.5
	417169	R13550	Hs.246773	ESTs	2.5
45	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	2.5
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
50	446346	AI290205	Hs.309940	ESTs	2.5
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	2.5
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	2.5
	425523	AB007948	Hs.158244	KIAA0479 protein	2.5
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.5
55	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.5
	425657	T89839	Hs.119471	ESTs	2.5
	401254				2.5
	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	2.5
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	2.5
60	433138	AB029496	Hs.59729	semaphorin sem2	2.5
	425804	BE501698	Hs.258189	ESTs	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	454305	BE062633	Hs.28338	KIAA1546 protein	2.5
65	455631	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	2.5
	401878				2.5
	450350	T97817	Hs.174880	ESTs	2.5
	436532	AA721522		gb:mv54h12.r1 NCLCGAP_Ew1 Homo sapiens	2.5
70	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	2.5
	427304	AA761526	Hs.163853	ESTs	2.5
	419721	NM_001650	Hs.288650	aquaporin 4	2.5
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.5
75	434273	AA913143	Hs.26303	ESTs	2.5
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	2.5
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN I	2.5
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.5
	452232	AW020603	Hs.158423	radial spoke protein 3	2.5
80	433764	AW753676	Hs.39982	ESTs	2.5
	412050	H96503	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.5
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.5

	408813	AI580090	Hs.48295	RNA helicase family	2.5
	414109	BE250744		gb:600943376F1 NIH_MGC_17 Homo sapiens c	2.5
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.5
5	419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.s.a	2.5
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.5
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
10	445865	AI262584	Hs.145575	ESTs	2.5
	451800	AW977435	Hs.323867	ESTs	2.5
	456987	AI557290	Hs.173536	ESTs	2.5
	403568				2.5
	435209	AW027809	Hs.187698	Homo sapiens cytomegalovirus partial fus	2.5
15	430371	D87466	Hs.240112	KIAA0276 protein	2.5
	418033	W58180	Hs.259855	elongation factor-2 kinase	2.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.5
	453619	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	2.5
	431071	AA491379		gb:aa6505.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
20	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.5
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.4
	417318	AW953937	Hs.12891	ESTs	2.4
25	413382	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.4
	406748	AW339106	Hs.217493	annexin A2	2.4
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.4
	441817	AW969706	Hs.293332	ESTs	2.4
	450551	AJ010046	Hs.25155	neuroepithelial cell transforming gene 1	2.4
30	457940	AL360159	Hs.306517	Homo sapiens TRIPartite motif protein ps	2.4
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	2.4
	436907	AA737171	Hs.131809	ESTs	2.4
	429399	AA452244	Hs.16727	ESTs	2.4
	448782	AL050295	Hs.22039	KIAA0758 protein	2.4
35	434404	AW445034	Hs.256578	ESTs	2.4
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	2.4
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.4
40	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.4
	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (J	2.4
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascidin	2.4
	458986	AI802772	Hs.208655	ESTs	2.4
	443861	AW449462	Hs.134743	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
45	415250	F02614	Hs.27319	ESTs	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	2.4
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.4
	400385	NM_020389	Hs.283104	putative capacitative calcium channel	2.4
50	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
	435559	AF209198	Hs.42636	zinc finger protein 277	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	448005	AW207437	Hs.170378	ESTs	2.4
55	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.4
	449486	AI652715	Hs.270811	ESTs	2.4
	421516	AI362418	Hs.105379	FT005 protein	2.4
	412167	AW897230		gb:CM0-NN0057-150400-335-a11 NN0057 Homo	2.4
60	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	2.4
	400641				2.4
	430576	AA767125	Hs.293574	ESTs	2.4
	434423	NM_006769	Hs.3844	LJM domain only 4	2.4
65	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.4
	441499	AW298235	Hs.101689	ESTs	2.4
	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	2.4
	417819	AI253112	Hs.133540	ESTs	2.4
	431728	NM_007351	Hs.268107	multimerin	2.4
70	425025	AW953168	Hs.12407	ESTs	2.4
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.4
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.4
	408867	AA437199	Hs.656	cell division cycle 25C	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
75	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.4
80	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.4
	453864	AW021407	Hs.21058	hypothetical protein	2.4
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.4
	426503	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	2.4

	447357	AK375922	Hs.159367	ESTs	2.4
	452631	AI188658	Hs.87496	ESTs	2.4
	405041				2.4
	405472				2.4
5	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	437119	AI379921	Hs.177043	ESTs	2.4
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.4
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.4
10	434936	AI285970	Hs.183817	ESTs	2.4
	408918	BE216603	Hs.279708	ESTs	2.4
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.4
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.4
	430299	W28673	Hs.105747	serine carboxypeptidase 1 precursor prot	2.4
15	446659	AI335361	Hs.226376	ESTs	2.4
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	2.4
	434995	AW974995		gb:EST387100 MAGE resequences, MAGN Homo	2.4
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.4
	444755	AA431791	Hs.113823	CipX (caseinolytic protease X, E. coli)	2.4
20	427131	AA448460	Hs.112017	GE36 gene	2.4
	442039	AW276240	Hs.128352	ESTs	2.4
	448595	AB014544	Hs.21572	KIAA0644 gene product	2.4
	432949	AA570749	Hs.298866	ESTs	2.4
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.4
25	417420	T85150	Hs.268814	ESTs	2.4
	427551	T96203		gb:ye48b07.r1 Soares fetal liver spleen	2.4
	420057	AA806899	Hs.184387	ESTs	2.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo	2.4
	425497	AA524596		gb:nh34b02.s1 NCI_CGAP_Pt3 Homo sapiens	2.4
30	438214	H06076	Hs.26320	TRABID protein	2.4
	416100	H18700	Hs.268799	ESTs	2.4
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	2.4
35	419179	AW275291	Hs.113009	hypothetical protein FLJ22527	2.4
	436391	AJ227892	Hs.146274	ESTs	2.4
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	2.4
	447499	AW262580	Hs.147674	protocadherin beta 16	2.4
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.4
40	412877	BE011168		gb:PM3-BN0218-100500-003-d08 BN0218 Homo	2.4
	435985	AA703154	Hs.191934	ESTs	2.4
	440674	BE561546		gb:601347208F1 NIH_MGC_8 Homo sapiens cD	2.4
	446476	AW294072	Hs.141376	ESTs	2.4
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.4
45	435731	AA699581	Hs.186811	ESTs	2.4
	437105	AA744554	Hs.222127	ESTs	2.4
	406091				2.4
	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
50	419556	U29615	Hs.91093	chitinase 1 (chitinotrioidase)	2.4
	424943	AU077260	Hs.153924	death-associated protein kinase 1	2.4
	444229	AV648613	Hs.282397	ESTs	2.4
	404860				2.4
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.4
55	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.4
	420843	H96982	Hs.42321	ESTs	2.4
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
60	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	2.4
	409073	AA063458		gb:zd71a07.s1 Soares_pineal_gland_N3HPG	2.3
	418782	AF792648	Hs.14665	ESTs	2.3
65	447870	BE139479	Hs.161492	ESTs	2.3
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	2.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	2.3
	424049	AB014524	Hs.138380	KIAA0624 protein	2.3
70	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.3
	430702	U56979	Hs.250651	H factor 1 (complement)	2.3
	409620	AA076278	Hs.13277	hypothetical protein FLJ22054	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.3
75	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.3
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	2.3
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	2.3
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.3
80	404513				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	448506	AI524673	Hs.38170	ESTs	2.3
	434811	AW971205	Hs.114280	ESTs	2.3

5	457065	AI476318	Hs.192480	ESTs	2.3
	407945	X69208	Hs.606	ATPase, Cu ⁺⁺ transporting, alpha polypep	2.3
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.3
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H]	2.3
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.3
	435867	AA954229	Hs.114052	ESTs	2.3
	440196	N72847	Hs.125221	ESTs	2.3
	401213				2.3
10	407291	AA001464		gb:ze45b01.r1 Soares retina N2b4HR Homo	2.3
	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.3
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.3
	438138	R98299	Hs.177502	ESTs	2.3
	440283	AI732892	Hs.190489	ESTs	2.3
	447039	AV661798	Hs.282915	ESTs	2.3
15	412777	AI335773	Hs.270123	ESTs	2.3
	421424	AW452690	Hs.258775	ESTs	2.3
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.3
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	2.3
	451516	AI800515	Hs.12024	ESTs	2.3
20	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	2.3
	421046	AA810854	Hs.89081	ESTs	2.3
	423604	AA486585	Hs.258901	ESTs	2.3
	409029	BE087807		gb:QV1-BT0681-290400-181-g02 BT0681 Homo	2.3
25	444206	AW301017	Hs.146492	ESTs	2.3
	451836	T63673	Hs.173220	ESTs	2.3
	454784	AW820626		gb:RCO-ST0299-190100-012-e10 ST0299 Homo	2.3
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.3
	436671	AW137159	Hs.146151	ESTs	2.3
30	434988	AI418055	Hs.161160	ESTs	2.3
	452862	AW378065	Hs.8687	ESTs	2.3
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	2.3
	410606	AW418779	Hs.114889	ESTs	2.3
	426535	AL077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.3
35	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	2.3
	430217	N47863	Hs.336901	ribosomal protein S24	2.3
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
	438180	AA808189	Hs.272151	ESTs	2.3
40	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypothet	2.3
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	2.3
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	2.3
	448831	AL080123	Hs.22182	zinc finger protein 23 (KOX 16)	2.3
45	412953	Z45794	Hs.238809	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	2.3
	428595	AB037795	Hs.186547	KIAA1374 protein	2.3
	437887	AA811524	Hs.29263	hypothetical protein FLJ11896	2.3
50	447720	AL038765	Hs.161304	ESTs	2.3
	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.3
	408374	AW025430	Hs.155591	forkhead box F1	2.3
	440381	AA917808	Hs.190495	ESTs	2.3
	425478	AB007853	Hs.268840	ESTs	2.3
55	432231	AA339977	Hs.274127	CLST 11240 protein	2.3
	431757	AA196930	Hs.268526	Homo sapiens chromosome 21q22.1 anonymou	2.3
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.3
	452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	2.3
	417426	NM_002291	Hs.82124	laminin, beta 1	2.3
60	423739	AA398155	Hs.97600	ESTs	2.3
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	2.3
	425876	AW005887	Hs.234058	ESTs	2.3
	457411	AW085961	Hs.130093	ESTs	2.3
65	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	2.3
	420313	AB023230	Hs.96427	KIAA1013 protein	2.3
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
	436331	AI239495	Hs.120189	ESTs	2.3
70	439275	AF086093	Hs.141566	ESTs	2.3
	449272	AW137656	Hs.197645	ESTs	2.3
	454352	AW389668		gb:RC2-ST0168-071299-013-406 ST0168 Homo	2.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	2.3
	407242	M18728		gb:Human nonspecific crossreacting antig	2.3
75	445326	AI220072	Hs.165893	ESTs	2.3
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.3
	452607	AI160029	Hs.61438	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	418851	AI417828	Hs.192435	ESTs	2.3
80	458332	AI000341	Hs.220491	ESTs	2.3
	432565	AA553477	Hs.152428	ESTs	2.3
	437511	AI807500	Hs.125247	ESTs	2.3
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.3
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	2.3

	448225	AJ476429	Hs.19238	ESTs	2.3
	408955	BE315170	Hs.8087	NAG-5 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
5	419699	AA248998	Hs.173044	ESTs, Weakly similar to 138022 hypothetical	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	440348	AW015802	Hs.47023	ESTs	2.3
	436340	R42246	Hs.21606	ESTs	2.3
10	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	2.3
	438462	AJ624122	Hs.89578	general transcription factor IIIH, polype	2.3
	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN IIII	2.3
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.3
	412505	AA974491	Hs.21734	ESTs	2.3
	418236	AW994005	Hs.337534	ESTs	2.3
15	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	2.3
	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.3
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.3
	433404	T32982	Hs.102720	ESTs	2.3
	409517	X90780	Hs.120036	troponin I, cardiac	2.3
20	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
	445641	AJ245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	2.3
	437770	AA767881	Hs.122897	ESTs	2.3
25	409064	AA062954	Hs.141883	ESTs	2.3
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.3
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	2.3
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	2.3
	418251	AA832123	Hs.177723	ESTs	2.3
30	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	2.3
	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.3
	415980	R52414		gb:yg80b05.r1 Soares infant brain 1N1B H	2.3
	449232	AW192780	Hs.196080	ESTs	2.3
35	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.3
	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.3
	438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	2.3
	400238				2.3
	404488				2.3
40	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586i1518 (f	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
45	426567	AA381579	Hs.182962	ESTs	2.3
	435708	AI362949	Hs.75169	ESTs	2.3
	441417	AJ733297	Hs.144474	ESTs	2.3
	445117	AJ208754	Hs.147369	ESTs	2.3
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.2
50	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	2.2
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	2.2
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	2.2
	420553	AI224532	Hs.88550	ESTs	2.2
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.2
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	2.2
55	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
60	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446164	AW273539	Hs.288750	hypothetical protein FLJ23577	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	402745				2.2
65	434008	AA740878	Hs.112982	ESTs	2.2
	439492	AF086310	Hs.103159	ESTs	2.2
	436853	BE328074	Hs.148661	ESTs	2.2
	417648	R06552		gb:ylf09e12.r1 Soares fetal liver spleen	2.2
70	427690	AI253134	Hs.283410	ESTs	2.2
	414217	AI309298	Hs.278898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.2
	450229	R18717	Hs.8929	hypothetical protein FLJ11362	2.2
	400756				2.2
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.2
	403388				2.2
75	433643	AJ821787	Hs.175586	ESTs	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
	439920	H05430	Hs.288433	neurotrophin	2.2
80	432436	AW300248	Hs.181693	ESTs	2.2
	429493	AL134708	Hs.145998	ESTs	2.2
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	2.2

	442757	A1739528	Hs.28345	ESTs	2.2
	430212	AA469153		gb:nc67f04.s1 NCL_CGAP_Pr1 Homo sapiens	2.2
	437146	AA730977		gb:ncw55f05.s1 NCL_CGAP_Ew1 Homo sapiens	2.2
5	432101	A1918950	Hs.123642	EphA3	2.2
	459644				2.2
	453887	BE564037	Hs.36237	hypothetical protein	2.2
	431170	AW971246	Hs.291022	ESTs	2.2
	428062	AA420683	Hs.88321	hypothetical protein FLJ14103	2.2
10	443682	A1383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	2.2
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	2.2
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.2
	425810	A1923627	Hs.31903	ESTs	2.2
	433037	NM_014158	Hs.279938	HSPC067 protein	2.2
15	407162	N63855	Hs.142634	zinc finger protein	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	A1347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	2.2
	454766	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414221	AW450979		gb:U1-H-B13-ata-a-12-0-U1.s1 NCL_CGAP_Su	2.2
20	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: harry2)	2.2
	400639				2.2
	406149				2.2
	424027	AW337575	Hs.201591	ESTs	2.2
	427531	AA405097	Hs.97957	ESTs	2.2
25	448353	BE407125	Hs.231510	ESTs	2.2
	417689	T99898		gb:ye68g01.r1 Soares fetal liver spleen	2.2
	449550	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	2.2
	452335	AW188944	Hs.61272	ESTs	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
30	447748	A1422023	Hs.161338	ESTs	2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
35	444540	A1693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.2
	439443	AF086261	Hs.127892	ESTs	2.2
	418824	AW751661	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	2.2
40	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.2
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.2
	432702	AW973953	Hs.293744	ESTs	2.2
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.2
	425570	AA359558		gb:EST68590 Fetal lung II Homo sapiens c	2.2
45	414935	C15671		gb:C15671 Clontech human aorta polyA+ mR	2.2
	453153	N53893	Hs.24360	ESTs	2.2
	430832	A1073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.2
	439867	AA847510	Hs.161292	ESTs	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
50	433420	A1674093	Hs.293961	ESTs, Moderately similar to putative DNA	2.2
	434590	A1887679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	431688	AA513906		gb:ng67c08.s1 NCL_CGAP_Lip2 Homo sapiens	2.2
55	403133				2.2
	414885	AA157531	Hs.269276	ESTs, Moderately similar to S65657 alpha	2.2
	432111	AW972777		gb:EST384871 MAGE resequences, MAGL Homo	2.2
	410073	AW408163	Hs.58488	catenin (cadherin-associated protein), a	2.2
60	448869	A1792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.2
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.2
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfot	2.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	2.2
	403378				2.2
65	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.2
	438580	AA811262	Hs.299202	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Casp1n	2.2
	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	2.2
	411966	AA099113	Hs.118609	ESTs	2.2
70	443915	Z40763	Hs.135292	ESTs	2.2
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.2
	446094	AK001760	Hs.13801	KIAA1685 protein	2.2
	436486	AA742221	Hs.120633	ESTs	2.2
	411139	AW819461		gb:RC5-ST0293-061299-031-C03 ST0293 Homo	2.2
75	409070	AA063003	Hs.224560	ESTs	2.2
	432713	AL118623	Hs.29494	PRO1912 protein	2.2
	419384	AA490866	Hs.39429	ESTs	2.2
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.2
	408444	AW661839	Hs.253204	ESTs	2.2
80	432128	AA127221	Hs.117037	ESTs	2.2
	418027	AB037807	Hs.83293	hypothetical protein	2.2
	446060	Z42061	Hs.27004	ESTs	2.2
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.2
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.2

5	443401	AI394067	Hs.160159	ESTs	2.2
	424665	AW368576	Hs.139851	caveolin 2	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
	414564	AA164803	Hs.71994	ESTs, Weakly similar to I38022 hypotheti	2.2
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	2.2
	419160	AA911342	Hs.35524	KIAA1559 protein	2.2
	420111	AA255652		gb:z21h11.1 NCI_CGAP_GC81 Homo sapiens	2.2
10	442879	AF032922	Hs.8813	synlaxin binding protein 3	2.2
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.2
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	2.2
	432074	AA525248	Hs.149723	ESTs	2.2
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	2.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.2
15	409723	AW885757	Hs.257862	ESTs	2.2
	425627	AF019612	Hs.297007	membrane-bound transcription factor prot	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	449369	AA001256	Hs.27260	ESTs	2.2
	425514	AF112345	Hs.158237	integrin, alpha 10	2.2
20	455821	BE143341		gb:MR0-HT0182-191099-002-d04 HT0162 Homo	2.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.2
	432284	AA532807	Hs.105822	ESTs	2.2
	403467				2.2
25	436032	AA150797	Hs.109276	latexin protein	2.2
	404356				2.2
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	2.2
	405257				2.2
	402103				2.2
30	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.2
	432985	T92363	Hs.178703	ESTs	2.2
	417649	AW239285	Hs.82359	tumor necrosis factor receptor superfam	2.2
	431277	AA501806	Hs.249965	ESTs	2.2
	454056	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	2.2
	401694				2.2
35	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
40	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.2
	404555				2.2
	418186	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fis, clone H	2.2
	419981	AA897581	Hs.128773	ESTs	2.2
45	449581	AI989517	Hs.181605	ESTs	2.2
	419229	AI827237	Hs.282684	ESTs	2.2
	403691				2.2
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.2
	443479	AF027219	Hs.9443	zinc finger protein 202	2.2
50	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fis, clone HE	2.2
	453345	AA302862	Hs.90063	neurocalcicin delta	2.2
	424335	AW021508	Hs.28170	ESTs	2.2
	451072	AA013451	Hs.117929	ESTs	2.2
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.2
55	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
	438035	AA938198	Hs.146123	poly(A) polymerase gamma	2.2
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.2
	400241				2.2
60	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.1
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo sapiens c	2.1
65	414891	R27124	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	2.1
	430172	AA468591	Hs.161889	ESTs	2.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.1
	422985	AU076411	Hs.1602	dihydropyrimidine dehydrogenase	2.1
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	2.1
70	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	2.1
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	2.1
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.1
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.1
75	415892	C05837	Hs.145807	hypothetical protein FLJ13593	2.1
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.1
	437132	AL049353	Hs.297268	ESTs	2.1
	415304	T66079	Hs.12799	ESTs	2.1
	450152	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	2.1
80	421147	AW592167	Hs.293299	ESTs	2.1
	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.1
	451750	AA280851	Hs.226930	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1

	406945	K01383	Hs.173451	metallothionein 1A (functional)	2.1
	452449	AW068658	Hs.20943	ESTs	2.1
	436009	H57130	Hs.120925	ESTs	2.1
	418637	T86737	Hs.193536	ESTs	2.1
5	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 f	2.1
	449203	AI634578	Hs.282121	ESTs	2.1
	437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	428412	AA428240	Hs.126083	ESTs	2.1
10	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript)	2.1
	441967	AA972742	Hs.209786	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
15	431229	AA496479	Hs.259929	ESTs	2.1
	435148	AI918049	Hs.124961	ESTs	2.1
	436349	AI445255	Hs.115315	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
	448582	AI538880	Hs.94812	ESTs	2.1
20	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	2.1
	451874	AW963137	Hs.194233	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.1
	443484	AI091458	Hs.134559	ESTs	2.1
25	430686	NM_001942	Hs.2633	desmoglein 1	2.1
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	2.1
	407624	AW157431	Hs.248941	ESTs	2.1
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.1
30	428923	BE047698	Hs.188785	ESTs	2.1
	422496	AA311301	Hs.278827	ESTs	2.1
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	2.1
	408418	AW963897	Hs.44743	KIAA1435 protein	2.1
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.1
35	427434	BE536374	Hs.301732	hypothetical protein MGC5306	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	459325	AW088369	Hs.282184	ESTs	2.1
	416996	W91892	Hs.59609	ESTs	2.1
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.1
40	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	2.1
	418894	W73921	Hs.50743	ESTs	2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.1
	437378	AJ198823	Hs.160473	ESTs	2.1
	454100	AI693231	Hs.126043	chromosome 21 open reading frame 51	2.1
45	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	2.1
	437311	AA3770041	Hs.9456	SWI/SNF related, matrix associated, acti	2.1
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.1
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	2.1
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	2.1
50	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.1
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	2.1
	449911	AI262106	Hs.12653	ESTs	2.1
	449509	AA001615	Hs.84561	ESTs	2.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	2.1
55	422839	AI674784	Hs.298908	ESTs	2.1
	435040	AI932350	Hs.152825	ESTs	2.1
	401200				2.1
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.1
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.1
60	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	2.1
	453908	AW613920	Hs.282178	ESTs	2.1
	446965	BE242873	Hs.16877	WD repeat domain 15	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
65	418378	AW982081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	455995	BE179408		gb:IL3-HT0618-060500-125-B07 HT0618 Homo	2.1
	422411	AW749443	Hs.22511	ESTs	2.1
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.1
	446893	AI610818	Hs.7110	ESTs	2.1
	442992	AI914699	Hs.13297	ESTs	2.1
70	407021	U52077		gb:Human mariner1 transposase gene, comp	2.1
	436938	AW139680	Hs.161393	ESTs	2.1
	433194	AB040883	Hs.83243	KIAA1450 protein	2.1
	454790	AW820852		gb:RC2-ST0301-120200-011-112 ST0301 Homo	2.1
75	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	2.1
	434739	AA804487	Hs.144130	ESTs	2.1
	406468				2.1
	457023	AA001732	Hs.173233	hypothetical protein FLJ10970	2.1
	416226	N55342	Hs.34372	ESTs	2.1
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.1
80	432810	AA863400	Hs.23054	ESTs	2.1
	412894	R09778	Hs.186510	ESTs	2.1
	430602	D13752	Hs.184927	cytochrome P450, subfamily XIB (steroid	2.1
	436981	AA740891	Hs.293316	ESTs	2.1

	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	2.1
	449838	AB020653	Hs.24024	KIAA0846 protein	2.1
	447160	AA330310	Hs.24181	ESTs	2.1
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	2.1
5	440137	AA866199	Hs.171397	ESTs	2.1
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	2.1
	436471	AA719813	Hs.117662	ESTs	2.1
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.1
10	426782	R14614	Hs.191254	ESTs	2.1
	430027	AB023197	Hs.227743	KIAA0980 protein	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.1
	413252	BE074910		gb:RC5-BT0560-170300-021-F12 BT0580 Homo	2.1
	427115	AW972853	Hs.112237	ESTs	2.1
15	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.1
	400451				2.1
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	450159	AI702418	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	418375	NM_003081	Hs.84389	synaposomal-associated protein, 25kD	2.1
	442835	AI021989	Hs.131903	ESTs	2.1
20	400196				2.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.1
	415189	L34657	Hs.78148	platelet/endothelial cell adhesion molec	2.1
	438940	AF075045	Hs.271609	ESTs	2.1
25	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	2.1
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	2.1
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.1
	419088	AI538323	Hs.52620	Integrin, beta 8	2.1
30	447373	AI381922	Hs.158781	ESTs	2.1
	457465	AW301344	Hs.122908	DNA replication factor	2.1
	413918	AW015898	Hs.71245	ESTs	2.1
	402820				2.1
35	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	428552	AW274560	Hs.129520	ESTs	2.1
	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	2.1
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.1
	420838	AW118210	Hs.5244	ESTs	2.1
40	428231	U17989	Hs.183105	nuclear autoantigen	2.1
	434933	R91095	Hs.4276	KIAA1701 protein	2.1
	444870	AI200621	Hs.148504	ESTs	2.1
	425354	U82027	Hs.155935	complement component 3a receptor 1	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	2.1
45	439155	H81076	Hs.269001	ESTs	2.1
	442787	W93048	Hs.250723	hypothetical protein MGC2747	2.1
	429864	AA460039	Hs.286	ribosomal protein L4	2.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.1
	437140	AA312799	Hs.283689	activator of CREM in testis	2.1
50	421991	NM_014918	Hs.110488	KIAA0990 protein	2.1
	446534	AI307356	Hs.175225	ESTs	2.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.1
	444838	AV651680	Hs.208558	ESTs	2.1
	402318				2.1
55	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	421306	AA806207	Hs.125889	ESTs	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	429088	D61542	Hs.227716	KIAA0934 protein	2.1
60	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.1
	428060	AA420616	Hs.249483	ESTs	2.1
	419953	BE287154	Hs.125752	ESTs	2.1
	443718	AI083580	Hs.221373	ESTs	2.1
	444187	AW138466	Hs.151274	ESTs	2.1
65	428048	AA705745		gb:z141b11.s1 Soares_fetal_heart_NbHH18W	2.1
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.1
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.1
	430335	D80007	Hs.239499	KIAA0185 protein	2.1
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.1
70	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.1
	410945	AW811552		gb:QV2-ST0145-071299-017-h10 ST0145 Homo	2.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.1
	433374	AI821409	Hs.332789	EST	2.1
75	445644	R77766	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.1
	450271	AI683900	Hs.200920	ESTs	2.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	2.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	2.1
	430998	AF128847	Hs.204038	Indolethylamine N-methyltransferase	2.1
80	435542	AA687376	Hs.269533	ESTs	2.1
	443544	AI078315	Hs.16359	ESTs	2.1
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	2.1
	405759				2.1
	446242	N86336	Hs.7360	ESTs	2.1

5	457938	AI373638	Hs.133900	ESTs	2.1
	433017	Y15067	Hs.279914	zinc finger protein 232	2.1
	435729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	2.1
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.1
	439224	AW471088	Hs.145950	ESTs, Highly similar to T08692 hypotheti	2.1
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.1
	454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo	2.1
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.1
10	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.1
	446891	AL036877	Hs.282878	ESTs	2.1
	434294	AJ271379	Hs.76194	ribosomal protein S5	2.1
	449057	AB037784	Hs.22941	KIAA1363 protein	2.1
	432769	AA620814	Hs.144959	ESTs	2.1
	441224	AU076964	Hs.7753	calumenin	2.1
15	407891	AA486620	Hs.41135	endomucin-2	2.1
	429017	AA463605	Hs.66295	multi-PDZ-domain-containing protein	2.1
	406817	AI936028		gb:wo47a09.x1 NCL CGAP_Gas4 Homo sapiens	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
20	449208	AW263635	Hs.48643	ESTs	2.1
	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.1
	452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.1
	444779	AI192105	Hs.147170	ESTs	2.0
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	2.0
25	415954	AA171850	Hs.42251	ESTs	2.0
	420273	AI652864	Hs.197257	ESTs	2.0
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.0
	422389	AF240635	Hs.115897	protocadherin 12	2.0
	446994	AV650435	Hs.16755	MBIP protein	2.0
30	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	2.0
	422654	AA314316	Hs.163725	ESTs	2.0
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	2.0
	405634				2.0
	451562	H04150	Hs.107708	ESTs	2.0
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.0
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.0
	442010	AI032680	Hs.132213	ESTs	2.0
	442891	BE281238	Hs.8886	hypothetical protein FLJ20424	2.0
	425312	AA354940	Hs.145958	ESTs	2.0
40	415191	AA190381	Hs.120810	ESTs	2.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.0
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1	2.0
	413753	U17760	Hs.75517	laminin, beta 3 (lncin (125kD), kalinin	2.0
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	2.0
45	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.0
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
50	429418	AI381028	Hs.118769	ESTs	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.0
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	2.0
	400462				2.0
55	422003	AA361760	Hs.296326	ESTs	2.0
	444585	AW170015	Hs.6594	ESTs	2.0
	444898	AI201548	Hs.308338	ESTs	2.0
	403525				2.0
60	443031	AW134696	Hs.49418	ESTs	2.0
	430818	AI311928		gb:qp89h04.x1 NCL CGAP_Kid5 Homo sapiens	2.0
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	2.0
	440941	BE268362	Hs.7535	COBW-like protein	2.0
	409627	AW997628	Hs.313637	ESTs	2.0
65	433258	AI806626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN IIII	2.0
	412863	AA121673	Hs.69757	zinc finger protein 281	2.0
	436478	AA326108	Hs.33829	bHLH protein DEC2	2.0
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.0
	417280	AW173116	Hs.262206	ESTs	2.0
70	423528	AB011137	Hs.300938	KIAA0565 gene product	2.0
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.0
	446019	AI362520	Hs.279789	histone deacetylase 3	2.0
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.0
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.0
75	430473	AW130690	Hs.59962	ESTs	2.0
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.0
	438118	AW753311	Hs.259415	ESTs	2.0
	400859				2.0
	405829				2.0
80	415258	AW752247	Hs.293853	ESTs	2.0
	420314	HB1671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	2.0
	453118	AW195849	Hs.252757	ESTs	2.0

5	430706	NM_003540	Hs.247816	H4 histone family, member C	2.0
	420568	F09247	Hs.247735	protocadherin alpha 10	2.0
	452759	AW590773	Hs.258996	ESTs	2.0
	408496	AI683802	Hs.136182	ESTs	2.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	2.0
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.0
	450086	AW016343	Hs.233301	ESTs	2.0
	410853	H04588	Hs.30469	ESTs	2.0
10	438607	AW080237	Hs.252884	ESTs	2.0
	422232	D43945	Hs.113274	transcription factor EC	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
	402490				2.0
	446551	AI308176	Hs.65636	ESTs	2.0
15	438315	R56795	Hs.82419	ESTs	2.0
	445261	T79759	Hs.282939	ESTs, Weakly similar to I38022 hypothe	2.0
	401986				2.0
	420335	AA258771	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
20	435413	AI267476	Hs.46669	ESTs	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	2.0
	417494	AI369494	Hs.222137	ESTs	2.0
	416045	H15990	Hs.31403	ESTs	2.0
25	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	2.0
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-l	2.0
	411578	AW238524		gb:exp27c05.x1 NCL_CGAP_HN10 Homo sapiens	2.0
	453116	AI276680	Hs.146086	ESTs	2.0
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.0
30	435608	AW183971	Hs.250896	ESTs	2.0
	402102				2.0
	458308	AI828155	Hs.211055	ESTs	2.0
	438177	BE327015	Hs.281391	ESTs	2.0
	415205	H71616	Hs.135233	ESTs	2.0
	427244	AA402400	Hs.178045	ESTs	2.0
35	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	2.0
	438979	AW976218	Hs.32565	ESTs	2.0
	400285				2.0
	405966				2.0
40	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	427739	AW196755	Hs.98105	NYD-SP14 protein	2.0
	433584	AW295399		gb:U1-H-BI2-ahv-h-03-0-ULs1 NCL_CGAP_Su	2.0
	448956	AK001674	Hs.22630	cofactor required for Sp1 transcription	2.0
	439474	AI824060	Hs.211501	ESTs	2.0
45	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.0
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.0
	418836	AI655499	Hs.161712	ESTs	2.0
	453108	AI311457	Hs.99472	ESTs	2.0
	447101	N72185	Hs.44189	ESTs	2.0
50	408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, del	2.0
	426226	AA769045		gb:aa80h07.s1 NCL_CGAP_GCB1 Homo sapiens	2.0
	401157				2.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.0
	425646	AW157044	Hs.158512	cyclin-dependent kinase-like 2 (CDC2-rel	2.0
55	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	2.0
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.0
	402855				2.0
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	2.0
	445672	AI907438	Hs.282862	ESTs	2.0
60	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
	411941	AW876909	Hs.25201	ESTs, Weakly similar to FAT DROME CADHER	2.0
	430664	AW969834	Hs.303303	ESTs	2.0
	402812				2.0
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	2.0
65	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	402048				2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
70	437373	H87505	Hs.191979	KIAA1733 protein	2.0
	439217	AF086041	Hs.42975	ESTs	2.0
	446609	BE395090	Hs.15535	Homo sapiens clone 24582 mRNA sequence	2.0

75 TABLE 3B: List of accession numbers for primers lacking uniqueID's for Table 3A. For such a probe set is listed a gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubletWist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

80 Pkey: Unique Eos probe set identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT number Accession

5	408690	107490_1	AW864542 AA056557 AW882724
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	409073	109851_1	AA063458 AA063018 AA444822
	409519	113722_1	AA075368 AA075369
	409595	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
10	410008	116812_1	AA079552 BE142525 BE142527
	410615	1212203_1	AW772721 AW873372 H89212
	410672	1214882_1	AW794600 AW794730
	410784	1221005_1	AW803201 BE079700 BE062940
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
15	410888	1225955_1	AW861207 AW809508
	410901	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
	410934	1227240_1	AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
	410945	1227561_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
	410999	1228809_1	AW811552 AW811470 AW811523 AW811482 AW811514 AW811456 AW811525
20	411004	1228975_1	AW813004 AW812962 AW812951
	411018	1229132_1	AW813242 BE146089 AW813195 AW813173 AW813206 BE145953 BE146212 AW813196 AW854582 AW813241 BE061582
	411139	1233781_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	411151	1234022_1	AW819461 AW819478 AW819479 AW819559 AW819505
	411479	1247077_1	AW866497 AW819775 AW819868 AW866602 AW866561
25	411514	1248638_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
	411578	125013_1	AW848905 AW848214
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	411880	1263110_1	AW238524 AA094059 RS9022
	411905	1265181_1	AW857826 AW859896
30	412167	1280605_1	AW872477 BE088101 T05990
	412209	1283610_1	BE265067 BE264978 AW875420
	412248	1285000_1	AW897230 AW897252 AW897244 AW897231 AW897263
	412282	1287679_1	AW901456 AW901450 AW901441
	412303	1288130_1	BE176480 AW903298 AW903313
35	412566	1306469_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	412877	1333953_1	AW936336 AW936339
	412879	1334272_1	AW962574 BE073261
	413087	1348720_1	BE011168 BE006371 BE011172 BE011313 BE011166
	413136	1350379_1	BE092219 BE092361 BE006789
40	413252	1355877_1	BE064655 BE153953
	413382	1365954_1	BE066941 BE066911 BE066979 BE066929 BE066925
	413488	1373234_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
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	413618	1380384_1	BE144017 BE185527 BE144023
45	413638	1381238_1	BE144884 H97942
	413642	1381386_1	BE154078 BE154006 BE153891 BE153523 BE153983
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	416288	1585983_1	F13168 R21289 T77628
	416337	1589299_1	AA381209 AA381245 AA167683
	416441	159480_1	R52414 R61681 H12009 T74429
	416548	1600181_1	H51299 H44619 H46391 R86024 H51892 T72744
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	416871	1626761_1	BE407197 AA182474 AA180369 BE275628 BE276131
	416913	163001_1	H62953 N76608 N72413
	416972	163668_1	H69044 T47567 H75691 T50292
	417561	168747_2	H98716 N90792 N24283
65	417648	1691070_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	417669	1692157_1	BE019670 AA191284 AA191255
	417859	1703724_1	AW974345 BE154500 T97088 AA639076
	418378	174655_1	R06552 T98985 R08656
	418636	177402_1	T99898 T92080 T91447 R07806 R07779
70	419546	185765_1	T26453 Z44226 R20425
	419637	186639_1	AW962081 AA218925 AA354237
	419807	188252_1	AW749855 AA225995 AW750208 AW750206
	420111	190755_1	AA244199 AA244272 H57440
	420621	195113_1	W27493 AA248063 AA249685 AA429679
75	420637	195241_1	R77402 AA262462 AA250988 R06794
	421065	198936_1	AA255652 AA280911 AW967920 AA262684
	422063	210852_1	AA278808 BE082076 BE081812 BE081581
	422156	212379_1	AW976153 AA278945 AA747691
	423121	225175_1	AA329711 AA287436 AA283148
80	423422	215498_1	BE156476 BE156473 BE156474 BE156475 AA302839
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	423977	223410_1	A1334966 W32951 H62656 H53902 R88904 AW835732
			AA309272 AA309312 AW961837
			AA310527 AW962295 Z44865 H06841
			AA631498 A1017191 AA491211 AA715555 AA768099 AA808288 A1934089 AA570223 AA574389 AA582438 A1745348 AW964510
			AA319642 AW853758 H56414
			AW864848 AA322213 AA322209 AW961624

	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
	423352	229382_1	BE090503 BE090490 BE090483 BE090501 BE090500 BE090365 BE090505 BE090509 BE090499 BE090502 BE090504 BE090497 AA327285
	423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
5	423841	232507_1	AW753967 AA370795 AA331630 AW962550
	423867	232732_1	AA331886 AW962659 AW962655 T89841
	424872	244505_1	AA347923 AA347928 AW961769
	425201	247933_1	AA352111 AW962247 AA429695
	425497	252499_1	AA524596 AA358494 AA513507
10	425570	253248_1	AA359558 AA359819 AW963122
	426226	262918_1	AA769045 AA372590 AW963633
	426497	268121_1	AA379913 AA379981 AW963523
	426603	269825_1	AA382291 AA994657
	427551	280163_1	T96203 AA405343 T96121
15	428048	286394_1	AA705745 AA420850 AA420433
	428679	294049_1	AA431765 AA432015
	430212	314437_1	AA469153 AI718503 AA469225
	430818	324239_1	AI311928 AA936030 T51931 AA609816 AA487195 AA664207
	430844	324570_1	T94960 AA487679 T95013
20	430933	325757_1	AW863635 BE179901 BE179402 AW863789 AA489179 BE010747 BE010748
	431071	327550_1	AA491379 H86020 AW969148
	431169	328799_1	AW971240 AA493843 AA493723
	431322	331543_1	AW970622 AA503009 AA502998 AA502805 T92188
	431595	335512_1	AA508196 BE142920 AI280311 AI205616 D51709
25	431688	336609_1	AA513906 AA847734 AI357044
	432111	341618_1	AW972777 AA526795 AA526305
	432189	342819_1	AA527941 AI810608 AI620190 AA635266
	432222	343347_1	AI204995 AW827539 AW869908 AW440776 AA528756
	432779	354024_1	AW979241 AA565006 AA847102
30	432803	354267_1	AA565398 AW894072 H97930
	432869	355475_1	AW974094 AA569074 AA602574
	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433492	367934_1	AW605849 AW262898 N41060 AA594852
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
35	433644	371919_1	AW342028 AA641080 AA603282
	433687	373061_1	AA743991 AA604852 AW272737
	434138	380572_1	AA625804 AW418787 AW074833 AI675642 AI393368
	434374	384889_1	AA631439 AI086355 AI082577
	434613	389550_1	AI821826 AA640657 AA658836 AA650055 AI821079
40	434638	38990_1	H50758 AF147434 H50666
	434950	396061_1	AW974892 AA654375
	434995	397210_1	AW974995 AI821880 AI821932 AI791196 AA659617 AI821137 AA558925
	435079	399783_1	AA664192 H60250 T71388
	435463	406582_1	AA682507 AW851124
45	435634	409239_1	T82384 R05307 AA693714
	436532	421802_1	AA721522 AW975443 T93070
	437146	43371_1	AA730977 AI261584 AA334473 Z43263 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920 AA167612
	438005	447553_1	AI239729 AI251752 AA485791 BE568425 AW962958
50	438458	457837_1	BE151746 BE336853 D63271 T94955 AA774994
	438909	46884_1	AW975186 AA807807 D29548
	438993	467651_1	AF085839 R69137 AW188788 R69254
	440320	491930_1	AA828995 AA834879 AI926381
	440674	49997_1	AA879294 N67538 AI474541
55	443613	575391_1	BE561546 Z25124 AI307139 Z28800
	443657	576685_1	AI079356 W23287
	444314	600667_1	R14973 R14967 AI081006
	444610	612257_1	AI140497 AW749625 AW749626 AW749644
	444910	624951_1	AI174783 R83569 R12271
60	446096	661959_1	AI201849 BE069007 AW946544
	446901	697809_1	AI276454 AI633717 AI275116
	447197	711623_1	AI347274 AW844024
	448404	761515_1	R36075 AI366546 R36167
	449540	80945_2	BE089973 AI498612 AW805032
65	450024	82296_1	AA001713 H63836
	450458	83586_1	AA005129 AA679084 AA694399
	450622	837264_1	AA009926 BE149301
	451024	85565_1	AI698839 AI909260 AI909259
	451487	87131_1	AA442176 AA259181
70	452453	918300_1	AA018072 N46370 R84847
	452542	921410_1	AI902519 AI902518 AI902516
	453823	982526_1	AW812256 AW812257 AI906423 AI906422
	453901	986414_1	AL137967 BE064160 BE064186
75	454190	1049995_1	BE065902 AW749032 AW003637
	454193	1050256_1	AW177821 AW177896 AW177867
			BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091
			AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
			AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129
			AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108
			AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178155
			AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
80	454352	1129667_1	AW389668 AW389657 AW609198 AW389649
	454359	1130674_1	N71277 AW390764
	454389	115682_1	AW752571 AW847602 AA077979
	454403	1170435_1	BE065585 BE065944 BE066008 BE066083 BE066093

5	454455	1206965_1	AW752710 BE180336 BE180186
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821
			AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617
			AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754
			AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674
			AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756
			AW807835 AW807608 AW807753 AW807601 AW807956
	454574	1225636_1	AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132
10	454600	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809684 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
			AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960
	454678	1228915_1	AW813089 W28102
	454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	454714	1230493_1	AW815098 BE154843 BE154831
15	454766	1234022_1	AW866497 AW819775 AW819868 AW866602 AW866561
	454784	1234630_1	AW820626 AW820621 AW820608
	454790	1234752_1	AW820852 AW820773 AW821088
	454835	1236509_1	AW833711 AW833620 AW833699
	454962	1246750_1	AW847645 AW847791 AW854083 AW853945
20	455047	1250536_1	AW852530 AW852527 AW852526
	455092	1252971_1	BE152428 AW855572 AW855607
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	455107	1253874_1	BE154113 AW856797 AW856847 AW861128 AW856817
	455114	1254106_1	AW857121 AW857123 AW861238
25	455170	1256906_1	AW860972 AW852598 AW852599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
	455226	1262534_1	AW902103 AW869012 AW869139
	455252	1266222_1	AW876627 AW876630 AW876631 AW876625
	455286	1273576_1	BE144384 AW887474 AW887403 BE144386
30	455310	1278168_1	AW893961 AW893998 AW894034 AW894019
	455431	1289854_1	AW938484 BE001245 BE001190
	455488	129372_1	AA102322
	455511	1321229_1	BE144762 AW979091
35	455512	1321443_1	AW983608 AW983628 AW983610 AW983688 AW983601 AW983645 AW983607 AW983640 AW983625 AW983612 AW983642 AW983687
			AW983602 AW983624 AW983634 AW983637 AW983632 AW983617 AW983635 AW983630 AW983636 AW983639 AW983616 AW983689
			AW983641 AW983621 AW983603 AW983609 AW983623 AW983644 AW983618 AW983615 AW983611 AW983604 AW983686 AW983622
			AW983619 AW983633 AW983589 AW983605 AW983626 AW983643 AW983631 AW983627 AW983613 AW983614 AW983685 AW983593
			AW983590 AW983594 AW983620 AW983638 AW983592 AW983588
			BE003714 BE003721 BE003720 BE003716
40	455571	1331885_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
	455631	1347545_1	BE066007 BE066017 BE066074
	455678	1349716_1	BE066976 BE066928 BE066927
	455685	1350393_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
	455807	1370914_1	BE143341 BE143344 BE143378 BE143358
	455821	1372714_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
45	455866	1377119_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997
	455992	1398552_1	BE179408 BE179798 BE179980
	455995	1398903_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368
	456034	142696_1	BE011362 BE011215 BE011355 BE011363
50	458804	75803_1	AL157625 N72696 BE622492
	458861	798085_1	AI630223 AI630470
	459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
	459201	925883_1	AW391177 W45021
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 29C

60	Pkey:	Unique number corresponding to an Eos probaset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
	NI_position:	Indicates nucleotide positions of predicted exons.	
65	Pkey	Ref	Strand
	400451	8113550	Minus
	400462	9929659	Minus
	400608	9887666	Minus
70	400639	9887597	Plus
	400641	8117693	Plus
	400756	8119084	Minus
	400859	9757499	Minus
	400880	9931121	Plus
75	400889	9958234	Minus
	400983	8081198	Plus
	401045	8117619	Plus
	401049	7232177	Plus
	401078	3687273	Plus
80	401094	9955511	Plus
	401103	8568122	Minus
	401157	9438289	Minus
	401189	9690246	Minus

	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401213	9858408	Plus	98243-98380,98489-98619
	401254	9796309	Plus	152209-152383
5	401323	9212516	Plus	213509-214450
	401335	9884881	Plus	15736-16352
	401497	7381770	Plus	92607-92813
	401517	7677912	Plus	29278-29770
	401526	7770561	Plus	91570-93177
10	401575	7229804	Minus	76253-76364
	401694	3540172	Minus	64056-64168
	401793	7263888	Minus	102945-103083
	401862	7770606	Minus	55839-55993,59145-59293
	401878	8099802	Minus	162268-162474,163089-163195
	401986	4406829	Minus	31137-31293
15	402046	8072415	Plus	166394-166556,168167-168395
	402048	8072512	Plus	43936-44078
	402102	8117771	Minus	174566-174740
	402103	7249203	Plus	14453-15414
20	402230	9966312	Minus	29782-29932
	402318	7582559	Minus	12843-13403
	402490	9797648	Plus	149982-150929
	402745	9212200	Minus	76516-76690
	402800	6010175	Plus	43921-44049,46181-46273
	402812	6010110	Plus	25026-25091,25844-25920
25	402820	6456853	Minus	82274-82443
	402855	9662953	Minus	59763-59909
	403133	7331427	Plus	38314-38634
	403271	7230852	Plus	134283-134485
30	403277	8072597	Minus	27494-27642
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403356	8569930	Plus	92839-93036
	403378	9438244	Minus	44264-44443
35	403388	9438331	Plus	112733-113001,114599-114735
	403467	9929556	Minus	73431-73602
	403515	7656757	Minus	173358-179553
	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
40	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403637	8671936	Minus	142647-142771,145531-145762
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
45	403760	7712202	Minus	45910-46260,47563-47824
	403776	7770611	Minus	1414-1513,1624-1756
	403895	7381715	Minus	3502-4002,4070-4308
	403937	7711761	Minus	12609-12773
	404043	9558573	Plus	29042-29135,46597-46699
50	404097	7770701	Plus	55512-55781
	404200	6010176	Minus	7066-7210
	404249	8655533	Plus	64270-64633
	404274	9885189	Plus	104127-104318
	404285	2326514	Plus	32282-32416
55	404288	2769644	Plus	3512-3691
	404356	7630858	Minus	126433-126623
	404443	7579073	Minus	87198-87441
	404476	8080699	Plus	101841-102043
	404488	8113286	Minus	64835-64994
60	404513	8151941	Minus	112837-113339
	404548	8570305	Minus	83896-84162
	404555	7243881	Minus	63963-64157
	404561	9795980	Minus	69039-70100
	404588	6456726	Minus	40059-40210
65	404593	9944086	Minus	74922-75788
	404599	8705107	Plus	110443-110733
	404860	8979555	Plus	65852-66081
	404916	7341826	Plus	91057-91188
	404957	7407927	Plus	147512-148011
70	405041	7547195	Plus	121230-121714
	405059	7656683	Plus	349-822
	405090	8072525	Minus	38552-39202
	405257	7329310	Plus	73121-73273
	405336	6094635	Plus	33267-33563
	405472	8439781	Plus	106297-106447,108462-108596
75	405494	8050952	Minus	70284-70518
	405547	1054740	Plus	124361-124520,124914-125050
	405621	5523811	Plus	59362-59607
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
80	405692	4314424	Plus	61379-62562
	405759	3288022	Minus	18283-18399
	405829	7109593	Minus	15628-16127
	405848	7651809	Minus	28135-28244

5	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
	406018	6758904	Minus	37795-38168
	406091	9123919	Minus	197370-197935
	406092	9123919	Plus	251370-251797,252168-252882
10	406149	7144791	Minus	44464-45164
	406195	7289992	Minus	36293-36827
	406333	9213235	Plus	64689-64788
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406506	7711374	Minus	6843-8077
15	406554	7711566	Plus	106956-107121
	406603	8272659	Minus	39508-39694

TABLE 30A: ABOUT 1840 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO HYPERSENSITIVITY PNEUMONITIS (HP)

Table 30A lists about 1840 genes that are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with hypersensitivity pneumonitis (HP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 Gene Chip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" hypersensitivity pneumonitis sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" hypersensitivity pneumonitis level was set to the 90th percentile amongst hypersensitivity pneumonitis samples.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to HP (hypersensitivity pneumonitis)

Pkey	ExAccn	Unigene ID	Unigene Title	R1
450478	AW451709	Hs.271200	ESTs	20.2
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
405654				11.8
440209	H05049	Hs.22269	neurexin 3	10.8
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	10.4
439608	W79123	Hs.58561	G protein-coupled receptor 87	10.3
425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	10.2
426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	9.5
416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
420481	U05025	Hs.98201	Human BRCA2 region, mRNA sequence CG029	9.2
403574				9.1
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
419519	AI198719	Hs.176376	ESTs	8.2
435256	AF193766	Hs.13872	cytokine-like protein C17	8.1
423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	8.1
429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
405443				7.8
428766	AA477989	Hs.98800	ESTs	7.7
441802	AA968636	Hs.127877	ESTs	7.6
453649	Y07494	Hs.34114	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (+)	7.5
447410	AJ470235	Hs.172698	EST	7.2
442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
405494				6.9
442377	AA993807	Hs.167367	ESTs	6.9
409928	AL137163	Hs.57549	hypothetical protein dJ473B4	6.8
420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	6.8
415236	R41400		gb:Y94b12.s1 Soares Infant brain 1N1B H	6.8
451562	H04150	Hs.107708	ESTs	6.8
403310				6.7
445189	AI938450	Hs.147482	ESTs	6.7
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	6.7
439780	AL109688		gb:Homo sapiens mRNA full length insert	6.6
402076				6.6
415025	AW207091	Hs.72307	ESTs	6.5
406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	6.5
438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	6.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	6.4
409545	BE296182	Hs.19002	hypothetical protein MGC4675	6.4
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.4
411866	AA099113	Hs.118609	ESTs	6.4
440274	R24595	Hs.7122	scrapie responsive protein 1	6.3
442879	AF032922	Hs.8813	synaptobrevin binding protein 3	6.3
419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
420185	AL044056	Hs.158047	ESTs	6.3
415672	N53097	Hs.193579	ESTs	6.2
455488	AA102322		gb:Z190103.r1 Stratagene colon (937204)	6.2
420026	AI831190	Hs.166676	ESTs	6.1
446888	AV660737	Hs.135100	ESTs	6.1
431622	AW979271	Hs.293184	ESTs	6.1
407265	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	6.1
421300	AW297398	Hs.96617	ESTs	6.0
416045	H15990	Hs.31403	ESTs	6.0

5	414175	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	436397	AA715013	Hs.169835	ESTs	6.0
	440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H α -transp	6.0
	409718	D86840	Hs.56045	src homology three (SH3) and cysteine ri	6.0
10	403625				6.0
	418986	AI123555	Hs.81796	ESTs	5.9
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.9
	400292	AA250737	Hs.72472	ESTs	5.9
	442849	R10099	Hs.269805	ESTs	5.9
15	440887	AI799488	Hs.135905	ESTs	5.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes p/a	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	431374	BE258532	Hs.251871	CTP synthase	5.7
	444963	AI916973	Hs.213603	ESTs	5.7
20	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	5.6
	444992	R37658	Hs.21375	ESTs	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
25	445466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	5.5
	404043				5.5
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	5.5
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	5.5
	434683	AW298724	Hs.202639	ESTs	5.5
30	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.5
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	5.5
	428895	AA437124	Hs.187247	ESTs	5.4
	450018	AA421842	Hs.24309	hypothetical protein FLJ11106	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
35	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	403637				5.3
	414725	AA769791	Hs.125300	ring finger protein 21, interferon-respo	5.3
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	5.3
40	403329				5.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	5.3
	459664				5.3
	401497				5.3
	410797	AW857191		gb:RC2-CT0304-080100-011-b12 CT0304 Homo	5.2
45	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	435202	AI971313	Hs.170204	KIAA0551 protein	5.1
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.1
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	5.1
50	434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.1
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Sle20-lik	5.0
	437636	AA764781	Hs.291844	ESTs	5.0
55	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.0
	418771	AA807881	Hs.25329	ESTs	5.0
	434820	AI821863		gb:ns90f05.x5 NCI_CGAP_Pr3 Homo sapiens	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
60	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
65	401878				4.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	4.9
	451325	AA021283	Hs.59788	ESTs	4.9
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	4.9
	406333				4.9
70	409105	AW467539	Hs.255877	ESTs	4.8
	408000	L11690	Hs.820	bullous pemphigoid antigen 1 (230/240kD)	4.8
	421482	AL135462	Hs.104715	Inversin	4.8
	442757	AI739528	Hs.28345	ESTs	4.8
	459717				4.8
75	436637	AI783629	Hs.26766	ESTs	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	450101	AV649989	Hs.24385	Human hbc547 mRNA sequence	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
80	441640	AI733345	Hs.144104	ESTs	4.8
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	4.8
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	411965	BE467339	Hs.280115	ESTs	4.7
	403341				4.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	4.7
	443271	BE568568	Hs.195704	ESTs	4.7

5	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	426097	BE327369	Hs.112238	ESTs	4.7
	439199	R40373	Hs.26299	ESTs	4.7
	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	4.6
	434381	AA631834		gb:np77h05.s1 NCL_CGAP_Py2 Homo sapiens	4.6
10	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	431242	AA987742	Hs.251278	KJAA1201 protein	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	442360	AJ374621	Hs.29055	ESTs	4.6
15	452171	AJ863302	Hs.211930	EST	4.6
	440801	AA906366	Hs.190535	ESTs	4.5
	411738	AW659353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	431447	AA505138	Hs.291341	ESTs	4.5
	433485	AI93076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
20	401365				4.5
	408281	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	4.5
	411657	AW855583		gb:CM4-CT0278-221099-027-07 CT0278 Homo	4.5
	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	4.5
	428528	AJ004034	Hs.98638	ESTs	4.5
25	454035	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	417252	AA195014	Hs.85971	ESTs	4.5
	417135	AA422067	Hs.50547	ESTs	4.5
	403089				4.4
	420691	AA829433	Hs.275343	ESTs	4.4
30	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	4.4
	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	435434	AA680387	Hs.187850	ESTs	4.4
35	420828	AA280778	Hs.186878	ESTs	4.3
	435586	AJ279137	Hs.151498	ESTs	4.3
	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	416170	H42454	Hs.220645	ESTs	4.3
	408891	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	4.3
40	428912	AW103117	Hs.98949	ESTs, Weakly similar to MEA6 [H.sapiens]	4.3
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	4.3
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	4.3
	401189				4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
45	447863	AL047611	Hs.28885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	422654	AA314316	Hs.163725	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	417919	AJ928203	Hs.86379	ESTs	4.3
	405784				4.3
50	431853	AA521034	Hs.70834	ESTs	4.3
	408629	AW449589	Hs.279724	ESTs	4.2
	403281				4.2
	427173	BE255017	Hs.97540	ESTs	4.2
	433717	AF063536		gb:AF063536 Homo sapiens library (Yu Y)	4.2
55	406777	T23625	Hs.150580	putative translation initiation factor	4.2
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	4.2
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae)	4.2
	449762	N93057	Hs.54888	ESTs	4.2
60	421106	AA877124	Hs.172844	ESTs	4.2
	439382	BE247684	Hs.103070	ESTs	4.1
	404957				4.1
	436332	AL049679	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
65	452728	AJ915676	Hs.239708	ESTs	4.1
	456386	W28481		gb:47a1 Human retina cDNA randomly prime	4.1
	406288	AW068311	Hs.311054	Homo sapiens mRNA full length Insert cDN	4.1
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
70	403344				4.1
	438993	AA828995		gb:od77b08.s1 NCL_CGAP_Ov2 Homo sapiens	4.1
	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.1
	401596	AA172106	Hs.110950	Rag C protein	4.1
	418693	AJ750878	Hs.87409	thrombospondin 1	4.1
75	414299	AA142989	Hs.71730	ESTs	4.1
	452744	AJ267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	458552	AW136139	Hs.245856	ESTs	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
80	441201	AW118822	Hs.128757	ESTs	4.0
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	4.0
	440472	AA888169	Hs.169071	ESTs	4.0
	418379	AA218940	Hs.137516	filagellin-like 1	4.0
	435878	R08330	Hs.20152	ESTs	4.0
	437263	AA747822		gb:nx97a04.s1 NCL_CGAP_GCB1 Homo sapiens	4.0
	444087	AV647899	Hs.282375	ESTs	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0

5	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010656, mRNA,	4.0
	405521				4.0
	411597	AW852925		gb:PM0-CT0248-131099-001-110 CT0248 Homo	4.0
	415655	W05433	Hs.49890	ESTs	4.0
	404822				4.0
10	441107	AA917075	Hs.190520	ESTs	4.0
	404834				4.0
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-43882	4.0
	428102	AA968441	Hs.126866	ESTs	4.0
	436511	AA721252	Hs.291502	ESTs	4.0
15	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	4.0
	453098	Z25935	Hs.86379	ESTs	3.9
	410811	AW805687	Hs.300648	ESTs	3.9
	425048	H05468	Hs.164502	ESTs	3.9
	431071	AA491379		gb:aa65f05.r1 NCL_CGAP_GCB1 Homo sapiens	3.9
20	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	452768	AW069459	Hs.61539	ESTs	3.9
	455241	AW876249		gb:PM4-PT0019-131299-006-B05 PT0019 Homo	3.9
	409070	AA063003	Hs.224560	ESTs	3.9
25	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
	403188				3.9
	418857	D10216	Hs.89394	POU domain, class 1, transcription factor	3.9
30	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
35	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.9
	451221	AI949701	Hs.210589	ESTs	3.9
	455475	AW948126		gb:RC0-MT0013-280300-031-a12 MT0013 Homo	3.9
	433197	AB040889	Hs.281022	KIAA1456 protein	3.9
	429881	T80112	Hs.192245	ESTs	3.9
40	415598	AI433165	Hs.9856	ESTs	3.9
	431220	N52937	Hs.102679	ESTs	3.9
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	404443				3.9
45	407340	AA810168	Hs.284289	villig-associated protein VIT-1	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	3.9
	427167	AI239607	Hs.99196	hypothetical protein MGC11324	3.9
	438090	AA777534	Hs.191992	ESTs	3.8
50	407938	AA905097	Hs.85050	phospholamban	3.8
	440454	AI733037	Hs.129990	ESTs	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	407762	AW235638	Hs.29475	ESTs	3.8
55	420727	H75701	Hs.99886	complement component 4-binding protein,	3.8
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	3.8
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	3.8
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
60	430205	AB025804	Hs.235168	carbonic anhydrase XIV	3.8
	437458	AL390131	Hs.128751	Homo sapiens cDNA FLJ12235 fis, clone MA	3.8
	451073	AI758905	Hs.206083	ESTs	3.8
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypothei	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
65	444414	AW293214	Hs.8752	transmembrane protein 4	3.8
	402815				3.7
	410585	AW770523	Hs.337501	ESTs	3.7
	425168	R96368		gb:yq37d04.s1 Soares fetal liver spleen	3.7
	449729	R72032	Hs.29235	ESTs	3.7
70	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439001	AF075068		gb:Homo sapiens full length insert cDNA	3.7
	443657	R14973		gb:y42f10.s1 Soares fetal liver spleen	3.7
	404193				3.7
75	416379	N38857	Hs.203933	ESTs	3.7
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	3.7
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	3.7
	412589	R28660	Hs.24305	ESTs	3.7
	421037	AI684808	Hs.197653	ESTs	3.7
80	427088	AA398085	Hs.142390	ESTs	3.7
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heraguin	3.7
	451882	AI821324	Hs.100445	ESTs	3.7
	419983	V55956	Hs.94030	Homo sapiens mRNA: cDNA DKFZp586E1624 (f	3.7
	405001	U58196	Hs.296281	interleukin enhancer binding factor 1	3.7
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	3.7

	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.7
	432781	NM_014133	Hs.278940	PRO0618 protein	3.7
	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.7
5	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	430682	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.7
	430503	AA533574	Hs.152274	ESTs	3.7
10	443305	AI050693	Hs.133318	ESTs	3.7
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.7
	452280	AI911410	Hs.167224	ESTs	3.6
	432189	AA527941		gb:nh30c04.s1 NCLCGAP_Pr3 Homo sapiens	3.6
	406992	S62472		gb:beta-pol=DNA polymerase beta (exon a	3.6
15	441416	AI990139	Hs.148609	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	413998	AW103807	Hs.243933	ESTs	3.6
	440385	AA884283	Hs.192136	ESTs	3.6
	431673	AW971302	Hs.293233	ESTs	3.6
20	401887				3.6
	404793				3.6
	422054	AA322506		gb:EST25146 Cerebellum II Homo sapiens c	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
	449645	AI961092	Hs.196155	ESTs	3.6
	404476				3.6
25	449336	AL119995	Hs.15260	ESTs, Highly similar to AC007228.2 BC372	3.6
	401200				3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
30	443394	AI055865	Hs.133485	ESTs	3.6
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156405	Human DNA sequence from clone 1198H6 on	3.6
	436269	AA707472	Hs.190760	ESTs	3.6
35	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	3.6
	416394	H64111		gb:yr57f03.r1 Soares fetal liver spleen	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
40	435766	R11673	Hs.186498	ESTs	3.6
	448067	R68568	Hs.183373	src homology 3 domain-containing protein	3.6
	441605	AA984647	Hs.128801	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
45	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.5
	450350	T97817	Hs.174880	ESTs	3.5
	451704	AI755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	459037	AW439497	Hs.290656	EST	3.5
	419247	S65791	Hs.89764	fragile X mental retardation 1	3.5
50	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	426724	AA383623	Hs.293616	ESTs	3.5
	434273	AA913143	Hs.26303	ESTs	3.5
	438042	AW296971	Hs.255593	ESTs	3.5
	410500	R09442		gb:yr26c09.r1 Soares fetal liver spleen	3.5
55	416154	Z46122		gb:HSCOV8031 normalized Infant brain cDN	3.5
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.5
	454447	BE163567		gb:QV3-HT0460-Z30200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	444338	AI937026	Hs.146642	ESTs	3.5
60	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	415929	AA724373	Hs.49344	hypothetical protein FLJ11008	3.5
	416009	Z43062		gb:HSC12E041 normalized Infant brain cDN	3.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	3.5
	403515				3.5
65	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	439953	AA918129	Hs.124638	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypothell	3.5
	453931	AL121278	Hs.25144	ESTs	3.5
70	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.5
	413468	BE504766		gb:hz40g01.x1 NCLCGAP_GC6 Homo sapiens	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.5
	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	3.5
75	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	440364	AA910460	Hs.126626	ESTs	3.5
	408190				3.5
80	430762	AI343652	Hs.105667	ESTs	3.5
	451182	D52562	Hs.296317	KIAA1789 protein	3.4
	432437	W07088	Hs.293685	ESTs	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
	407676	AW064111	Hs.279823	ESTs	3.4

5	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	458371	R20991		gb:yg06h01.r1 Soares Infant brain 1NIB H	3.4
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.4
10	423841	AW753957		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.4
	420430	AJ703192		gb:wd92h04.x1 NCL CGAP_Lu24 Homo sapiens	3.4
	443921	AI091310	Hs.134848	ESTs	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
	443475	AI066470	Hs.134482	ESTs	3.4
15	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.4
	453263	R91778	Hs.99369	ESTs	3.4
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	3.4
	456303	AA224872	Hs.115088	ESTs	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
20	439702	AW085525	Hs.134182	ESTs	3.4
	458797	AW001835	Hs.13323	hypothetical protein FLJ22059	3.4
	430140	AW298771	Hs.221999	ESTs	3.4
	423871	AA331806		gb:EST35805 Embryo, 8 week 1 Homo sapien	3.4
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.4
25	446672	T05514		gb:EST03403 Fetal brain, Stratagene (cat	3.4
	431548	AI834273	Hs.9711	novel protein	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	417663	R07483	Hs.180461	ESTs	3.3
30	405455				3.3
	426235	AI631964	Hs.34447	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
	444848	AW451176	Hs.195954	ESTs	3.3
	451426	AW205003	Hs.208063	ESTs	3.3
35	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.3
	401626				3.3
	405780				3.3
	417991	AA731452	Hs.190008	ESTs	3.3
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	3.3
40	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c05 HT0272 Homo	3.3
	426701	AI988103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.3
	445510	AA946676	Hs.282824	ESTs	3.3
45	418663	AK001100	Hs.41690	desmocollin 3	3.3
	447617	AI400762	Hs.176675	ESTs	3.3
	448150	AI472167	Hs.302739	ESTs	3.3
	401040	AL134435	Hs.22269	neuradin 3	3.3
	443283	BE568610		gb:601342622F1 NIH_MGC_63 Homo sapiens c	3.3
50	454777	AW820027		gb:QV0-ST0294-240300-173-g04 ST0294 Homo	3.3
	410767	AJ001873	Hs.66185	Homo Sapiens mRNA, partial cDNA sequence	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
55	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.3
	411880	AW872477		gb:hmc30f03.x1 NCL CGAP_Thy4 Homo sapiens	3.3
	433567	AF073299	Hs.103132	solute carrier family 9 (sodium/hydrogen	3.3
	433805	AA706910	Hs.112742	ESTs	3.3
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.3
60	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	456555	AW592167	Hs.293299	ESTs	3.3
	419189	T95862	Hs.112318	6.2 kd protein	3.3
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	3.3
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.3
65	413200	AA127395	Hs.222414	ESTs	3.3
	416421	AA134006	Hs.79305	eukaryotic translation initiation factor	3.3
	416737	AF154335	Hs.79691	LIM domain protein	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
70	432488	AA551010	Hs.216640	ESTs	3.3
	433386	AW360833		gb:PM1-CT0243-201099-004-d08 CT0243 Homo	3.3
	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	446190	AJ279299	Hs.256584	ESTs	3.3
75	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kd	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
80	434294	AJ271379	Hs.76194	ribosomal protein S5	3.3
	452372	AI885742	Hs.228474	ESTs	3.3
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	3.2
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	3.2
	430548	AW450575	Hs.163203	ESTs, Weakly similar to B34087 hypotheti	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	437845	AA769578	Hs.90488	ESTs	3.2

5	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	414394	AJ904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.2
	417175	R44558	Hs.94002	ESTs	3.2
	456536	AW135986	Hs.257859	ESTs	3.2
	401132				3.2
10	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	450947	AJ745400	Hs.204662	ESTs	3.2
	456605	AJ827786	Hs.259044	ESTs	3.2
	452879	AW905328	Hs.180842	ribosomal protein L13	3.2
15	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.2
	429479	AA453488	Hs.99333	ESTs	3.2
	448090	AJ608821	Hs.270289	ESTs	3.2
	401324				3.2
	404731				3.2
20	419936	AJ792788		gb:cl91d05.y5 NCI_CGAP_K0d5 Homo sapiens	3.2
	455571	BE003714		gb:CV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	433990	AA889328	Hs.112950	ESTs	3.2
	415239	R42608	Hs.139270	ESTs	3.2
	418878	W20090	Hs.6616	ESTs	3.2
25	438079	R09664	Hs.191223	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	3.2
	454145	AA046872	Hs.62798	ESTs	3.2
	446577	AB040933	Hs.15420	KIAA1500 protein	3.2
30	430664	AW969834	Hs.303303	ESTs	3.2
	404588				3.2
	407834	AW084991	Hs.26100	ESTs	3.2
	413087	BE064855		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	440790	AW593050	Hs.128580	ESTs	3.2
35	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	3.2
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone L	3.2
	419261	X07876	Hs.89791	wingless-type MMTV integration site faml	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	444771	AB023201	Hs.11912	KIAA0984 protein	3.2
40	445233	AV653034	Hs.297559	ESTs	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.2
45	403623				3.2
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.2
	444050	AW138295	Hs.135024	ESTs	3.2
	421036	AA810560	Hs.303577	ESTs	3.2
	401459				3.1
50	404404				3.1
	450438	AI696071	Hs.253800	ESTs	3.1
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibitor	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
55	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
	431906	AW328038	Hs.37486	ESTs	3.1
60	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	450271	AI693900	Hs.200920	ESTs	3.1
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	3.1
	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
65	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.1
	446364	AB006624	Hs.14912	KIAA0286 protein	3.1
	436638	AI271945	Hs.134984	ESTs	3.1
	418079	R40058	Hs.6911	ESTs	3.1
	448466	AI522109	Hs.171066	ESTs	3.1
70	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
	415046	R40018	Hs.56400	ESTs	3.1
	448134	AJ470790	Hs.34494	ESTs	3.1
	456027	BE327387	Hs.13913	KIAA1577 protein	3.1
	458023	AW978161	Hs.268555	5'-3' exonuclease 2	3.1
75	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.1
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.1
	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	449138	AW294215	Hs.195631	ESTs	3.1
	455756	BE079307		gb:RC1-BT0623-120200-011-g09 BT0623 Homo	3.1
80	428170	H05530	Hs.12565	ESTs	3.1
	429878	AA460188	Hs.127263	ESTs	3.1
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	3.1
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptid	3.1
	415840	R15955	Hs.21758	ESTs	3.1
	444955	AW002844	Hs.148641	ESTs	3.1
	436020	AA778177	Hs.121724	ESTs	3.1
	453051	AW196690	Hs.224269	ESTs	3.1

	425178	H16097	Hs.161027	ESTs	3.1
	402145				3.1
	410685	AA497117	Hs.129600	ESTs, Moderately similar to ALU1_HUMAN A	3.1
	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
5	456737	BE247203	Hs.124831	CGI-67 protein	3.1
	438214	H06076	Hs.26320	TRABID protein	3.1
	436250	AY004867	Hs.85844	neurotrophic tyrosine kinase, receptor,	3.1
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (lr	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
10	449357	AI076363	Hs.288806	Homo sapiens cDNA FLJ11778 fis, clone HE	3.0
	418950	T78517	Hs.13941	ESTs	3.0
	431508	NM_012481	Hs.182979	ribosomal protein L12	3.0
	405090				3.0
	445409	AI949081	Hs.147862	ESTs	3.0
15	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.0
	408235	AA053381	Hs.75969	proline-rich protein with nuclear target	3.0
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	3.0
20	452073	AA625150	Hs.82098	ESTs	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	427244	AA402400	Hs.178045	ESTs	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sap	3.0
	421376	AA287948	Hs.134110	ESTs	3.0
25	441519	AA972740	Hs.127092	ESTs	3.0
	404367				3.0
	453502	AL039786	Hs.21273	transcription factor NYD-sp10	3.0
	421948	L42583	Hs.334309	keratin 6A	3.0
30	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	400608				3.0
	404042				3.0
	405229				3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
	415452	F09134	Hs.12839	ESTs	3.0
35	430371	D87466	Hs.240112	KIAA0276 protein	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	429014	AI800518	Hs.118158	ESTs	3.0
	405605				3.0
40	400227				3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	427533	R36022	Hs.179566	hypothetical protein FLJ22624	3.0
45	418355	L42563	Hs.1165	ATPase, H ⁺ /K ⁺ transporting, nongastric,	3.0
	433536	AI732163	Hs.188909	ESTs, Weakly similar to alternatively sp	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	449623	C00719	Hs.120440	EST	3.0
	445568	H00918	Hs.268744	KIAA1796 protein	3.0
50	440448	AA885428	Hs.125646	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	444148	AW003204	Hs.151167	ESTs	3.0
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	3.0
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	3.0
	440925	AW511090	Hs.130419	ESTs	3.0
55	428398	AI249368	Hs.98558	ESTs	3.0
	415913	H70302		gb:yr95f07.r1 Soares fetal liver spleen	3.0
	418145	AF121260	Hs.83577	cysteine and glycine-rich protein 3 (car	3.0
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	3.0
	400335	Y13187	Hs.248067	Homo sapiens dmd gene, Intron 11	3.0
60	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	437980	R50393	Hs.278436	KIAA1474 protein	3.0
	455955	BE162394		gb:PM2-HT0451-170100-004-s08 HT0451 Homo	3.0
	414899	AW975433	Hs.36288	ESTs	2.9
65	403786				2.9
	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.9
70	457041	AA399018	Hs.250835	ESTs	2.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.9
	422336	AI761322	Hs.115285	dihydroliipoamide S-acetyltransferase (E2	2.9
	451684	AA889081	Hs.153952	5' nucleotidase (CD73)	2.9
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.9
75	455249	AW876538		gb:RC3-PT0028-190100-012-b05 PT0028 Homo	2.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.9
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	2.9
	405302				2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
80	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9

	425793	AA363946	Hs.20969	ESTs	2.9
	401462				2.9
	458817	A1522129	Hs.173119	ESTs	2.9
5	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.9
	419875	AA853410	Hs.93557	proenkephalin	2.9
	423047	NM_005323	Hs.123064	H1 histone family, member T (testis-spec	2.9
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.9
	401368				2.9
10	418531	R96760	Hs.183758	ESTs	2.9
	447290	AA76732	Hs.263912	ESTs	2.9
	411143	AI027604	Hs.159650	ESTs	2.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	2.9
	405783				2.9
15	444459	AI680624	Hs.148676	ESTs	2.9
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	2.9
	425745	U4060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.9
	444827	R09764	Hs.20416	ESTs	2.9
	451195	U10492	Hs.438	mesenchyme homeo box 1	2.9
20	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh50f07.s1 NCL_CGAP_Pr6 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.9
	455699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	2.9
25	459440	BE048054		gb:tz46c03.y1 NCL_CGAP_Brn52 Homo sapien	2.9
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	437913	AJ140825	Hs.121623	ESTs	2.9
30	443185	NM_006134	Hs.284142	chromosome 21 open reading frame 4	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	2.9
	437183	AJ928184	Hs.122011	ESTs	2.9
	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
35	442726	AW136066	Hs.19145	ESTs	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441115	R69910	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	2.9
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.9
	415628	F13080		gb:HSC3ID041 normalized Infant brain cDN	2.9
40	423637	AL137279	Hs.130187	Homo sapiens mRNA: cDNA DKFZp434O1214 (f	2.9
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypotheti	2.9
	450877	AJ799608	Hs.29178	ESTs	2.9
	439063	AF085922	Hs.113968	ESTs	2.9
	401526				2.9
45	408751	N91553	Hs.258343	ESTs	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.9
50	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	452589	BE159915	Hs.61406	ESTs, Weakly similar to 2004399A chromos	2.8
	403011				2.8
	436154	AA764950	Hs.119898	ESTs	2.8
	408221	AA912183	Hs.47447	ESTs	2.8
55	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.8
	415399	T26994	Hs.177198	ESTs	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	443558	AA256769	Hs.94949	methylmalonyl-CoA epimerase	2.8
	455092	BE152428		gb:CM0-HT0323-161299-126-b04 HT0323 Homo	2.8
60	439703	AF086538	Hs.196245	ESTs	2.8
	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.8
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.8
	434715	BE005346	Hs.116410	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
65	439235	N45513	Hs.46608	ESTs	2.8
	453736	AL118874	Hs.34871	zinc finger homeobox 1B	2.8
	404967				2.8
	437783	AJ683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.8
70	426942	AA393551	Hs.97450	ESTs	2.8
	403513				2.8
	419077	AA233885	Hs.164526	ESTs	2.8
	421823	N40850	Hs.28625	ESTs	2.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	2.8
75	451007	H38108	Hs.32759	ESTs	2.8
	407803	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	2.8
	409642	AW450809	Hs.257347	ESTs	2.8
	439492	AF086310	Hs.103159	ESTs	2.8
	420814	AA721155	Hs.190440	ESTs	2.8
80	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	2.8
	428350	AW873520	Hs.112017	GE36 gene	2.8
	405456				2.8
	442459	AI264628	Hs.125428	ESTs	2.8
	415763	Z42285	Hs.5181	proliferation-associated 2G4, 38kD	2.8

5	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	435720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	449539	W80363	Hs.58446	ESTs	2.8
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.8
	408749	H65489	Hs.250659	ESTs	2.8
10	404652				2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	2.8
	402131				2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
15	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	444217	AV648751	Hs.282395	ESTs	2.8
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypothel	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-101 DT0041 Homo	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
20	433513	AI566356	Hs.171437	ESTs	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	451496	AW503407		gb:U1-HF-BNO-akw-d-11-0-U1.r1 NIH_MGC_50	2.8
	420273	AI652864	Hs.197257	ESTs	2.8
	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	2.8
25	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	425012	T77668	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.8
	41609	AA946764	Hs.133460	ESTs	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
30	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypothel	2.8
	457314	AA479597	Hs.193659	hypothetical protein DKFZp586J1119	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
	418888	AU076801	Hs.89435	cadherin 17, LI cadherin (liver-intestin	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
35	459450	AA426429	Hs.98463	EST	2.8
	424188	AW954552	Hs.142634	zinc finger protein	2.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	2.7
	427443	AA402713	Hs.97872	ESTs	2.7
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.7
40	413091	BE065063		gb:RC1-BT0313-110500-017-e02 BT0313 Homo	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.7
45	408243	Y00787	Hs.624	interleukin 8	2.7
	407308	H67394	Hs.331325	ESTs, Weakly similar to I38022 hypothel	2.7
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.7
	404587	M99587	Hs.104134	homeo box (H6 family) 1	2.7
	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.7
50	416431	AW384459	Hs.172004	titin	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	441218	BE327561	Hs.202345	ESTs	2.7
	440911	AA909536	Hs.143562	ESTs	2.7
	411131	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo	2.7
	438602	AI167149	Hs.123374	ESTs, Weakly similar to mariner transpos	2.7
60	441191	AI693930	Hs.148816	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	429905	AL080128	Hs.225998	DKFZP434C153 protein	2.7
65	449396	BE169100	Hs.195029	ESTs	2.7
	450777	AA255646	Hs.60478	ESTs, Moderately similar to S47073 finge	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	405523				2.7
	434849	AW292765	Hs.8053	ESTs	2.7
70	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypothel	2.7
	438055	AA776655	Hs.270942	ESTs	2.7
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	2.7
	405738				2.7
	417806	AI867277	Hs.183733	ESTs	2.7
75	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kgd1 Homo sapiens	2.7
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	446092	N33522	Hs.145894	ESTs	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.7
80	444931	AV652066	Hs.75113	general transcription factor IIIA	2.7
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.7
	453264	AA034137	Hs.271955	ESTs	2.7
	438370	AA843242	Hs.485523	ESTs	2.7
	406092				2.7
	454874	AW836407	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7

5	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.7
	441884	AW172630	Hs.144884	ESTs	2.7
	416211	R14625		gb:yg45c03.r1 Soares Infant brain 1N18 H	2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	2.7
10	453696	AI989482	Hs.146266	kinesin family member 13A	2.7
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.7
	425876	AW005887	Hs.234058	ESTs	2.7
	450458	AA009926		gb:zi07a05.r1 Soares_fetal_liver_spleen_	2.7
	406603				2.7
15	410181	AA68210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	410871	D78367	Hs.66739	keratin 12 (Meesmann corneal dystrophy)	2.7
	412706	R97106	Hs.167546	ESTs	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	436329	AI798750	Hs.163960	Homo sapiens heat shock transcription fa	2.7
20	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	2.7
	419296	AA236115	Hs.120785	ESTs	2.7
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.7
25	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	411409	AW844803		gb:RC3-CN0056-170300-015-f08 CN0056 Homo	2.7
	426662	AA879474	Hs.122710	ESTs	2.7
	400268				2.7
	438782	AA828380	Hs.126733	ESTs	2.7
30	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	2.7
	412486	AF210650	Hs.150858	NAG19 protein	2.7
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	2.7
	457900	AW976692	Hs.291665	ESTs	2.7
	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	2.7
35	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	435608	AW183971	Hs.250896	ESTs	2.7
	413627	BE182082	Hs.246973	ESTs	2.7
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
40	441396	AW293577	Hs.186890	ESTs	2.6
	452046	AB018345	Hs.27657	KIAA0802 protein	2.6
	454936	AW846082		gb:MR3-CT0176-081099-002-d01 CT0176 Homo	2.6
	454434	AA083558	Hs.261286	ESTs	2.6
	436888	AI942357	Hs.187870	ESTs	2.6
45	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 Integrin	2.6
	416690	H84078	Hs.108551	ESTs	2.6
	436471	AA719813	Hs.117662	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
50	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.6
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.6
	455544	AW993880		gb:RC3-BN0034-240400-017-d09 BN0034 Homo	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
55	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	2.6
	429864	AA460039	Hs.286	ribosomal protein L4	2.6
	456273	AF154846	Hs.1148	zinc finger protein	2.6
	402603				2.6
	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2.6
60	420621	AA278808		gb:zsa79c09.r1 NCL_CGAP_GC81 Homo sapiens	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
	438295	AI394151	Hs.37832	ESTs	2.6
	450181	H05254	Hs.201198	ESTs	2.6
65	433764	AW753676	Hs.39982	ESTs	2.6
	433229	AB040925	Hs.91625	KIAA1492 protein	2.6
	443718	AI083580	Hs.221373	ESTs	2.6
	418246	AI472179	Hs.121276	ESTs, Weakly similar to R5HU7A ribosomal	2.6
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	2.6
70	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.6
	419318	AW969742	Hs.291005	ESTs	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	404414				2.6
	446444	AI743737	Hs.24370	ESTs	2.6
75	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.6
	418310	AA814100	Hs.86693	ESTs	2.6
	454481	AW794878	Hs.314230	ESTs, Highly similar to clock (H.sapiens	2.6
	441216	BE299830	Hs.192908	ESTs	2.6
80	438257	AW474419	Hs.224794	ESTs	2.6
	442284	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	419505	AA243660	Hs.143061	ESTs	2.6
	417596	R07343	Hs.226823	ESTs, Moderately similar to I54374 gene	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	454887	AW835924		gb:PM1-LT0018-250200-002-e09 LT0018 Homo	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6

5	457630	AI680803	Hs.112627	ESTs	2.6
	424210	T71397	Hs.222707	KIAA1718 protein	2.6
	447748	AA22023	Hs.161338	ESTs	2.6
	411970	AA099142	Hs.13804	hypothetical protein dJ462023.2	2.6
	441233	AA972965	Hs.135568	ESTs	2.6
	400706				2.6
	436033	H75391	Hs.255748	ESTs	2.6
	440836	AW370882	Hs.222080	ESTs	2.6
10	431086	AI829692	Hs.211561	ESTs	2.6
	455110	BE154505		gb:PM0-HT0343-281299-003-e06 HT0343 Homo	2.6
	455878	BE056007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.6
	413088	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.6
15	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.6
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.6
	442690	AI014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.6
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	2.6
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.6
	403271				2.6
20	429761	AI276780	Hs.135173	ESTs	2.6
	437085	AA743935	Hs.202329	ESTs	2.6
	450822	AW771860	Hs.205130	ESTs	2.6
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	2.6
25	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	2.6
	430357	AW976789	Hs.165607	ESTs	2.6
	417249	N58198	Hs.182898	ESTs	2.6
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.6
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	2.6
30	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ25448 fis, clone H	2.6
	446302	AI285848	Hs.149757	ESTs	2.6
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6
	428944	AA780181	Hs.41182	Homo sapiens DC47 mRNA, complete cds	2.6
	419647	AA348947	Hs.91816	hypothetical protein	2.6
35	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	2.6
	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	2.6
	452450	AW854891	Hs.194720	ATP-binding cassette, sub-family G (WHIT	2.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	2.6
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	2.6
40	447505	AL049266	Hs.18724	Homo sapiens mRNA: cDNA DKFZp564F093 (fr	2.6
	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.6
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.5
45	447624	AI640326	Hs.62713	ESTs	2.5
	411736	AW859089		gb:MR1-CT0350-150200-002-d02 CT0350 Homo	2.5
	416334	H53139	Hs.36271	ESTs	2.5
	446818	AI342668	Hs.279765	ESTs	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
50	442278	AI733477	Hs.166313	ESTs	2.5
	453393	AW956392	Hs.110376	ESTs	2.5
	420854	AW296927		gb:UH-H-BW0-ajc-c-07-0-ULs1 NCL CGAP_Su	2.5
	408729	AA195764	Hs.72639	ESTs	2.5
55	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	2.5
	411660	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	409156	N76186	Hs.173518	M-phase phosphoprotein homolog	2.5
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.5
	430291	AV660345	Hs.238126	CGI-49 protein	2.5
60	401785				2.5
	402369				2.5
	439079	AF085937	Hs.38348	ESTs	2.5
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	2.5
	411463	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	2.5
65	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.5
	404988				2.5
	409446	AI581173	Hs.67688	ESTs	2.5
	412613	AA653507	Hs.285711	hypothetical protein FLJ13089	2.5
	417909	R35614		gb:yg65e08.r1 Soares infant brain 1N1B H	2.5
70	454743	AW818456	Hs.79347	KIAA0211 gene product	2.5
	406364				2.5
	404108				2.5
	411934	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.5
	415747	AA381209		gb:EST94257 Activated T-cells 1 Homo sap	2.5
75	443526	AW792804	Hs.134002	ESTs	2.5
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.5
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	2.5
	458771	AW295151	Hs.163612	ESTs	2.5
	414349	BE512968		gb:501172296F1 NIH_MGC_15 Homo sapiens c	2.5
80	426589	AW954460		gb:EST366530 MAGE resequences, MAGC Homo	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	2.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	2.5
	434784	AA649051	Hs.164007	ESTs	2.5

	429322	D86984	Hs.199243	KIAA0231 protein	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
5	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	449410	AA001356	Hs.18159	ESTs	2.5
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.5
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ca	2.5
	416944	N22809		gb:yyw41e07.s1 Weizmann Olfactory Epithel	2.5
10	423010	W25436	Hs.90725	ESTs, Moderately similar to I38022 hypot	2.5
	412505	AA974491	Hs.21734	ESTs	2.5
	446399	AI298405	Hs.150080	ESTs	2.5
	412139	BE044976		gb:hn25b10.x1 NCL_CGAP_Thy7 Homo sapiens	2.5
	403691				2.5
15	424025	AI701852	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	2.5
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular card	2.5
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.5
	457770	BE065030	Hs.124179	ESTs	2.5
20	427731	AA411750	Hs.20943	ESTs	2.5
	426920	AA393351	Hs.132121	ESTs	2.5
	427794	AA709186	Hs.282963	ESTs	2.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
25	414550	BE379808		gb:601159567T1 NIH_MGC_53 Homo sapiens c	2.5
	436391	AJ227892	Hs.146274	ESTs	2.5
	401889				2.5
	423346	AI267677	Hs.127416	synaptojanin 1	2.5
	444905	AW135863	Hs.209228	ESTs	2.5
30	424539	L02911	Hs.150402	activin A receptor, type I	2.5
	400861				2.5
	458426	AJ084514	Hs.249587	ESTs	2.5
	429520	AA160142	Hs.205058	hypothetical protein FLJ20075	2.5
	403568				2.5
35	430632	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.5
	451078	AJ927694	Hs.204470	ESTs	2.5
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.5
	427888	AA417088	Hs.137598	ESTs	2.5
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.5
40	422840	U44059	Hs.121481	thyrotrophic embryonic factor	2.5
	404708				2.5
	405008				2.5
	453772	BE281431	Hs.16323	Homo sapiens, Similar to G antigen 8, cl	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
45	444575	AI284847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tl49a12.x1 NCL_CGAP_GC6 Homo sapiens	2.5
	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.5
	454566	AW807605		gb:MR4-ST0059-120100-001-b06 ST0059 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
50	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.4
	407851	NM_014496	Hs.40434	ribosomal protein S6 kinase, 90kD, polyp	2.4
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.4
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-lin	2.4
	406468				2.4
55	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.4
	408617	R61738	Hs.124128	ESTs	2.4
	409627	AW997628	Hs.313637	ESTs	2.4
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.4
60	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	2.4
	428709	BE268717	Hs.104918	hypothetical protein FLJ21940	2.4
	429654	AI435046	Hs.164318	ESTs	2.4
	432253	AW090822	Hs.274174	transcription elongation factor (SII) e	2.4
65	439786	AV652707	Hs.33756	Homo sapiens mRNA full length Insert cDN	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
	453052	R63050	Hs.223813	ESTs	2.4
	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.4
70	452843	AI796769	Hs.208320	ESTs	2.4
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	2.4
	449695	AA164569	Hs.34550	ESTs	2.4
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.4
	400641				2.4
75	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.4
	432808	NM_015985	Hs.278973	angiopoietin-3	2.4
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411561	H81184	Hs.285017	hypothetical protein FLJ21799	2.4
80	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheti	2.4
	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	435663	AI023707	Hs.134273	ESTs	2.4
	455879	BE153275		gb:PMO-HT0335-180400-008-e11 HT0335 Homo	2.4
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.4

	409041	AB033025	Hs.50081	KIAA1199 protein	2.4
	423244	AL039379	Hs.209502	ESTs, Weakly similar to ubiquitous TPR m	2.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.4
5	448889	BE140902		gb:IL1-HT0028-240699-001-C11 HT0028 Homo	2.4
	439481	AF086294	Hs.125844	ESTs	2.4
	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.4
	403053	R58624	Hs.2185	eukaryotic translation elongation factor	2.4
	409298	AA070211		gb:znm68c04.s1 Stratagene neuroepithelium	2.4
10	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	447640	AJ417187		gb:lg75g11.x1 Soares_NhHMPu_S1 Homo sapi	2.4
	447849	AJ538147	Hs.164277	ESTs	2.4
	458763	AJ693417	Hs.293309	ESTs	2.4
	404638				2.4
15	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.4
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.4
	408238	W95901		gb:ze43d11.r1 Soares retina N2b4HR Homo	2.4
	436747	AW977192	Hs.291343	ESTs	2.4
20	437048	AA743240	Hs.91582	ESTs	2.4
	413143	BE067232		gb:PM3-BT0347-170200-001-b05 BT0347 Homo	2.4
	404561				2.4
	444009	AJ380792	Hs.135104	ESTs	2.4
	400250				2.4
25	403891				2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AJ927629	Hs.57873	ESTs	2.4
	441227	AW295407	Hs.128893	ESTs	2.4
	445038	AJ635444	Hs.143917	dJ467N11.1 protein	2.4
30	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458824	AJ362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	2.4
	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.4
35	450068	AW207212	Hs.280925	ESTs	2.4
	444750	AW242684	Hs.243623	ESTs	2.4
	414591	AJ888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	407264	L34727		gb:Homo sapiens T-cell receptor beta (TC	2.4
40	443169	AJ038687	Hs.133338	ESTs	2.4
	426536	AJ949749	Hs.44441	ESTs	2.4
	449752	AJ668626	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	2.4
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF 1 [2.4
	429504	X99133	Hs.204238	ipocalin 2 (oncogene 24p3)	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
45	430484	D82880	Hs.241548	RAS p21 protein activator 2	2.4
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.4
	447375	AJ376660	Hs.257822	ESTs	2.4
	444230	H95537	Hs.146067	ESTs	2.4
	439911	AA854024	Hs.189110	ESTs	2.4
50	421296	NM_002666	Hs.103253	perilipin	2.4
	449385	AJ650471	Hs.270370	ESTs	2.4
	430044	AA464510	Hs.152812	ESTs	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	409103	AF251237	Hs.112208	XAGE-1 protein	2.4
55	421354	AA766485	Hs.269664	ESTs	2.4
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	2.4
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein	2.4
	441358	AW173212	Hs.129041	ESTs	2.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.4
60	414290	AJ568801	Hs.71721	ESTs	2.4
	427342	AL110150	Hs.176680	Homo sapiens mRNA; cDNA DKFZp586D0724 (f	2.4
	459459	AA460445		gb:zx66h11.r1 Soares_tetal_fetus_Nb2HP8_	2.4
	434638	H50758		gb:yp86e08.r1 Soares fetal liver spleen	2.4
	442717	R88362	Hs.180691	ESTs, Weakly similar to T23976 hypotheti	2.4
65	419537	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	458734	AJ554946	Hs.158794	ESTs	2.4
	449529	AJ990559	Hs.232033	ESTs	2.4
70	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.4
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.4
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.4
	430957	AJ937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.4
	418188	AW139413	Hs.151880	ESTs	2.4
75	424103	NM_001918	Hs.139410	dihydrolipoamide branched chain transacy	2.4
	454324	AW608930	Hs.52184	hypothetical protein FLJ20618	2.4
	437369	AA765230	Hs.121742	ESTs	2.4
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	2.4
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.4
80	400462				2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	424195	U50536	Hs.142907	Human BRCA2 region, mRNA sequence CG011	2.4
	434163	AW974720	Hs.25206	group XII secreted phospholipase A2	2.4

	435985	AA703154	Hs.191834	ESTs	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	458661	AI299789	Hs.166999	ESTs, Moderately similar to I38344 tfin	2.4
	459023	AW968226	Hs.60798	ESTs	2.4
5	406005				2.4
	456561	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypothei	2.4
	452161	R43077	Hs.221747	ESTs	2.4
	436590	AI393115	Hs.127655	ESTs	2.4
	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo	2.4
10	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	433479	AW511459	Hs.249972	ESTs	2.4
	441676	BE564206	Hs.49889	ESTs	2.4
	407965	W21483	Hs.41707	heat shock 27kD protein 3	2.4
	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
15	452958	AA883929	Hs.40527	ESTs	2.4
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.4
	405347				2.4
	440577	AA889945	Hs.326381	EST	2.4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
20	457024	AA397546	Hs.119151	ESTs	2.4
	404249				2.4
	437511	AI807500	Hs.125247	ESTs	2.4
	421338	AA287443		gb:zs52c10.r1 NCL CGAP_GCB1 Homo sapiens	2.4
	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	2.4
25	428277	AA425220	Hs.179203	ESTs	2.4
	444870	AI200621	Hs.148504	ESTs	2.4
	402090				2.4
	458507	AI185703	Hs.206957	ESTs	2.4
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.4
30	446534	AI307356	Hs.175225	ESTs	2.4
	453111	AB014588	Hs.31720	hephaestin	2.4
	405230				2.4
	405935				2.4
35	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	420724	AA279694	Hs.191540	ESTs	2.4
	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone Z2453 mariner transposon	2.4
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.3
40	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRNA	2.3
	440621	AW296024	Hs.150434	ESTs	2.3
	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	2.3
	424131	AA335714	Hs.199665	ESTs	2.3
	450737	AW007152	Hs.203330	ESTs	2.3
	453687	T55674	Hs.283108	hemoglobin, gamma G	2.3
45	442704	AI015463	Hs.130987	ESTs	2.3
	457756	AA126136	Hs.38125	Interferon-Induced protein 75, 52kD	2.3
	412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo	2.3
	418998	F13215	Hs.287849	ESTs, Weakly similar to T22074 hypothei	2.3
50	419751	AW195581	Hs.93121	KIAA0761 protein	2.3
	429485	AW197086	Hs.99338	ESTs	2.3
	433377	AI752713	Hs.43845	ESTs	2.3
	434896	AW022054	Hs.136591	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
55	444711	AI188739	Hs.148488	ESTs	2.3
	445621	AI733818	Hs.145549	ESTs	2.3
	449182	AW292381	Hs.224150	ESTs	2.3
	430987	Y08564	Hs.248190	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.3
	404068				2.3
60	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.3
	438315	R56795	Hs.82419	ESTs	2.3
	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	447998	AI768289	Hs.304389	ESTs	2.3
	410150	AW382942	Hs.6774	ESTs	2.3
65	432792	AA448114	Hs.278950	protocadherin beta 1	2.3
	443363	AI792629	Hs.133293	ESTs	2.3
	440729	AA904739	Hs.128204	ESTs	2.3
	411045	AW854691	Hs.115325	RAB7, member RAS oncogene family-like 1	2.3
	459207	AW138410	Hs.45051	ESTs	2.3
70	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.3
	458684	BE281115	Hs.98855	hypothetical protein FLJ20909	2.3
	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.3
	401899				2.3
	432116	AA902953	Hs.308538	ESTs	2.3
75	404196				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	413308	W28131		gb:4217 Human retina cDNA randomly prime	2.3
	430264	AA470519		gb:nc71f1f10.s1 NCL CGAP_Pr1 Homo sapiens	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
80	453305	R39224	Hs.267997	EHM2 gene	2.3
	451963	AI825440	Hs.224952	ESTs	2.3
	453043	AW136440	Hs.224277	ESTs	2.3
	435559	AF209198	Hs.42638	zinc finger protein 277	2.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	2.3

5	434120	AI435050	Hs.143937	ESTs	2.3
	429768	AA805719	Hs.192154	ESTs	2.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.3
	455841	BE145836		gb:MR0-HT0208-101299-202-b08 HT0208 Homo	2.3
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
	430706	NM_003540	Hs.247816	H4 histone family, member C	2.3
	428268	AA424957	Hs.294132	ESTs	2.3
	458833	AW236702	Hs.171431	ESTs, Weakly similar to A46010 X-linked	2.3
10	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	2.3
	444109	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.3
	428411	AW291464	Hs.10338	ESTs	2.3
	433098	AW190593	Hs.151143	ESTs	2.3
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	2.3
	453178	AA496086	Hs.61648	ESTs	2.3
15	404569				2.3
	413841	M34276	Hs.75576	plasminogen	2.3
	424068	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	2.3
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	2.3
20	442710	AI015631	Hs.23210	ESTs	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451284	AI768235		gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.3
	454784	AW820626		gb:RCO-ST0299-190100-012-e10 ST0299 Homo	2.3
	429080	AA446228	Hs.99057	ESTs	2.3
	404166				2.3
25	416327	R99822	Hs.36172	ESTs	2.3
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.3
	438504	AW665281	Hs.224625	ESTs	2.3
	435325	AI038388	Hs.119309	ESTs	2.3
30	421253	AI188102	Hs.31028	ESTs	2.3
	427046	BE246180	Hs.121385	ESTs	2.3
	432711	AA563785	Hs.152465	ESTs, Weakly similar to I38022 hypotheti	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	2.3
35	448458	AW614367	Hs.171054	ESTs	2.3
	452542	AW812256		gb:RCO-ST0174-191099-031-a07 ST0174 Homo	2.3
	417768	R24732	Hs.175139	ESTs	2.3
	427374	AI150033	Hs.143586	ESTs	2.3
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.3
40	423600	AI633559	Hs.310359	ESTs	2.3
	413006	W03857	Hs.34298	ESTs	2.3
	434698	BE044674		gb:hm46f02.x1 NCI_CGAP_RDF1 Homo sapiens	2.3
	407639	AW205369	Hs.312830	ESTs	2.3
	455121	BE156459		gb:QVO-HT0368-040100-082-f06 HT0368 Homo	2.3
45	448117	H49129	Hs.172982	ESTs	2.3
	443931	H23213	Hs.22657	ESTs	2.3
	450795	AW173371	Hs.60435	ESTs	2.3
	418632	AW118745	Hs.9460	Homo sapiens mRNA: cDNA DKFZp547C244 (fr	2.3
	419441	AW023731	Hs.274368	MSTP032 protein	2.3
50	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	2.3
	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.3
	455964	BE168924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.3
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
55	449272	AW137656	Hs.197645	ESTs	2.3
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	2.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.3
	444715	AV650947	Hs.282464	ESTs	2.3
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	2.3
60	444140	AV648089	Hs.282383	ESTs	2.3
	423949	AI014546	Hs.130912	ESTs	2.3
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	445711	T79811	Hs.193691	ESTs	2.3
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.3
65	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.3
	429180	AA808287	Hs.58893	ESTs	2.3
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.3
	425523	AB007948	Hs.158244	KIAA0479 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
70	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248938	Hs.173044	ESTs, Weakly similar to I38022 hypotheti	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	436294	AA708310		gb:zg07b07.s1 Soares_pineal_gland_N3HPG	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	433939	AL133887	Hs.254122	hypothetical protein	2.3
75	450048	AI693269	Hs.202273	ESTs	2.3
	451640	AA185601	Hs.26771	Human DNA sequence from clone 747H23 on	2.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.3
	405920				2.3
80	405747				2.3
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.3
	420457	AA482280	Hs.191856	ESTs	2.3
	407726	AA435679	Hs.88594	ESTs	2.3
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.3

	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	435352	AI056599	Hs.120893	ESTs	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
5	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.3
	449015	AL038958	Hs.22858	protein tyrosine phosphatase, non-recept	2.3
	411377	AW841462		gb:RC5-CN0014-080300-012-B09 CN0014 Homo	2.3
10	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.3
	411815	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.3
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
15	445117	AI208754	Hs.147359	ESTs	2.3
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.2
	420230	AL034344	Hs.284186	forkhead box C1	2.2
	411517	AW850267		gb:IL3-CT0219-161199-031-A09 CT0219 Homo	2.2
	403678				2.2
20	457003	S78234	Hs.172405	cell division cycle 27	2.2
	404531	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Th	2.2
	423045	AW987472	Hs.183302	PCTAIRE protein kinase 2	2.2
	409427	AW389668		gb:RC2-ST0168-071299-013-f08 ST0168 Homo	2.2
25	434745	AW974445	Hs.185155	ESTs, Weakly similar to T12482 hypothet	2.2
	400696				2.2
	407259	L02256		gb:Human Fab fragment binding syncytial	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
30	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	458303	AI264628	Hs.125428	ESTs	2.2
	405692				2.2
	403572				2.2
35	415380	F07953	Hs.16085	putative G-protein coupled receptor	2.2
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.2
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.2
	456472	AK001714	Hs.95744	hypothetical protein similar to ankyrin	2.2
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.2
40	428231	U17989	Hs.183105	nuclear autoantigen	2.2
	454086	AW885909	Hs.6975	PRO1073 protein	2.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.2
	416348	H65887	Hs.272163	ESTs	2.2
	403780				2.2
45	414262	AW975616	Hs.291469	ESTs	2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	419216	AI076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
50	416588	H66558		gb:yu16e04.r1 Soares fetal liver spleen	2.2
	425368	AB014595	Hs.155976	cutlin 4B	2.2
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.2
	441638	AW293202	Hs.133451	ESTs	2.2
	446845	AI343645	Hs.156108	ESTs	2.2
55	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	2.2
	436574	AW293527	Hs.126465	ESTs	2.2
	424584	H10692	Hs.13310	ESTs	2.2
	456347	U00803	Hs.89426	lym-related kinase	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
60	459364	W69284		gb:zd46c03.r1 Soares_fetal_heart_NbHH19W	2.2
	430686	NM_001942	Hs.2633	desmoglein 1	2.2
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	2.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.2
	403525				2.2
65	453343	AA905353	Hs.121622	ESTs	2.2
	421574	AJ000152	Hs.105924	defensin, beta 2	2.2
	449327	AI638743	Hs.224672	ESTs	2.2
	454769	AW819848		gb:QV0-ST0294-070300-151-b04 ST0294 Homo	2.2
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	2.2
70	401614				2.2
	404767				2.2
	403534				2.2
	410694	AW770778	Hs.281238	ESTs	2.2
	436193	AA706059	Hs.255286	ESTs	2.2
75	439626	N22415	Hs.189080	ESTs	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
	441453	AW176106	Hs.285459	ESTs	2.2
	424946	M54572	Hs.153932	protein tyrosine phosphatase, non-recept	2.2
	437332	AA814943		gb:oc07d06.s1 NCI_CGAP_GC81 Homo sapiens	2.2
	454419	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	2.2
80	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	2.2
	450579	AW136774	Hs.48614	ESTs	2.2
	400664				2.2
	447613	AL041057	Hs.33363	DKFZP434N093 protein	2.2

	402669	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	2.2
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.2
	432797	AA565264	Hs.136443	ESTs	2.2
	405608				2.2
5	426365	AA376667	Hs.10283	RNA binding motif protein 8B	2.2
	405634				2.2
	423646	H02364		gb:yf35d06.r1 Soares placenta Nb2HP Homo	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
10	436572	AA723274	Hs.278596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
15	433781	AA609379	Hs.192083	ESTs	2.2
	450587	AI828854	Hs.258538	striatin, calmodulin-binding protein	2.2
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	2.2
	448756	AI739241	Hs.171480	ESTs	2.2
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.2
20	454471	AW802125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.2
	419107	AW085152	Hs.292987	ESTs	2.2
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.2
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	2.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.2
25	456056	AA463650	Hs.337532	ESTs, Weakly similar to A47582 B-cell gr	2.2
	409998	M78345	Hs.98265	KIAA1877 protein	2.2
	422352	AA766296	Hs.99200	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	433919	AA746311		gb:oa56d12.r1 NCL_CGAP_GCB1 Homo sapiens	2.2
30	455771	BE084820	Hs.186711	hypothetical protein FLJ120070	2.2
	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fls, clone HE	2.2
	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.2
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	2.2
	458037	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	2.2
35	434239	AF119910	Hs.283047	hypothetical protein PRO2964	2.2
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fls, clone HE	2.2
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.2
	400697				2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
40	447039	AV681798	Hs.282915	ESTs	2.2
	404593				2.2
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.2
	421976	AL138443	Hs.23450	mitochondrial ribosomal protein S25	2.2
	401673				2.2
45	425001	U55184	Hs.154145	hypothetical protein FLJ11585	2.2
	447816	NM_007233	Hs.274329	TP53 target gene 1	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
	419118	AA234223	Hs.139204	ESTs	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
50	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	454749	AW818649		gb:RC1-ST0278-040400-018-e02 ST0278 Homo	2.2
	456933	AA363946	Hs.20969	ESTs	2.2
	402942				2.2
	437064	AI023264		gb:ov64h08.s1 Soares_testis_NHT Homo sap	2.2
55	458623	AI305223	Hs.148056	ESTs	2.2
	415257	F03016	Hs.27513	ESTs	2.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	2.2
	442783	AI017586	Hs.131181	ESTs	2.2
	444313	AI140494	Hs.197955	KIAA0704 protein	2.2
60	453444	AL036531		gb:DKFZp564I1162_r1 564 (synonym: hibr2)	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
	430013	AA463833	Hs.151275	ESTs, Weakly similar to TRHY_HUMAN TRUCH	2.2
	437138	AI935622	Hs.271245	ESTs	2.2
	406298				2.2
65	409723	AW885757	Hs.257862	ESTs	2.2
	414481	AW451956	Hs.8383	bromodomain adjacent to zinc finger doma	2.2
	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fls, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
70	445061	AI253094	Hs.145227	ESTs	2.2
	442617	AW340093	Hs.130538	ESTs	2.2
	438298	H23542	Hs.181788	ESTs	2.2
	454916	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	2.2
	428017	AA424983	Hs.98312	ESTs	2.2
75	451149	AL047586	Hs.10283	RNA binding motif protein 8B	2.2
	418076	R61388	Hs.6724	ESTs	2.2
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	2.2
	441811	AI073548	Hs.164597	ESTs	2.2
	434763	AA648618		gb:ns07a11.r1 NCL_CGAP_Ew1 Homo sapiens	2.2
80	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.2
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.2
	415424	Z44766		gb:HSC28G081 normalized infant brain cDN	2.2
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	2.2
	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	2.2

	429509	AF002246	Hs.210863	cell adhesion molecule with homology to	2.2
	448700	BE614182	Hs.123075	ESTs	2.2
	457741	BE044740		gb:hm55g10.x1 NCL_CGAP_RDF1 Homo sapiens	2.2
5	437927	AI039789	Hs.25982	hypothetical protein FLJ21031	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
10	438290	AA843719	Hs.122341	ESTs	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	455735	BE161124		gb:PMO-HT0425-141299-001-A06 HT0425 Homo	2.2
	458455	AV648310	Hs.213488	ESTs	2.2
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.2
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	2.2
15	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	2.2
	441874	AA970389	Hs.128055	ESTs	2.2
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	433629	R13140	Hs.13359	ESTs	2.2
	415266	AA164199	Hs.270152	ESTs	2.2
20	440633	AI140686	Hs.263320	ESTs	2.2
	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.2
	401240				2.2
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
	436992	AA741074	Hs.120750	ESTs	2.2
30	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	2.1
	400040				2.1
	458762	AW802754		gb:IL2-UM0076-030400-061-H01 UM0076 Homo	2.1
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.1
35	419953	BE267154	Hs.125752	ESTs	2.1
	410648	AW792909		gb:CM0-UM0001-010300-258-c05 UM0001 Homo	2.1
	423717	AA330036	Hs.152003	ESTs	2.1
	436683	AW991278	Hs.57787	ESTs	2.1
	445225	AJ216555	Hs.202398	ESTs	2.1
40	410991	AW812790		gb:RC3-ST0186-141299-014-g08 ST0186 Homo	2.1
	412639	AW961284	Hs.296235	ESTs	2.1
	447777	AJ424223		gb:te95a05.x1 NCL_CGAP_Pr28 Homo sapiens	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	404526	AJ912555	Hs.157195	peptide YY, 2 (seminalplasmin)	2.1
45	452492	BE063096		gb:CM4-BT0266-091199-039-e02 BT0266 Homo	2.1
	417154	AI674701	Hs.21388	ESTs	2.1
	428152	AA422030		gb:zv26h05.r1 Soares_NhiHMPu_S1 Homo sapi	2.1
	442312	AI820617	Hs.129216	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	456513	AA279143	Hs.88561	ESTs	2.1
50	430712	AW044847	Hs.196284	ESTs	2.1
	441445	AI221959	Hs.187937	ESTs	2.1
	420288	AW071225	Hs.245558	ESTs	2.1
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.1
	447033	AI357412	Hs.157601	ESTs	2.1
55	436853	BE328074	Hs.148661	ESTs	2.1
	455189	AW864176		gb:PMO-SN0014-260400-002-b08 SN0014 Homo	2.1
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	2.1
	458356	AI024855	Hs.131575	ESTs	2.1
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.1
60	424480	AA341442	Hs.205299	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fs, clone PL	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
65	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
	417725	R25257	Hs.21503	ESTs	2.1
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.1
	439474	AJ824060	Hs.211501	ESTs	2.1
70	446895	AA166655	Hs.282803	ESTs	2.1
	448582	AI538880	Hs.94812	ESTs	2.1
	452783	AA028167	Hs.61486	ESTs	2.1
	442430	R89164	Hs.48320	double ring-finger protein, Dorf	2.1
	428908	AW303529	Hs.144955	ESTs	2.1
	427335	AA448542	Hs.251677	G antigen 7B	2.1
75	428336	AA503115	Hs.183752	microsomal protein, beta-	2.1
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.1
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.1
	439950	AW937417	Hs.293561	ESTs	2.1
	458227	Z40670	Hs.181340	ESTs	2.1
80	447179	AW015633	Hs.157299	ESTs	2.1
	454950	AW847460		gb:RC3-CT0208-270999-021-e04 CT0208 Homo	2.1
	404453				2.1
	420844	AA595522		gb:nh22c09.s1 NCL_CGAP_Pr1 Homo sapiens	2.1

5	426456	AA580748	Hs.130658	ESTs	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	430879	BE149423	Hs.10554	hypothetical protein FLJ12761	2.1
	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
10	453853	AL040600	Hs.188083	ESTs	2.1
	414083	AL121282	Hs.257786	ESTs	2.1
	401645				2.1
	436577	W84774	Hs.17643	ESTs	2.1
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.1
15	409168	N94037	Hs.312938	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	410276	AI554545	Hs.68301	ESTs	2.1
	443372	AI792557	Hs.133107	ESTs	2.1
	422093	AF151852	Hs.111449	CGI-94 protein	2.1
	402333				2.1
20	409374	R87083	Hs.19081	ESTs	2.1
	412011	NM_000406	Hs.73064	gonadotropin-releasing hormone receptor	2.1
	412798	AW998557	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
25	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	452374	AL037405	Hs.339639	ESTs	2.1
	450061	AI797034	Hs.201115	ESTs	2.1
	450180	AW449644	Hs.257182	ESTs	2.1
	405120				2.1
30	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.1
	458890	AW855523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.1
	435600	AL047034	Hs.119747	ESTs	2.1
	440964	AI733106	Hs.130218	ESTs	2.1
	417455	AW007056	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.1
35	436461	AW511956	Hs.293261	ESTs	2.1
	436777	AA731199	Hs.293130	ESTs	2.1
	427521	AW973352	Hs.290585	ESTs	2.1
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.1
	413231	D87461	Hs.75244	BCL2-like 2	2.1
40	423969	AI830571	Hs.331633	hypothetical protein DKFZp566N034	2.1
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.1
	443777	AV646510	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	2.1
	416148	H22453	Hs.169187	ESTs	2.1
	402528				2.1
45	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	446209	AI375025	Hs.153368	ESTs	2.1
	453362	H14988	Hs.107375	ESTs	2.1
	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.1
50	401069				2.1
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.1
	410966	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo	2.1
	447124	AW976438	Hs.17428	RBP1-like protein	2.1
	449939	T86420	Hs.272139	ESTs	2.1
55	411693	AW857271		gb:CMO-CT0307-210100-158-g09 CT0307 Homo	2.1
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	2.1
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	2.1
	404694				2.1
60	406668	T62745	Hs.184411	albumin	2.1
	441092	T99289	Hs.126556	EST	2.1
	454843	BE006345		gb:RC2-BN0127-240300-011-d05 BN0127 Homo	2.1
	426646	AA382787	Hs.122713	ESTs	2.1
	431605	AW972407		gb:EST384498 MAGE resequences, MAGL Homo	2.1
65	414452	AA454038	Hs.29032	ESTs	2.1
	401991				2.1
	457176	AA438837		gb:zv57g07.s1 Soares_testis_NHT Homo sep	2.1
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	428208	AA442327	Hs.104854	ESTs	2.1
70	445049	AV652718		gb:AV652718 GLC Homo sapiens cDNA clone	2.1
	419116	AF292402	Hs.283093	neuromedin U receptor 2	2.1
	427894	AL135709	Hs.28921	zinc finger protein	2.1
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.1
	424323	AA338791	Hs.177788	ESTs	2.1
75	404582				2.1
	418631	AA225921	Hs.115105	ESTs	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	452539	AW105321	Hs.49367	ESTs	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
80	440310	AA878939	Hs.125406	ESTs	2.1
	433297	AV658581	Hs.282633	ESTs	2.1
	410900	AW810169		gb:MR4-ST0124-040500-007-h07 ST0124 Homo	2.1
	419386	AA236867	Hs.143868	ESTs, Weakly similar to I38022 hypotheti	2.1
	402451				2.1
	447842	AW160804	Hs.247302	twisted gastrulation	2.1
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	2.1
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1N1B H	2.1

	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.1
	400612				2.1
	402318				2.1
5	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	412029	AW886238		gb:RC5-OT0076-280300-022-F01 OT0078 Homo	2.1
	414494	AA768491	Hs.5783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
10	444498	AI151413	Hs.26330	ESTs	2.1
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.1
	425324	M89470	Hs.155644	paired box gene 2	2.1
	430719	AA488988	Hs.293796	ESTs	2.1
	432577	BE208545	Hs.317590	hypothetical protein FLJ14640	2.1
15	407593	AW044083	Hs.237008	ESTs	2.1
	401098				2.1
	440299	AJ871778	Hs.250112	ESTs	2.1
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.1
	428627	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1
20	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	2.1
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	2.1
	439831	AW136488	Hs.25545	ESTs	2.1
	451829	AW964081	Hs.247377	ESTs	2.1
	404595				2.1
25	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	456083	U46922	Hs.77252	fragile histidine triad gene	2.1
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	2.1
	406413				2.1
	439483	T69980	Hs.58323	Homo sapiens cDNA FLJ11613 fis, clone HE	2.1
30	446242	N66338	Hs.7360	ESTs	2.1
	449625	NM_014253	Hs.23796	odc (odd Oz/ten-m, Drosophila) homolog 1	2.1
	457938	AJ373638	Hs.133900	ESTs	2.1
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	2.1
	408350	AW183350	Hs.250127	ESTs	2.1
35	419812	NM_000562	Hs.93210	complement component 8, alpha polypeptid	2.1
	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A recepto	2.1
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	2.1
	409955	U60665	Hs.57692	chromosome 6 open reading frame 10	2.1
	435579	AJ332373	Hs.156924	ESTs	2.1
40	436088	AA704687	Hs.191294	ESTs	2.1
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.1
	416100	H18700	Hs.268799	ESTs	2.1
	403218	AL134878	Hs.119500	ribosomal protein, large P2	2.1
	409747	H60964	Hs.331250	ESTs	2.1
45	428764	W21550		gb:zb52f12.r1 Soares_fetal_jung_NbHL19W	2.1
	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.1
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.1
	428299	AL038004	Hs.29419	ESTs	2.1
	406817	AI936028		gb:wo47a09.x1 NCL_CGAP_Gas4 Homo sapiens	2.1
50	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AI768015	Hs.92127	ESTs	2.1
	414012	AW452334	Hs.128148	ESTs	2.1
	421966	AA904519	Hs.130710	ESTs	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
55	456606	AA292862	Hs.275369	ESTs	2.1
	451604	T65365	Hs.172851	arginase, type II	2.0
	440926	AW196772	Hs.131323	ESTs	2.0
	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.0
	459082	BE561721	Hs.282149	ESTs	2.0
60	413241	BE073771	Hs.302414	Homo sapiens clone FLB8945 PRO2411 mRNA,	2.0
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	447552	AJ394125	Hs.160413	ESTs	2.0
	420905	AA521307	Hs.186651	ESTs	2.0
	428052	AA420477	Hs.26993	ESTs	2.0
65	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.0
	432527	AW975028	Hs.102754	ESTs	2.0
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	2.0
	446610	AV659433	Hs.282984	ESTs, Weakly similar to I38022 hypotheti	2.0
	427961	AW293165	Hs.143134	ESTs	2.0
70	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.0
	445564	AB028957	Hs.12896	KIAA1034 protein	2.0
	412811	H06382	Hs.21400	ESTs	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
75	429418	AJ381028	Hs.118769	ESTs	2.0
	431511	NM_012386	Hs.258581	Homo sapiens p95 paxillin-kinase linker	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	453123	AI953718	Hs.221849	ESTs	2.0
80	455401	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	2.0
	406666	V00495	Hs.184411	albumin	2.0
	445688	AI248205	Hs.153244	ESTs	2.0
	446131	NM_000929	Hs.290	phospholipase A2, group V	2.0
	440388	AI693520	Hs.223000	ESTs	2.0

5	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.0
	404416				2.0
	444187	AW138466	Hs.151274	ESTs	2.0
	431552	AJ815863	Hs.259873	axonal transport of synaptic vesicles	2.0
	455814	BE141689		gb:CM1-HT0092-220999-016-b09 HT0092 Homo	2.0
10	454759	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	2.0
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.0
	404420				2.0
	408112	AW451982	Hs.248613	ESTs	2.0
	432702	AW973953	Hs.293744	ESTs	2.0
15	448587	AI539652	Hs.28338	KIAA1546 protein	2.0
	446854	BE268103	Hs.208914	hypothetical protein MGC10999	2.0
	410569	AA766825	Hs.205675	ESTs	2.0
	432596	AJ224741	Hs.278461	matrilin 3	2.0
	402341				2.0
20	452919	AW962167		gb:EST374240 MAGE resequences, MAGG Homo	2.0
	433632	AA649921	Hs.112553	ESTs	2.0
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.0
	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.0
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.0
25	450895	N66727	Hs.10957	ESTs	2.0
	408459	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypothetical	2.0
	400842				2.0
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.0
	400859				2.0
30	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
	416093	R60685	Hs.268698	ESTs, Moderately similar to ALLUC_HUMAN I	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypothetical	2.0
35	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolog	2.0
	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	2.0
40	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	2.0
	419886	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0
	415173	AW501735	Hs.253015	ESTs	2.0
	449011	AI655376	Hs.192693	ESTs	2.0
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.0
45	416057	AI927382	Hs.29857	ESTs	2.0
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.0
	408531	AW207553	Hs.253639	ESTs	2.0
	434663	AA641972	Hs.130058	ESTs	2.0
	428085	AA421081	Hs.12388	ESTs	2.0
50	425006	R38685	Hs.332622	ESTs	2.0
	446139	H77395	Hs.39749	ESTs	2.0
	400049				2.0
	428333	AW972668	Hs.293044	ESTs	2.0
	429458	BE161832	Hs.292689	ESTs	2.0
55	425087	R62424	Hs.126059	ESTs	2.0
	457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	400310	X63966	Hs.135631	H.sapiens synthetic gene for platelet-de	2.0
	451805	AI968300	Hs.208220	ESTs	2.0
	401986				2.0
60	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	429110	L29301	Hs.2353	opioid receptor, mu 1	2.0
65	433755	AW085934	Hs.120868	ESTs	2.0
	434118	AF116715	Hs.256256	Homo sapiens PRO2829 mRNA, complete cds	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	443748	AW206447		gb:UH-BH1-afg-g-02-0-UI.s1 NCI_CGAP_Su	2.0
	445205	D83776	Hs.12413	KIAA0191 protein	2.0
70	458175	AW296024	Hs.150434	ESTs	2.0
	446419	AW576760	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE	2.0
	441627	AA947552	Hs.58086	ESTs	2.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.0
	455614	AI693369	Hs.202274	ESTs	2.0
75	449899	AI610700	Hs.103280	ESTs	2.0
	420111	AA255652		gb:z621h11.r1 NCI_CGAP_GCB1 Homo sapiens	2.0
	437354	AA749215	Hs.291886	ESTs	2.0
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.0
	419691	W03298	Hs.193521	ESTs	2.0
80	439724	AF086565	Hs.60351	EST	2.0
	413362	BE088812		gb:CM2-BT0693-230300-129-d08 BT0693 Homo	2.0
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	2.0
	434361	AF129755	Hs.117772	ESTs	2.0
	442479	AF069484		gb:AF069484 Homo sapiens astrocytoma fib	2.0
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.0
	459323	AW062490		gb:MR0-CT0065-100899-001-d01 CT0065 Homo	2.0
	449438	AA927317	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	2.0

	400285				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
5	417383	W02642	Hs.136102	KJAA0853 protein	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447313	U92981	Hs.16081	Homo sapiens clone DT1P186 mRNA, CAG rep	2.0
	455696	BE067870		gb:RCO-BT0362-021299-031-b06 BT0362 Homo	2.0
	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
10	449815	A1871000	Hs.199739	ESTs	2.0
	425398	AL049569	Hs.156369	hypothetical protein similar to Ienascn	2.0
	400238				2.0
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.0
	445073	AW291389	Hs.13056	hypothetical protein FLJ13920	2.0
15	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.0
	413174	AA723564	Hs.191343	ESTs	2.0
	435810	BE349853	Hs.2785	keratin 17	2.0
	418687	R61650	Hs.22581	ESTs	2.0
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.0
20	431750	AA514986	Hs.283705	ESTs	2.0
	453242	T98327	Hs.18343	ESTs	2.0
	437074	AI286235	Hs.128905	hypothetical protein FLJ13204	2.0
	459411	N52920		gb:yy34h09.s1 Soares fetal liver spleen	2.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.0
25	409929	R38772	Hs.172619	myelin transcription factor 1-like	2.0
	406378				2.0
	459208	BE261314	Hs.149039	ESTs, Weakly similar to I38022 hypothetical	2.0
	45260	AI218133	Hs.147617	ESTs	2.0
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.0
30	445020	AI205655	Hs.147221	ESTs	2.0
	402048				2.0
	412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	2.0
	416408	R94725	Hs.35354	ESTs	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
35	427836	AA416642	Hs.116176	ESTs	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	436902	AW247145	Hs.192729	ESTs	2.0
	440122	AI733011	Hs.127678	ESTs	2.0
	442901	AI023654	Hs.114191	ESTs	2.0
40	444097	AW517412	Hs.150757	ESTs	2.0
	447278	AI934935	Hs.158669	ESTs	2.0
	451361	AA053854		gb:z52f02.r1 Soares retina N2b4HR Homo	2.0
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.0
	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0
45	458801	N98548	Hs.276860	ESTs, Weakly similar to C Chain C, Human	2.0

TABLE 30B

50	Key:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
55	Key	CAT number	Accession
	407593	1003161_1	AW044083 AW044094 AW370634
	407594	1003220_1	AW057584 AW057585 AW044153 R34370
	407639	1006924_1	AW205369 AW058599 AW207608
	407676	1008294_1	AW064111 AW064450 AW064429
60	407721	10108_1	Y12735 NM_003582 AW238970 R38268 R41411 R41419 T16717 AA002193 H62028 AJ359545 AW105201 AW087158 AA699728 AI095264 AA002065 H62029 AJ289101 AA884804 AA904950 AA609872 AI139874 H77896
	407726	101126_1	AA435679 AA470655 H22526 AA044031 AA876426 W63767 AI221140 AI418990 H42329 H88910 AL041066 H88909 W94610 AW352277 W94548 W94167 AW952568 AI418653 AA335501 AA393641 AA044353 H41626 H22525 R58582 AW297645 C75230 AW368034 AW468904 AI272755
65	407762	101439_1	AW235638 AA346882 AW866803 AA361281 AW963163 AA044373 AA136755
	407764	1014849_1	BE008347 BE008320 BE083307 BE083311 AW075968
	407788	10163_1	BE514982 BE614814 AW393078 AW238480 AA055637 N27644 AA641158 M87068 AA161019 AA161003 AA587315 AA176746 AA593632 AJ354870 AW183492 Y07755 NM_005978 AW872948 AI608987 H64656 AF086003 AA643149 AI819402 H64555 AA858398 AA594885 AA36747 BE122811 AA587026 AW857106 AJ950679 AA596012 AA654004 AW238238 AI971395 AA459074 AA458884 AI608591 BE181995 BE181970 AW195797 CX0271 BE182043
70	407803	1017498_1	AW081681 N36967 N36959
	407809	1017982_1	AW082279 AW082688
	407811	10180_1	AW190902 AJ802788 AI041650 AI037867 AF110137 NM_013372 H99469 N35377 AW151676 AI678451 AW078795 AW087935 AI884505 AW044602 AB032372 AF045800 AI621183 AI750578 AA376403 AI910477 AA373348 AA373673 AI752124 AL359060 W48619 AA373298 AA373975 AW604409 AW604404 AW368603 AA545734 AW361415 AA373557 AW956164 AW853798 AI750595 AL359059 AA344024 N31127 AW580737 N27040 AA071138 AI753050 AA599801 W48852 AA669811 AA112124 AI940705 W52686 AA084001 C01826 AI940729 AA373544 AW957491 AW383224 AW383164 AW383192 AW383125 AW383194 AW842507 AI940795 H80042 AW631119 W47324 W42884 AI750594 AI754387 AI753734 AA372833 AW069006 AI750577 AW473621 AI888605 AA600082 AI041803 W51909 W25447 AI521673 AI087351 AA670070 W47325 AA071381 W42791 AI090390 AI085102 AI302125 AA788723 AW069430 AW069485 AI754608 AA373014 BE140150 BE140166 BE140102 BE140143 BE140157 BE140117 BE140098 AW005943 BE140108 BE140176 BE140171 BE140144 BE140175 BE140160 BE140152 BE140099 BE140177 BE140167 BE140145 BE140109 BE140163 BE140172 BE140161 BE140179 BE140147 BE140107 BE140146 BE140155 BE140173 BE140148 BE140174 BE140158 BE140149 BE140118 BE140156 BE140105 BE140103 BE140164 AW138508 BE140153 AW806557 BE140121 BE140162 C01953 AW806500 BE140124 AA329219 AW955642 AW069165 AI968107 N21113 AI754594 AW069264 AI754660 BE551937 AA543066 AA703927 AW130486 AI814434 AI924946 AA789056 AW173667 AW069841 AI022286 AI753523 AI753558 AI753482 AW068940 AI753002 AA669866
75			
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AW051234 Z41044 AA876777 F03579 AI680446 AA745688 T24075 T35116 T35115 R02091 Z30229 AI872774 AW772549 AI540411 AI784282 R25646 AA541817 T77442 R26596 BE168424 T77229 R23696 AA399018 AW242359 AI868208 AW020951 AA412180 AI026157 AA838752 AI146272 AA910825 AI266100 N24580 H97503 BE327388 AI697814 W56675 AA423842 AA423880 H40134
15	456481 456510	192210_1 19507_1	
20	456513 456536 456551 456561	195409_1 198330_1 199748_1 200378_1	
25	456605 456606 456737	203819_1 203847_1 22551_1	
30	456869	24619_1	
35	456933 457003	256540_2 27203_1	
40			
45			
50			
55	457024 457030	274501_1 27473_1	
60			
65			
70	457039 457040	275248_1 27530_2	
75			
80	457041 457122	275843_1 287827_1	

5	457128	28930_1	AJ932995 BE064464 AW371902 AW371841 AJ885885 BE064457 AA524113 AA721037 AA504343 AA778099 AJ800598 AJ693112 AJ864633 AJ690228 AJ400990 AW969089 AW371927 AW371912 AW383562 BE151089 AW383568 BE218503 AW383570 AW371899 BE151097 AW371900 AW293095 AW292008 AA434179 AA714780 R45868 W01182 AW957767 AW119223 AJ207854 W01578 AA354403 AA805177 AJ613299 AW269636 AA481528 AW079101 AF131777 R60489 T81289 AA481594 BE181020 AA465433 AW808125 T84992 AA749191
	457176	296527_1	AA436837 AA442594
	457187	298994_1	AA443927 AA444106
	457225	30546_1	AW820035 T20260 T20259 AL049415 AA737756 W46965 W00799 AW340968 AW027417 AW263261 AJ420674 AA814921 AA736509 N69991 AW368643 W47065 AJ090172 AJ924139 BE468071 AA375842 AA375767 AW628849 AJ422731 AA494558 AA569233 AJ142954 AJ161089 AJ167233 W94484 AJ681576 AA249694 AJ695943 AA832347 AA76621 AA937792 AJ702870 AA455748 AW195100 AJ638530 BE502479 AJ383418 AA039630 C20777
10	457314	318637_1	AA479597 Z45151 H28821
	457460	340038_1	AJ143312 AJ394343 AW205239 AA523980 AJ831223 AJ347180 BE263197 AA765781 AJ654500
	457506	34672_1	AF131757 T79901
	457620	371514_1	AA602711 BE078290
15	457630	373784_1	AJ680803 AJ703329 AA609004 AJ305245 AJ457796 AW295787
	457652	37972_1	AF116656 AJ114583 AW838134 AW838525 AW885447 H83251 AW838349 AW838378 AW838175 H83252
	457653	37979_2	AJ820719 AJ273515 AW592687 AJ263784 AJ351926 R46866
	457741	395767_1	BE044740 AW827360 AW827623 BE161439 BE044718 BE046207 BE046551 AA653908 BE166581
20	457756	3_1	AA126136 H62964 BE245159 AF280094 AA431918 BE386201 AA707576 AJ074267 AA969194 AA693596 H62844 AW134991 AA126014 AJ077443 AA699881 AJ037956 AA961277 AW204185 AJ540791 AJ273273 AW627957 AA926890 AJ014851 AW081056 AA443705 AW137571 BE139390 AJ583851 AJ583822 AJ583814 AW268341 AJ590502 AW302642 AJ053871 AJ254692 AJ591255 AJ590260 AJ583359 AJ583341 AJ583752 AJ224227 AW302089 AW466960 AA810124 AW302684 AJ272921 AJ141003 AW589738 AA074714 AA621482 AJ796501 AW024557 AA821074 T62627 AA639206 AJ913538 AA075135 R54613 AA352975 AW206892 AJ868280 AW449243 AA907317 AW134573 AJ590492 AJ610050 AJ834309 AJ375556 AJ284991 AW968038
25	457770	402530_1	BE065030 AA670100 AA781546 AJ022472 AA846803 AJ497780 N68386 AJ382890
	457802	410073_1	T78013 AA699327 W87785 W88613
	457900	434061_1	AW976692 AA806542 AA745856
	457938	439837_1	AJ373638 AJ073389 AJ087143 AA764776 AA913318
30	458023	463717_1	AW978161 AW978165 AJ016938 AJ539270 AW294958 AW511089 AA814849
	458037	46627_1	AF074982 R27906 R31333 R31591 R27812
	458043	466952_1	AW979009 AA828038 AA828148
	458067	46875_2	AA393603 Z19481 AA252342 AJ807614 AJ913804 AA040176 AA971879 H53388 AF085972 AJ291424 H53349 AW015078 AA768307 AA127921 AA723700 AA040841 AA93954 AA213655 AA127972 AA913063 BE327712 AJ017585 AA988186 AA628183 AJ205930 AA833558 AA974107 AJ004390 H48931 AA724004
35	458175	498744_1	AW296024 AA897109 AJ015000
	458227	517913_1	Z40670 BE504110 BE219908 AW468668 AJ002334
	458257	526854_1	U48351 AA969182 BE327312 AW138276 BE467567 AJ680815 AJ422668
	458303	543175_1	AJ264628 AF017648 AJ872732
40	458356	555234_1	AJ024855 AJ024877
	458426	579269_1	AJ084514 N46645 AW183984
	458455	59100_1	AV648310 AV661871 AJ828475 AV647819 T55845
	458507	614471_1	AJ185703 AJ806813 AW292764
	458552	633259_1	AW136139 AJ216724
45	458623	662297_1	AJ305223 AJ458577 AJ275569
	458624	662652_1	AJ362790 AJ275996 N48887
	458661	677016_1	AJ299789 BE551384
	458684	68549_1	BE281115 T53860 AV659439 AV659421 BE539929
	458734	719515_1	AJ554946 AW362008 AW362553 AJ863342 AJ376781
50	458762	73076_1	AW802754 BE619228
	458763	731371_1	AJ693417 AJ418256 AW627792 F32978
	458771	737397_1	AW295151 AJ425004 AW470228 AJ693738 H50554 R99198 H50553 R99197
	458797	75398_2	AW001835 AW612725 AW136670 AJ789956 BE457368 AA280216 AJ216754 BE622057 AL121193 AW853470 AW853450 AW369075 AW369108 AW578479 AW369106 AW361242 AW361190 N79183 N98648 AJ458157 BE041652 BE218014 BE822355 AA369340 AA369515 AW962780 AW962704
55	458801	75669_1	AJ522129 T56009 R53849
	458817	764459_1	AW236702 AJ566105 Z40398
	458833	777505_1	AJ630223 AJ630470
	458861	798085_1	AW865523 AW865128 AW865467 AW865127 AW865466
	458890	812733_2	R15891 R61471 R81469 N69765 AJ014624 AA007214 AW592075 H09780 AA709038 AJ335898 H11055 AJ559229 F09750 T72573 AA935558
60	458925	82655_1	AA988654 AA826438 AJ002431 AJ299721
	459023	86727_1	AW968226 AJ139249 AJ701692 AA017303 AW469622 AA259148 AA811690 AA807996 AA744260 AA824494 AA731710 T25332 AA258101 AA970687
	459037	87417_1	AW439497 AJ826059 AA018402 AA837392
65	459082	889533_1	BE551721 H51878 AJ823338 C01488 AW813562
	459124	916575_1	AW301478 AW301560 AJ889207
	459207	926704_1	AW138410 AJ912712 N40186
	459208	92717_1	BE261314 AJ243408 AA027322
70	459275	97318_1	AJ808913 AW028342 W81290 AJ571379 AJ382808 AA037071 W78688 R48751 N31808 AJ870233 R48752 AW024895 AJ333754
	459278	9751_1	AW294659 AJ204928 AA351653 H51220 R68843 AA993182 U79298 R15294 F05089 Z42963 R17818 T77498 AA332319 W56049 AA331588 AW881873 AW881865 AW881876 R52345 AJ652070 AA400044 AA401512 T08151 W05486 N68378 T33846 AJ190920 R43021 AJ949580 Z39084 T63413 W37269 F01343 R66669 AJ621055 AW117593 AJ193211 AW297532 AJ500709 AA400056

75 Table 30C

80 Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
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	400462	9929659	Minus	197610-197785
	400608	9887666	Minus	96756-97558
	400612	9929648	Minus	151513-151662
5	400631	8247025	Minus	56203-56313,56424-56482,57073-57185,57513-57593,57747-57941
	400641	8117693	Plus	4786-4992
	400664	8118496	Plus	13558-13721,13942-14090,14554-14679
	400696	8118812	Minus	77737-77899
10	400697	8118812	Minus	79073-79198
	400706	7249204	Minus	78299-78686
	400816	8569993	Plus	161221-162078
	400842	1927148	Plus	90462-90673
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
	400861	9757506	Plus	163855-164016
15	400889	9958234	Minus	169782-170036
	401069	3927852	Minus	45682-45831
	401098	9955518	Minus	85632-86174
	401132	8705350	Minus	85679-85795
	401189	9690246	Minus	90815-90929
20	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401240	3355450	Plus	77433-77636
	401324	9863791	Plus	234057-234174
	401365	9796180	Minus	119572-119672
	401368	8670914	Minus	65508-65662
25	401459	9212270	Minus	182001-183323
	401462	6682291	Plus	112763-112909
	401497	7381770	Plus	92607-92813
	401528	7770561	Plus	91570-93177
	401596	3293210	Plus	63639-63890
30	401614	7839924	Plus	17350-17735
	401626	8575943	Minus	238100-238432
	401645	7657839	Minus	34986-35133
	401673	7689903	Minus	122587-122705,122765-123047
	401694	3540172	Minus	64056-64168
35	401765	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401878	8099802	Minus	162268-162474,163089-163195
	401887	7229981	Plus	93973-94120
	401899	7230209	Minus	155620-155815
	401986	4406829	Minus	31137-31293
40	401989	4309954	Minus	118611-118821
	401991	4158128	Plus	2398-2513
	402048	8072512	Plus	43936-44078
	402076	8117410	Plus	128316-128627
45	402090	7249154	Minus	104806-104939,106898-107052
	402112	8139750	Plus	10507-10713
	402131	7704961	Minus	33114-33209,33496-33678
	402145	8018280	Plus	113086-114800
	402318	7582559	Minus	12843-13403
50	402333	8844110	Minus	165693-165856
	402341	7656696	Plus	22583-23699
	402369	9558577	Minus	50417-50522
	402451	9796677	Minus	48137-48343
	402528	7630857	Minus	169609-169742
55	402603	9909396	Minus	141663-141852
	402615	9926801	Plus	131390-132157
	402689	8348025	Minus	5885-6209
	402942	9368398	Plus	102152-102386
	403011	6693597	Minus	3468-3623
60	403053	8748888	Plus	146568-146659,147539-147811
	403089	8954241	Plus	171964-172239
	403188	9838289	Minus	157618-157755
	403218	7630969	Plus	58039-58149
	403271	7230852	Plus	134283-134485
	403281	8072630	Minus	7521-7728
65	403306	8099945	Plus	127100-127251
	403310	8139936	Minus	183883-184026
	403317	8318526	Minus	50623-50834
	403329	8516120	Plus	96450-96598
70	403341	8569175	Plus	30699-30910
	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
	403525	7860440	Plus	152431-153243
75	403534	8076917	Minus	46652-47332
	403568	8101145	Minus	85509-85658
	403572	8101156	Minus	1253-1675
	403574	8101156	Plus	5542-6176
80	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
	403637	8671936	Minus	142647-142771,145531-145762
	403678	7331517	Minus	119573-120430
	403691	7387384	Minus	88280-88463

	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
	403786	8083636	Minus	73028-73217
5	403891	7331467	Minus	191508-193220
	403937	7711761	Minus	12609-12773
	404042	9558573	Plus	5140-5208,8633-8763
	404043	9558573	Plus	29042-29135,46597-46699
	404068	3168621	Minus	18123-18766
10	404108	8247074	Minus	63603-64942
	404166	7596822	Plus	86147-86509
	404193	3881948	Minus	94185-94322
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
15	404367	9965011	Minus	114391-114628
	404404	7272262	Plus	82112-82244
	404414	7382165	Plus	143127-143398
	404416	7382420	Minus	143042-143216,144704-144853,145800-146048
	404420	7407952	Minus	129817-130586
20	404443	7579073	Minus	87198-87441
	404453	7657714	Plus	27768-29179
	404476	8080699	Plus	101841-102043
	404518	8151988	Plus	84494-84603
	404526	8152087	Plus	121918-122123,125198-125348
25	404531	8247909	Plus	20152-20362
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404582	9739220	Plus	53230-53424
	404587	8698840	Minus	69781-70096
30	404588	6456726	Minus	40059-40210
	404593	9944086	Minus	74922-75788
	404595	9958262	Minus	16764-16900
	404638	9796751	Minus	99433-99528,100035-100161
	404652	9796969	Minus	108172-108296
35	404694	9799957	Minus	128092-128227
	404708	9800828	Plus	77522-77658
	404731	7230299	Minus	168609-168781,182951-183081
	404767	7882827	Minus	23244-23759
	404793	7232206	Minus	61087-61590
40	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404957	7407827	Plus	147512-148011
	404987	7523744	Minus	89944-90729
	404988	4662677	Minus	72406-72600,72779-72856
45	405001	6015406	Minus	104646-104819
	405008	6088019	Minus	64091-64267
	405090	8072525	Minus	38552-39202
	405120	8099940	Plus	140176-140340
	405229	7249019	Plus	51081-51701
50	405230	7249032	Minus	97493-97682
	405302	2078453	Minus	121688-121840
	405347	2979602	Minus	977-1116
	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
	405456	7656676	Plus	150052-150208
55	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405605	5836195	Minus	117070-117270
60	405608	5815499	Minus	66822-66925
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405738	9943998	Plus	44370-45410
65	405747	8469069	Minus	153933-154060
	405780	7248203	Minus	48204-48371
	405783	5738434	Minus	27238-27885
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
70	405920	6758795	Plus	120621-120971
	405935	6758795	Minus	163112-163652
	405970	8247789	Minus	45795-46295
	406005	8247801	Minus	39912-40220
	406018	6758904	Minus	37795-38168
75	406076	9123123	Plus	89972-90319
	406092	9123919	Plus	251370-251797,252168-252882
	406190	7289992	Minus	22395-22901
	406288	7549620	Plus	111718-112008
	406298	5686278	Minus	30084-30770
80	406333	9213235	Plus	64689-64798
	406364	9256114	Minus	50715-50833
	406378	9256142	Minus	126408-126800
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11368-11509,11625-11880

406603 8272659 Minus 39506-39694

5 TABLE 31A: ABOUT 1884 GENES UP-REGULATED IN IPF COMPARED TO NSIP

Table 31A lists about 1884 genes whose expression levels are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with non-specific interstitial pneumonia (NSIP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" non-specific interstitial pneumonia sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" non-specific interstitial pneumonia level was set to the 90th percentile amongst non-specific interstitial pneumonia samples.

15 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to NSIP (non-specific interstitial pneumonia)

20	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	450478	AW451709	Hs.271200	ESTs	20.2
	405654				16.1
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
25	431548	AI834273	Hs.9711	novel protein	10.8
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
	403574				10.1
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
30	441233	AA972965	Hs.135568	ESTs	9.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	8.4
	432437	W07088	Hs.293685	ESTs	8.3
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	8.2
35	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	8.1
	403329				8.0
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
	441519	AA972740	Hs.127092	ESTs	7.9
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	7.8
40	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	7.7
	416379	N38857	Hs.203933	ESTs	7.7
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	7.5
	407305	AA715284		gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens	7.2
	434683	AW298724	Hs.202639	ESTs	7.2
45	441802	AA968636	Hs.127877	ESTs	6.9
	431242	AA987742	Hs.251278	KIAA1201 protein	6.9
	442377	AA993807	Hs.167367	ESTs	6.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	6.8
	428908	AW303529	Hs.144955	ESTs	6.8
50	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	6.7
	457673	AA551569	Hs.272034	hypothetical protein PRO2822	6.7
	458771	AW295151	Hs.163612	ESTs	6.6
	426800	AA385085		gb:EST98959 Thyroid Homo sapiens cDNA 5'	6.6
55	440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.6
	415025	AW207091	Hs.72307	ESTs	6.5
	438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
	416128	AA173632	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	6.4
	457242	AA457011		gb:aa90c11.r1 Stratagene fetal retina 93	6.3
60	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	6.3
	404793				6.2
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	6.2
	415672	N53097	Hs.193579	ESTs	6.2
	455488	AA102322		gb:z190f03.r1 Stratagene colon (937204)	6.2
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	6.1
65	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	6.1
	431622	AW979271	Hs.283184	ESTs	6.1
	405523				6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	436397	AA715013	Hs.169835	ESTs	6.0
70	456476	AA256753		gb:zs22b12.r1 NCI_CGAP_GC81 Homo sapiens	5.9
	434784	AA649051	Hs.164007	ESTs	5.9
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	5.9
	442849	R10099	Hs.269805	ESTs	5.9
	451519	AI800600	Hs.209573	ESTs	5.8
75	412474	AF791451		gb:n150c09.y5 NCI_CGAP_Ov2 Homo sapiens	5.8
	457081	AA916785	Hs.180610	splicing factor proline/glutamine rich (5.8
	444827	R09764	Hs.20416	ESTs	5.8
	404822				5.7
	402430				5.7
80	457900	AW976692	Hs.291665	ESTs	5.7
	400292	AA250737	Hs.72472	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	440172	AA888584	Hs.126154	ESTs	5.7

	431374	BE258532	Hs.251871	CTP synthase	5.7
	409816	AW500954		gb:UH-HF-BP0p-ahr-h-12-0-ULr1 NIH_MGC_5	5.6
	447613	AL041057	Hs.33363	DKFZP434N093 protein	5.6
5	417919	AI928203	Hs.86379	ESTs	5.6
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.6
	439063	AF085922	Hs.113968	ESTs	5.6
	406053				5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
10	451830	H18433	Hs.21542	KIAA1035 protein	5.5
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.5
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	5.5
	459458	AW270957	Hs.254577	ESTs, Weakly similar to B34087 hypotheti	5.5
	416154	Z46122		gb:HSCOV8031 normalized infant brain cDN	5.5
	404561				5.4
15	428895	AA437124	Hs.187247	ESTs	5.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	5.4
	440925	AW511090	Hs.130419	ESTs	5.4
20	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
	448477	BE612572		gb:601452090F1 NIH_MGC_66 Homo sapiens c	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	459664				5.3
	401497				5.3
25	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	5.3
	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	5.3
	452542	AW812256		gb:RC0-ST0174-191099-031-e07 ST0174 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
30	404957				5.2
	435445	AA922213	Hs.121735	ESTs	5.2
	442617	AW340093	Hs.130538	ESTs	5.2
	416045	H15990	Hs.31403	ESTs	5.2
	425178	H16097	Hs.161027	ESTs	5.2
35	441918	AI733373	Hs.128119	ESTs	5.2
	455464	AW983901		gb:RC1-HN0003-220300-011-110 HN0003 Homo	5.2
	420929	AI694143	Hs.296251	programmed cell death 4	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	430686	NM_001942	Hs.2633	desmoglein 1	5.2
40	405229				5.1
	417641	AA205015	Hs.54617	hypothetical protein FLJ20060	5.1
	434167	AA626334	Hs.116153	ESTs	5.1
	450438	AI696071	Hs.253800	ESTs	5.1
45	456394	W28506		gb:48f1 Human retina cDNA randomly prime	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	417420	T85150	Hs.268814	ESTs	5.0
	409545	BE296182	Hs.19002	hypothetical protein MGC4675	5.0
	426750	AA383950		gb:EST97403 Thymus II Homo sapiens cDNA	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
50	408959	AW890878	Hs.211610	CUG triplet repeat, RNA-binding protein	4.9
	454482	BE147919		gb:RC3-HT0230-160200-016-e08 HT0230 Homo	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstr	4.9
	452046	AB018345	Hs.27657	KIAA0802 protein	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
55	450090	AW448940	Hs.202259	ESTs	4.9
	406333				4.9
	434188	AI765848	Hs.281680	peroxisomal trans 2-enoyl CoA reductase;	4.8
	403344				4.8
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	4.8
60	405455				4.8
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	4.8
	426097	BE327369	Hs.112238	ESTs	4.8
	427768	T78402	Hs.174880	ESTs	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
65	415257	F03016	Hs.27513	ESTs	4.8
	441107	AA917075	Hs.190520	ESTs	4.8
	419519	AI198719	Hs.176376	ESTs	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
70	424188	AW954552	Hs.142634	zinc finger protein	4.8
	456987	AI557290	Hs.173536	ESTs	4.8
	405303				4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	451620	AW449888	Hs.257224	ESTs	4.7
75	421948	L42583	Hs.334309	keratin 6A	4.7
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	4.7
	443271	BE568568	Hs.195704	ESTs	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	402230				4.7
80	422246	AA461032	Hs.5306	hypothetical protein DKFZp586F1122 simil	4.7
	431508	NM_012481	Hs.182979	ribosomal protein L12	4.7
	415236	R41400		gb:y94b12.s1 Soares infant brain 1NIB H	4.7
	413101	BE065215		gb:RC1-BT0314-310300-015-01 BT0314 Homo	4.6
	444774	AW052174	Hs.196030	ESTs	4.6

5	444414	AW293214	Hs.8752	transmembrane protein 4	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	436853	BE328074	Hs.148661	ESTs	4.6
	445334	AI610081	Hs.9475	glucose transporter protein 10	4.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	404638				4.6
	447617	AI400762	Hs.176675	ESTs	4.6
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	4.6
	442360	AI374621	Hs.29055	ESTs	4.6
15	411738	AW859353		gb:MR1-CT0353-150300-102-e12 CT0353 Homo	4.5
	444157	AI125785	Hs.153351	ESTs	4.5
	401365				4.5
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF 1 [4.5
	436269	AA707472	Hs.190760	ESTs	4.5
20	459448	AA416773	Hs.275012	EST	4.5
	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.5
	414899	AW975433	Hs.36288	ESTs	4.5
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	4.5
	444898	AI201548	Hs.308338	ESTs	4.5
25	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	405605				4.5
	457982	AW856093	Hs.183617	ESTs	4.5
	427731	AA411750	Hs.20943	ESTs	4.4
30	420691	AA829433	Hs.275343	ESTs	4.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
35	453824	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	4.4
	458865	T05095	Hs.19597	KIAA1694 protein	4.4
	459037	AW439497	Hs.290656	EST	4.4
	403310				4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
40	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	4.4
	432020	AJ251509	Hs.272345	phosphodiesterase 11A	4.4
	453043	AW136440	Hs.224277	ESTs	4.4
	456293	AW131715	Hs.311561	ESTs, Weakly similar to CYA7_HUMAN ADENY	4.4
	447879	BE503405	Hs.170437	ESTs, Weakly similar to PRP4_HUMAN SALV	4.4
45	426646	AA382787	Hs.122713	ESTs	4.4
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	4.4
	404898				4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	443314	AW771701	Hs.54646	ESTs	4.3
50	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.3
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	4.3
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	4.3
	404767				4.3
	445189	AI936450	Hs.147482	ESTs	4.3
55	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	428740	AA433838		gb:zw53e12.r1 Soares_total_fetus_Nb2HF8_	4.3
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	4.3
	410615	AW772721		gb:hi95c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.3
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.3
60	406073				4.3
	405692				4.3
	436033	H75391	Hs.255748	ESTs	4.3
	410733	D84284	Hs.66052	CD38 antigen (p45)	4.3
	455587	BE007829		gb:QV0-BN0147-280400-213-d03 BN0147 Homo	4.3
65	459084	H01699	Hs.27289	CGI-125 protein	4.3
	401189				4.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heraguin	4.3
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
70	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	436659	AI217900	Hs.144464	ESTs	4.3
	435463	AA582507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	455675	BE065984		gb:RC3-BT0319-120200-014-e06 BT0319 Homo	4.3
	439481	AF086294	Hs.125844	ESTs	4.3
75	405287				4.3
	405784				4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	437636	AA764781	Hs.291844	ESTs	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
80	412999	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	4.2
	403281				4.2
	427531	AA405097	Hs.97957	ESTs	4.2
	451882	AI821324	Hs.100445	ESTs	4.2
	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	4.2
	405494				4.2
	456027	BE327387	Hs.13913	KIAA1577 protein	4.2
	414539	BE379046		gb:601236846F1 NIH_MGC_44 Homo sapiens c	4.2

	421106	AA877124	Hs.172844	ESTs	4.2
	409076	N57559	Hs.82273	hypothetical protein	4.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	4.2
5	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	4.1
	416614	T83391	Hs.111849	ESTs	4.1
	454434	AA083558	Hs.261286	ESTs	4.1
	404526	AJ912555	Hs.157195	peptide YY, 2 (seminaplasmin)	4.1
	445393	AW014174	Hs.301956	zinc finger protein	4.1
	405302				4.1
10	432669	AL043482	Hs.267115	ESTs	4.1
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	423841	AW753957		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	430484	D82880	Hs.241548	RAS p21 protein activator 2	4.1
15	403895				4.1
	420457	AA482280	Hs.191656	ESTs	4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	458421	AJ279978	Hs.22547	ESTs	4.1
	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.1
20	411382	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	4.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	4.1
	430749	AJ242956	Hs.259560	v-myc avian myelocytomatosis viral relat	4.1
	403625				4.1
	401887				4.1
25	403667				4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA: cDNA DKFZp434E082 (fr	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	432792	AA448114	Hs.278950	protocadherin beta 1	4.0
30	405443				4.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	4.0
	431822	AA516049		gb:mg65d01.s1 NCI_CGAP_Lip2 Homo sapiens	4.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.0
	448324	AI571356	Hs.34174	ESTs, Moderately similar to ALU8_HUMAN A	4.0
35	456536	AW135986	Hs.257859	ESTs	4.0
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	449327	AI638743	Hs.224672	ESTs	4.0
40	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	4.0
	433485	AI93076	Hs.201967	aldo-keto reductase family 1, member C2	4.0
	434849	AW292765	Hs.8053	ESTs	4.0
	400268				4.0
45	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	4.0
	445414	AV653692	Hs.146105	ESTs	4.0
	406470				3.9
	429809	AL162010	Hs.223603	Homo sapiens mRNA: cDNA DKFZp761D09121 (3.9
	453098	Z25935	Hs.86379	ESTs	3.9
50	402867				3.9
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-Interacting protein 1	3.9
55	426076	AW962714		gb:EST374787 MAGE resequences, MAGG Homo	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.9
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogen	3.9
	413499	BE144884		gb:CMO-HT0182-041099-065-e11 HT0182 Homo	3.9
60	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
	443323	BE560621	Hs.9222	estrogen receptor binding site associata	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	455993	BE179085		gb:RCO-HT0613-140300-021-d06 HT0613 Homo	3.9
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
65	403956	W28077	Hs.79389	nei (chicken)-like 2	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retrovru	3.9
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	3.9
	430140	AW296771	Hs.221999	ESTs	3.8
	457042	AI382130	Hs.97703	ESTs	3.8
70	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	413071	BE064032		gb:QV3-BT0296-010300-111-b08 BT0296 Homo	3.8
	437354	AA749215	Hs.291886	ESTs	3.8
75	403381				3.8
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	426365	AA376667	Hs.10283	RNA binding motif protein 88	3.8
	430757	AI458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	3.8
80	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	433887	AW204232	Hs.279522	ESTs	3.8
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.8
	404043				3.8

	431333	AA708488	Hs.120127	Homo sapiens cDNA: FLJ22769 fis, clone K	3.8
	451073	AJ758905	Hs.206063	ESTs	3.8
	417663	R07483	Hs.180461	ESTs	3.8
5	432363	AA534489		gb:mf76g11.s1 NCL_CGAP_Co3 Homo sapiens	3.8
	436975	AA740723	Hs.212644	ESTs	3.8
	405959				3.8
	400631	AF173937	Hs.109494	secreted protein of unknown function	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
10	446158	AJ277603	Hs.145990	ESTs, Weakly similar to I38022 hypothe	3.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.7
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.7
	436020	AA778177	Hs.121724	ESTs	3.7
	424989	AA985520	Hs.23575	ESTs	3.7
15	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.7
	441416	AI990139	Hs.148609	ESTs	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	3.7
	404453				3.7
20	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	421037	AJ684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
	453530	AW021633		gb:df26c02.y1 Morton Fetal Cochlea Homo	3.7
25	406984	M21305		gb:Human alpha satellite and satellite 3	3.7
	432291	AK001108	Hs.274274	hypothetical protein FLJ10246	3.7
	449623	C00719	Hs.120440	EST	3.7
	419691	W03298	Hs.193521	ESTs	3.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.7
30	403271				3.7
	453123	AI953718	Hs.221849	ESTs	3.7
	400462				3.7
	449804	AI535663	Hs.39379	ESTs	3.7
	443305	AI050693	Hs.133318	ESTs	3.7
35	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.6
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	403296				3.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.6
40	436026	AJ349764	Hs.217081	ESTs	3.6
	429864	AA460039	Hs.286	ribosomal protein L4	3.6
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	3.6
	442910	AJ365130	Hs.11307	ESTs, Weakly similar to T19326 hypothe	3.6
	446304	AW104432	Hs.149761	ESTs	3.6
45	441216	BE299830	Hs.192908	ESTs	3.6
	421494	AJ763322	Hs.152104	ESTs	3.6
	404476				3.6
	416327	R99822	Hs.36172	ESTs	3.6
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.6
50	417401	AA426026	Hs.187615	ESTs	3.6
	401200				3.6
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.6
	426306	AA447310	Hs.164059	Homo sapiens cDNA FLJ13338 fis, clone OV	3.6
	437918	AJ761449	Hs.121629	ESTs	3.6
55	447817	AL048037	Hs.164588	ESTs, Moderately similar to neuronal thr	3.6
	421328	BE466506	Hs.3981	ESTs	3.6
	447290	AA76732	Hs.263912	ESTs	3.6
	417229	AA976096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1196H6 on	3.6
60	403515				3.6
	419917	AA320068	Hs.93701	Homo sapiens mRNA: cDNA DKFZp434E232 (tr	3.6
	435554	AF208502	Hs.185708	early B-cell factor	3.6
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	3.6
	410500	R09442		gb:yr26c09.r1 Soares fetal liver spleen	3.6
65	439326	W07140	Hs.54721	ESTs	3.6
	426296	R14454	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.6
	411311	AW836491		gb:PM3-LT0032-281299-002-f02 LT0032 Homo	3.6
	418019	R68911	Hs.176275	ESTs	3.6
	417490	AA203335		gb:zx56g02.r1 Soares_fetal_liver_spleen_	3.6
70	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	416575	W02414	Hs.38383	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity 1, rec	3.5
	418405	AI868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	450350	T97817	Hs.174880	ESTs	3.5
75	451704	AJ755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	421013	M52397	Hs.1345	mutated in colorectal cancers	3.5
	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRN	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypothe	3.5
80	457141	AA521410	Hs.41371	ESTs	3.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	3.5
	440737	AJ375167	Hs.132221	hypothetical protein FLJ12401	3.5
	452728	AJ915676	Hs.239708	ESTs	3.5
	423266	AA323875	Hs.193574	ESTs	3.5

5	413543	AA130228	Hs.324611	ESTs, Moderately similar to ALU8_HUMAN A	3.5
	454447	BE163567		gb:OV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	415549	F11942		gb:HSC33F061 normalized Infant brain cDN	3.5
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	453211	W84829		gb:zh53104.r1 Soares_fetal_liver_spleen_	3.5
10	418717	AI334430	Hs.86984	ESTs	3.5
	400641				3.5
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	3.5
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
15	458340	AI457102	Hs.6986	Human glucose transporter pseudogene	3.5
	412281	AI810054	Hs.14119	ESTs	3.5
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	3.5
	416616	H68270		gb:yr61h09.r1 Soares fetal liver spleen	3.5
	444338	AI937026	Hs.146642	ESTs	3.4
20	436946	AW137748	Hs.125956	ESTs	3.4
	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	3.4
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	3.4
	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.4
25	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.4
	416100	H18700	Hs.268799	ESTs	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
30	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	440388	AI693520	Hs.223000	ESTs	3.4
	421072	AI215069	Hs.89113	ESTs	3.4
	424578	AK001973	Hs.150890	hypothetical protein	3.4
	436331	AI239495	Hs.120189	ESTs	3.4
35	444063	AI122614		gb:xq66b05.x1 Soares_fetal_heart_NbHH19W	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
	404196				3.4
	421282	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	3.4
	409555	AW410788	Hs.256185	ESTs	3.4
40	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	3.4
	416057	AI927382	Hs.29857	ESTs	3.4
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	3.4
	447738	AI871000	Hs.161330	ESTs	3.4
	430564	AW969834	Hs.303303	ESTs	3.4
45	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	3.4
	415769	H94186	Hs.5912	F-box only protein 7	3.4
	429382	AI791249	Hs.278054	ESTs, Weakly similar to I38022 hypotheti	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	3.4
50	442826	AI018777	Hs.131241	ESTs	3.4
	400608				3.4
	436111	AI803082	Hs.157212	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
	436577	W84774	Hs.17643	ESTs	3.4
55	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.4
	423871	AA331906		gb:EST35805 Embryo, 8 week 1 Homo sapien	3.4
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.4
	409623	AW449185		gb:UI-H-B13-ekg-e-05-0-UI.s1 NCI_CGAP_Su	3.4
60	416182	NM_004354	Hs.79089	cyclin G2	3.4
	420854	AW296927		gb:UI-H-BW0-ajc-c-07-0-UI.s1 NCI_CGAP_Su	3.4
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	432404	AA535248	Hs.50852	ESTs	3.4
	458695	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypotheti	3.4
65	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	3.3
	428766	AA477989	Hs.98800	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
	456231	H73183	Hs.129885	ESTs, Weakly similar to 2004399A chromos	3.3
	454318	AW367764	Hs.7857	erythrocyte membrane protein band 4.1-ii	3.3
70	411966	AA099113	Hs.118609	ESTs	3.3
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	3.3
	437037	T63804		gb:yc21e09.r1 Stratagene lung (937210) H	3.3
	407664	AW053476	Hs.279080	ESTs	3.3
	405780				3.3
75	426567	AA381579	Hs.182962	ESTs	3.3
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	3.3
	403358				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, I	3.3
	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
80	429875	AI091815		gb:xq58b06.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	433785	BE044593	Hs.112704	ESTs	3.3
	437876	AA770151	Hs.126424	ESTs	3.3
	444870	AI200621	Hs.148504	ESTs	3.3
	453324	W26592	Hs.232089	ESTs	3.3

5	437963	BE395279		gb:601309785F1 NIH_MGC_44 Homo sapiens c	3.3
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	3.3
	408813	A1580090	Hs.48295	RNA helicase family	3.3
	426692	AK001751	Hs.171835	hypothetical protein FLJ10889	3.3
	407456	AJ237589		gb:Homo sapiens mRNA for T-box transcrip	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
10	453242	T98327	Hs.18343	ESTs	3.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.3
	412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	3.3
	435070	A1821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	3.3
	444443	A1149286	Hs.55099	rab6 GTPase activating protein (GAP and	3.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibitor	3.3
15	454145	AA046872	Hs.62798	ESTs	3.3
	405264				3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	416816	T71168	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.3
20	435325	AJ038388	Hs.119309	ESTs	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AJ369472	Hs.65407	ESTs	3.3
	429105	AA446612		gb:zw55g07.s1 Soares_tetal_fetus_Nb2HF8_	3.3
25	405720				3.3
	400889				3.3
	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	422094	AF129535	Hs.272027	F-box only protein 5	3.3
	425374	A1904013		gb:MR-BT041-220199-104 BT041 Homo sapien	3.3
30	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	427374	A150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AJ336596	Hs.156294	ESTs	3.3
	457604	AJ004397	Hs.334552	Homo sapiens cDNA FLJ14930 fis, clone PL	3.3
35	452291	AF015592	Hs.28853	CDCT (cell division cycle 7, S. cerevisi	3.3
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	3.3
	458885	AA411303	Hs.30022	ESTs, Weakly similar to NAH6_HUMAN SODIU	3.3
	429608	U49250	Hs.210862	T-box, brain, 1	3.2
	437454	AL390159	Hs.269812	Homo sapiens mRNA; cDNA DKFZp761M0415 (I	3.2
40	430503	AA533574	Hs.152274	ESTs	3.2
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	3.2
	421698	T89677	Hs.324323	ESTs	3.2
	412321	AW936913		gb:RC1-DT0029-030200-012-f08 DT0029 Homo	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
45	454952	AW847645		gb:JL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	441705	AJ087052	Hs.55993	ESTs	3.2
	403619				3.2
	435608	AW183971	Hs.250896	ESTs	3.2
	426701	AJ968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.2
50	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (Ik	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.2
55	419936	AJ792788		gb:ol91d05.y5 NCL_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	408592				3.2
	446530	AV658909	Hs.282642	ESTs	3.2
	454466	AA984138	Hs.155101	ATP synthase, H+ transporting, mitochond	3.2
60	401449				3.2
	431196	AW974436	Hs.154929	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	459459	AA460445		gb:zx66h11.r1 Soares_tetal_fetus_Nb2HF8_	3.2
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.2
65	427335	AA448542	Hs.251677	G antigen 7B	3.2
	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	3.2
	425156	AA351364		gb:EST59099 Infant brain Homo sapiens cD	3.2
	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
70	444910	AJ201849		gb:qs76g04.x1 NCL_CGAP_Pr28 Homo sapiens	3.2
	426660	NM_002719	Hs.171734	protein phosphatase 2, regulatory subuni	3.2
	438315	R56795	Hs.82419	ESTs	3.2
	425523	AB007948	Hs.158244	KIAA0479 protein	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
75	425636	AK001243	Hs.158370	hypothetical protein FLJ10381	3.2
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	3.2
	457030	AJ301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	447375	AJ376660	Hs.257822	ESTs	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
80	410085	AA428482	Hs.58589	glycogenin 2	3.2
	410536	N39533		gb:yy27d04.s1 Soares fetal liver spleen	3.2
	448495	AW136516	Hs.208515	ESTs	3.2
	405634				3.2
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	3.2

	421581	U89331	Hs.105932	short stature homeobox	3.1
	440633	AJ140686	Hs.263320	ESTs	3.1
	453264	AA034137	Hs.271955	ESTs	3.1
5	411656	AW855576		gb:CM4-CT0278-221099-027-d01 CT0278 Homo	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothe	3.1
	426591	AA431127	Hs.98685	ESTs	3.1
	446966	C01448	Hs.300511	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
10	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.1
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.1
	423557	AL045128	Hs.1691	glucan (1,4-alpha-), branching enzyme 1	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
15	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	400315	U46120	Hs.193392	Human expressed unknown mRNA	3.1
	411965	BE467339	Hs.280115	ESTs	3.1
	416316	H58721	Hs.271628	ESTs	3.1
	400613				3.1
20	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	3.1
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.1
	418693	AI750878	Hs.87409	thrombospondin 1	3.1
	416258	N45661	Hs.90011	adenylosuccinate synthase	3.1
	405093				3.1
25	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	422654	AA314316	Hs.163725	ESTs	3.1
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	3.1
30	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.1
	402790				3.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	3.1
	447524	D80449	Hs.45177	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
35	415979	H16427	Hs.271501	ESTs, Weakly similar to I54374 gene NF2	3.1
	434479	AI138213	Hs.162035	olfactory receptor, family 52, subfamily	3.1
	426724	AA383623	Hs.293616	ESTs	3.1
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	3.1
	405608				3.1
	406506				3.1
40	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	3.1
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypothe	3.1
	404288				3.1
	429878	AA460188	Hs.127263	ESTs	3.1
	439834	AF754576	Hs.124523	ESTs	3.1
45	454584	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo	3.1
	450491	BE045604	Hs.202301	ESTs	3.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.1
	400579				3.1
	402953				3.1
50	404285				3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457770	BE065030	Hs.124179	ESTs	3.1
	435477	BE218708	Hs.117270	hypothetical protein FLJ14345	3.1
55	436391	AJ227892	Hs.146274	ESTs	3.1
	456083	U46922	Hs.77252	fragile histidine triad gene	3.1
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.1
	430101	AF110002	Hs.233363	guanylate cyclase activator 1C	3.1
	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
60	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	3.1
	456323	AW752389	Hs.87296	Homo sapiens cDNA FLJ20269 fis, clone HE	3.1
	429828	AB019494	Hs.225767	IDN3 protein	3.1
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	3.1
	452762	AW501435	Hs.276582	v-eld murine thymoma viral oncogene homo	3.1
	401344				3.1
65	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	3.1
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	3.1
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.1
	423600	AI633559	Hs.310359	ESTs	3.1
70	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	3.0
	407257	AB006834		gb:Homo sapiens mRNA for HRV Fab N6-VH,	3.0
	457041	AA399018	Hs.250835	ESTs	3.0
	421482	AL135462	Hs.104715	Inversin	3.0
	459062	AA059246	Hs.110293	ESTs	3.0
75	436475	R58806	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.0
	417489	AW953341	Hs.22573	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	3.0
	436394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.0
80	443741	AW451759	Hs.145420	ESTs	3.0
	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	445409	AI949081	Hs.147862	ESTs	3.0

	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.0
	406364				3.0
5	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.0
10	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	3.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.0
	426424	BE081745	Hs.272188	Homo sapiens cDNA FLJ12090 fis, clone HE	3.0
	419505	AA243660	Hs.143061	ESTs	3.0
	403743				3.0
15	415452	F09134	Hs.12839	ESTs	3.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	400227				3.0
20	436219	AK001695	Hs.146589	hypothetical protein FLJ10701	3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AJ741816	Hs.125897	ESTs	3.0
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.0
	403513				3.0
25	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.0
	440122	AJ733011	Hs.127678	ESTs	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.0
30	448130	AW271635	Hs.170717	ESTs	3.0
	420288	AW071225	Hs.245556	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	404513				3.0
35	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	3.0
	407762	AW235638	Hs.29475	ESTs	3.0
	403396				3.0
	436938	AW139680	Hs.161393	ESTs	3.0
40	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	3.0
	400706				2.9
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.9
	444600	R41398	Hs.6996	ESTs	2.9
	403786				2.9
45	430187	AI799909	Hs.158989	ESTs	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.9
	457503	AW970244	Hs.162188	ESTs	2.9
	446251	AW867156	Hs.282589	ESTs, Weakly similar to I38022 hypotheti	2.9
	406327				2.9
50	434671	R34758		gb:yg61g02.r1 Soares infant brain 1N18 H	2.9
	430175	AA468724		gb:ns08a06.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	2.9
	449459	BE546846	Hs.195048	ESTs	2.9
55	435934	R19382	Hs.117869	ESTs	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	414514	BE327365	Hs.280187	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
60	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32108, mRNA seq	2.9
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	2.9
	456186	W26642		gb:34b8 Human retina cDNA randomly prime	2.9
	412222	AA528283	Hs.292737	ESTs	2.9
65	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.9
	435579	AJ332373	Hs.156924	ESTs	2.9
	417027	AA192306	Hs.23926	triadin	2.9
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
70	445909	BE262656	Hs.32603	hypothetical protein MGC3279 similar to	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	403341				2.9
	445635	AJ769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
75	453830	AA534296	Hs.20953	ESTs	2.9
	455866	BE149024		gb:CMO-HT0249-291099-084-c04 HT0249 Homo	2.9
	407676	AW064111	Hs.279823	ESTs	2.9
	437913	AJ140825	Hs.121623	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
80	457049	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	2.9
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441874	AA970389	Hs.128055	ESTs	2.9
	416483	H58311	Hs.165077	ESTs	2.9

	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
	446447	AI300402	Hs.202250	ESTs	2.9
	439953	AA918129	Hs.124638	ESTs	2.9
	400643				2.9
5	436594	AI419982	Hs.156189	ESTs	2.9
	438402	D16902	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.9
	451353	N21043	Hs.42932	ESTs	2.9
	419791	AI579909	Hs.105104	ESTs	2.9
	415628	F13080		gb:HSC3ID041 normalized Infant brain cDN	2.9
10	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	454747	AW818535		gb:RC1-ST0278-140300-016-105 ST0278 Homo	2.9
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.9
	457178	AL039101	Hs.194625	dynein, cytoplasmic, light Intermediate	2.9
	401526				2.9
15	408751	N91553	Hs.258343	ESTs	2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
20	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	421847	NM_014717	Hs.108884	KIAA0390 gene product	2.8
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.8
	422225	BE245652	Hs.118281	zinc finger protein 266	2.8
	403011				2.8
25	405170				2.8
	435878	R08330	Hs.20152	ESTs	2.8
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	2.8
	400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA,	2.8
	411244	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	2.8
30	441817	AW969706	Hs.293332	ESTs	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	2.8
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.8
	402131				2.8
35	428959	AF100779	Hs.194680	WNT1 Inducible signaling pathway protein	2.8
	438160	AA779332	Hs.122671	ESTs	2.8
	407594	AW057684	Hs.160681	ESTs	2.8
	417877	AI025829	Hs.86320	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
40	451257	AA016255	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.8
	437113	AA744893		gb:ny26c10.s1 NCL_CGAP_GCB1 Homo sapiens	2.8
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	410672	AW794600		gb:RC8-UM0014-170300-022-C05 UM0014 Homo	2.8
45	412236	AW802583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.8
	417827	T79366	Hs.108258	actin binding protein; macrophilin (microf	2.8
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glu	2.8
	449676	AW380579	Hs.209657	ESTs	2.8
	454778	AW820199		gb:QV2-ST0296-190100-029-a07 ST0296 Homo	2.8
50	451203	AW070604	Hs.46517	ESTs	2.8
	450180	AW449644	Hs.257182	ESTs	2.8
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.8
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	450003	AA777809	Hs.191995	ESTs	2.8
55	401602				2.8
	413986	Z43567		gb:HSC1FC021 normalized Infant brain cDN	2.8
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.8
	415652	T79213	Hs.272073	ESTs	2.8
	404076				2.8
60	409416	AW388359	Hs.10667	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
	426960	AA393713		gb:zt71h04.r1 Soares_testis_NHT Homo sap	2.8
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.8
	448597	BE613250	Hs.98265	KIAA1877 protein	2.8
65	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	2.8
	433077	AA314262	Hs.301917	YDD19 protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	447410	AI470235	Hs.172698	EST	2.8
	414652	AI620599	Hs.72068	ESTs	2.8
70	430454	AW469011	Hs.105635	ESTs	2.8
	412417	AA102268	Hs.158622	ESTs	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
	401098				2.8
75	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	2.8
	403549				2.8
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
80	433513	AI566356	Hs.171437	ESTs	2.8
	446677	AI800311	Hs.156291	ESTs	2.8
	457758	AA126136	Hs.38125	Interferon-induced protein 75, 52kD	2.8
	450895	N66727	Hs.10957	ESTs	2.8
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.8

	449358	AA001229	Hs.131436	ESTs	2.8
	422816	AA323585	Hs.93235	ESTs	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
5	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypothe	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	458023	AW978161	Hs.268555	5'-3' exonuclease 2	2.8
10	422260	AA315993	Hs.105484	regenerating gene type IV	2.8
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	411762	AW850972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
15	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	405992	S82472		gb:beta -pot=DNA polymerase beta (exon a	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429583	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
20	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	445017	AI205493	Hs.176860	ESTs	2.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	2.7
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	2.7
	416805	F13271	Hs.79981	Human clone Z3560 mRNA sequence	2.7
25	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	435689	AA694284		gb:z135c02.s1 Soares_fetal_liver_spleen_	2.7
	429282	N27596	Hs.21342	ESTs	2.7
	435731	AA699581	Hs.186811	ESTs	2.7
30	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	421274	BE160327	Hs.104572	ESTs	2.7
	403776				2.7
	409526	BE298751	Hs.55014	hypothetical protein FLJ10206	2.7
35	410201	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	447884	H29505		gb:ym60d10.r1 Soares Infant brain 1N1B H	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	447272	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.7
40	434890	AF161345	Hs.283930	Homo sapiens HSPC082 mRNA, partial cds	2.7
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	2.7
	413998	AW103807	Hs.243933	ESTs	2.7
	403677				2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
45	430698	AA492071		gb:zne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
	432591	AA643238	Hs.146144	ESTs	2.7
	446800	A1341635	Hs.156486	ESTs	2.7
	454938	AW846134		gb:QV0-CT0179-091199-049-d02 CT0179 Homo	2.7
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
50	445233	AV653034	Hs.297559	ESTs	2.7
	448756	AI739241	Hs.171480	ESTs	2.7
	418379	AA218940	Hs.137516	fidgulin-like 1	2.7
	435068	H16262	Hs.31415	ESTs	2.7
	406092				2.7
55	422036	AA302647	Hs.271891	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.7
	441541	AA938663	Hs.199828	ESTs	2.7
	451395	AI082419	Hs.114761	ESTs	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7
60	423949	AI014546	Hs.130912	ESTs	2.7
	435420	AI928513	Hs.59203	ESTs	2.7
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	2.7
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.7
	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.7
65	454767	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	2.7
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.7
	402429				2.7
	403760				2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
70	435448	H17132	Hs.27085	ESTs	2.7
	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	2.7
	422171	U50529	Hs.112434	Novel human gene mapping to chromosome 13	2.7
	459023	AW968226	Hs.60798	ESTs	2.7
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08580 hypothe	2.7
	404569				2.7
75	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	449880	AI673006	Hs.231948	ESTs	2.7
80	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	415268	R53935	Hs.287827	ESTs, Highly similar to MDR3_HUMAN MULTI	2.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.7
	452512	AW363486	Hs.337635	ESTs	2.7
	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	2.7

	419481	AI879195	Hs.90606	15 kDa selenoprotein	2.7
	454352	AW389668		gb:RC2-ST0168-071299-013-06 ST0168 Homo	2.7
	422831	R02504	Hs.332943	ESTs	2.7
5	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.7
	426872	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapien	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GC81 Homo sapiens	2.7
	446002	AI346468	Hs.145789	ESTs	2.7
10	454716	AW850684		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.7
	406664	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	2.7
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	2.7
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	2.7
	454754	AW819191		gb:CM1-ST0283-071299-061-008 ST0283 Homo	2.7
15	439451	AF086270	Hs.278554	heterochromatin-like protein 1	2.7
	445225	AI216555	Hs.202398	ESTs	2.7
	427175	H06924	Hs.23782	hypothetical protein FLJ12847	2.7
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.7
	438135	AI253025	Hs.190426	ESTs	2.7
20	405981				2.7
	406005				2.7
	430762	AI343652	Hs.105667	ESTs	2.7
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.7
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.7
25	434684	AA737282	Hs.190911	ESTs	2.7
	445660	AI702669	Hs.201955	ESTs	2.7
	400844				2.6
	415725	BE219771	Hs.237146	hypothetical protein FLJ12752	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
30	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 Integrin	2.6
	430052	AF102850	Hs.227933	Alg5, S. cerevisiae, homolog of	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	417252	AA195014	Hs.85971	ESTs	2.6
35	427167	AI239607	Hs.99196	hypothetical protein MGC11324	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.6
40	442240	AI791883	Hs.292719	ESTs	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	410238	N94320	Hs.144225	ESTs	2.6
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.6
	440801	AA906366	Hs.190535	ESTs	2.6
45	440274	R24595	Hs.7122	scrapie responsive protein 1	2.6
	411597	AW852925		gb:PM0-CT0248-131099-001-110 CT0248 Homo	2.6
	417956	AA210704	Hs.180465	ESTs	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GC81 Homo sapiens	2.6
50	425176	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcr	2.6
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	426098	NM_014906	Hs.166351	KIAA1072 protein	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
55	445550	AI242754	Hs.137306	ESTs	2.6
	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.6
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.6
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	2.6
60	418282	AA215535	Hs.98133	ESTs	2.6
	442757	AI739528	Hs.28345	ESTs	2.6
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Ho	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	441209	AA922939	Hs.135742	ESTs	2.6
65	458679	AW975460	Hs.143563	ESTs	2.6
	442279	AW867006	Hs.159970	ESTs	2.6
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.6
	411880	AW872477		gb:hm3003.x1 NCI_CGAP_Thy4 Homo sapiens	2.6
	404845				2.6
70	411693	AW857271		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	457630	AI680803	Hs.112627	ESTs	2.6
75	424015	N95698	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (tr	2.6
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.6
	413174	AA723564	Hs.191343	ESTs	2.6
	438875	AA827640	Hs.189059	ESTs	2.6
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	2.6
80	423257	AW161039	Hs.125878	synapsin III	2.6
	431086	AI828692	Hs.211561	ESTs	2.6
	409337	H71269	Hs.220535	ESTs	2.6
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.6
	410004	AI298027	Hs.5057	carboxypeptidase D	2.6

	455935	BE158687	gb:CMO-HT0395-280100-169-b09 HT0395 Homo	2.6
	403273			2.6
	445955	AA332209	Hs.158196 transcriptional adaptor 3 (ADA3, yeast h	2.6
5	425626	AI537536	Hs.173519 ESTs	2.6
	451531	AA018311	Hs.114762 ESTs	2.6
	428085	AA421081	Hs.12388 ESTs	2.6
	429761	AI276780	Hs.135173 ESTs	2.6
	437958	BE139550	Hs.121668 ESTs, Moderately similar to PC4259 ferri	2.6
10	442666	W74633	Hs.303720 ESTs	2.6
	413088	BE064962	gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	419107	AW085152	Hs.292987 ESTs	2.6
	435766	R11673	Hs.186498 ESTs	2.6
	452879	AW905328	Hs.180842 ribosomal protein L13	2.6
	440400	AA994364	Hs.125594 ESTs, Weakly similar to T25472 hypotheti	2.6
15	440460	H92571	Hs.234478 Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	424146	AA705092	Hs.202368 ESTs	2.6
	439950	AW937417	Hs.293561 ESTs	2.6
	410366	AI267589	Hs.302689 hypothetical protein	2.6
	417485	AA203304	Hs.32826 CGI-130 protein	2.6
20	412586	AW962574	gb:EST374847 MAGE resequences, MAGG Homo	2.6
	416498	U33632	Hs.79351 polasslum channel, subfamily K, member 1	2.6
	440397	AA884448	Hs.157239 ESTs	2.6
	451236	AI767406	Hs.207026 ESTs, Weakly similar to B56205 transcrip	2.6
	411819	AW947884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.6
25	430357	AW976789	Hs.165607 ESTs	2.6
	432869	AW974094	gb:EST386197 MAGE resequences, MAGM Homo	2.6
	427506	AK000134	Hs.179100 hypothetical protein FLJ20127	2.6
	401614			2.6
30	404531	Z25884	Hs.121483 chloride channel 1, skeletal muscle (Th	2.6
	426698	AA394104	Hs.97489 ESTs	2.6
	440479	AA886461	Hs.208161 ESTs	2.6
	443160	AI467915	Hs.36053 ESTs	2.6
	419323	AI092379	Hs.135275 ESTs	2.5
35	442813	AI018435	Hs.270970 ESTs	2.5
	436196	AK001084	Hs.333498 Homo sapiens cDNA FLJ10222 fis, clone HE	2.5
	433561	BE540937	Hs.20104 hypothetical protein FLJ00052	2.5
	434059	AA649162	Hs.236456 ESTs	2.5
	454836	AW833711	gb:QV4-TT0008-251199-043-a11 TT0008 Homo	2.5
40	458589	AV654623	Hs.288141 hypothetical protein MGC3156	2.5
	459716			2.5
	436340	R42246	Hs.21606 ESTs	2.5
	426020	L19058	Hs.181581 glutamate receptor, ionotropic, kainate	2.5
	416951	AA190926	Hs.190785 ESTs, Moderately similar to S65657 alpha	2.5
	401078			2.5
45	410644	AW902125	gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.5
	411660	AW855718	gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	425201	AA352111	gb:EST60061 Activated T-cells XX Homo sa	2.5
	455252	AW876627	gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
50	439096	AA830185	Hs.269680 ESTs	2.5
	442627	AI027990	Hs.132303 ESTs	2.5
	457799	AF220188	Hs.236510 uncharacterized hypothalamus protein HTM	2.5
	428799	AI478619	Hs.104677 ESTs	2.5
	450402	BE218027	Hs.89969 ESTs	2.5
55	411156	AW819939	Hs.273629 ESTs	2.5
	431673	AW971302	Hs.293233 ESTs	2.5
	415706	BE182587	Hs.57485 ESTs	2.5
	412882	BE006919	Hs.134106 ESTs	2.5
	441300	R35063	Hs.181536 ESTs	2.5
60	413257	BE075035	gb:PM3-BT0584-260300-002-g05 BT0584 Homo	2.5
	434662	AA641957	gbms18d08.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
	455255	AW877139	gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.5
	417137	U46265	Hs.81281 mitochondrial ribosomal protein S21	2.5
	417909	R35614	gb:yg66e08.r1 Soares infant brain 1N1B H	2.5
65	458043	AW979009	Hs.326108 ESTs	2.5
	417008	AW673606	Hs.80758 aspartyl-tRNA synthetase	2.5
	442006	AW975183	Hs.292663 ESTs, Weakly similar to S72482 hypotheti	2.5
	455756	BE079307	gb:RC1-BT0623-120200-011-g09 BT0623 Homo	2.5
	454032	W31790	Hs.194293 ESTs, Weakly similar to 154374 gene NF2	2.5
70	444963	AI916973	Hs.213603 ESTs	2.5
	443526	AW792804	Hs.134002 ESTs	2.5
	454532	AA344685	Hs.58831 regulator of Fas-induced apoptosis	2.5
	428832	AA578229	Hs.324239 ESTs, Moderately similar to ZN91_HUMAN Z	2.5
	442003	AW297497	Hs.201891 ESTs	2.5
75	452768	AW069459	Hs.61539 ESTs	2.5
	411355	AW838479	Hs.22692 ESTs	2.5
	458890	AW865523	gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.5
	400074			2.5
	405241			2.5
80	413096	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	2.5
	414349	BE512968	gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	422884	AW860975	Hs.13256 ESTs	2.5
	429515	AL031228	Hs.204370 DNA segment on chromosome 6 (unique, pse	2.5
	431925	AK000890	gb:Homo sapiens cDNA FLJ10028 fis, clone	2.5

	442653	BE269247		gb:601185486F1 NIH_MGC_8 Homo sapiens cD	2.5
	401882				2.5
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hlg	2.5
	405336				2.5
5	439492	AF086310	Hs.103159	ESTs	2.5
	455390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.5
	436359	Z83806		gb:H.sapiens mRNA for axonemal dynein he	2.5
	429322	D86984	Hs.199243	KIAA0231 protein	2.5
10	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	437107	AA745598	Hs.291840	ESTs, Weakly similar to I78865 serine/th	2.5
	441953	H11695	Hs.322901	disrupter of silencing 10	2.5
	442777	AW341541	Hs.271153	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
15	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	457824	R84938		gb:yt65f04.r1 Soares retina N2b4HR Homo	2.5
	428550	AW297880	Hs.98661	ESTs	2.5
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.5
	456359	AJ967991	Hs.93574	homeo box D3	2.5
20	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.5
	452528	AA742457	Hs.291479	ESTs	2.5
	408444	AW661839	Hs.253204	ESTs	2.5
	440327	R12581	Hs.191146	ESTs	2.5
	410406	AJ969703	Hs.1466	glycerol kinase	2.5
25	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fs, clone H	2.5
	418948	AI217097		gb:qd43h07.x1 Soares fetal heart NbHH19W	2.5
	435427	AA682573	Hs.188982	ESTs, Weakly similar to organic anion tr	2.5
	427791	AA412446	Hs.98138	ESTs	2.5
	403509	AF231919	Hs.18759	KIAA0539 gene product	2.5
30	436590	AJ393115	Hs.127655	ESTs	2.5
	455556	AW995423		gb:QV0-BN0042-010400-183-g08 BN0042 Homo	2.5
	405869				2.5
	408274	R17315		gb:cyg12g11.r1 Soares infant brain 1N1B H	2.5
	448015	AJ458065	Hs.23196	ESTs	2.5
35	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
	436154	AA764950	Hs.119898	ESTs	2.5
	406377				2.5
	437030	AA742577	Hs.303781	EST	2.5
	420815	AA280684	Hs.270584	ESTs	2.5
40	418421	R58620	Hs.85050	phospholamban	2.5
	423638	AJ003521	Hs.130310	Homo sapiens mRNA for cyclin B3 isoform	2.5
	415425	F08365		gb:HSCZSA121 normalized infant brain cDN	2.5
	404577				2.5
	403568				2.5
45	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.5
	449899	AJ610700	Hs.103280	ESTs	2.5
	451078	AJ927694	Hs.204470	ESTs	2.5
	453343	AA905353	Hs.121622	ESTs	2.5
	428728	NM_016825	Hs.191381	hypothetical protein	2.5
50	409642	AW450809	Hs.257347	ESTs	2.5
	426235	AJ631964	Hs.34447	ESTs	2.5
	452043	H86231		gb:yt03f02.r1 Soares retina N2b5HR Homo	2.5
	401992				2.5
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.5
55	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AJ264847	Hs.22545	Homo sapiens cDNA FLJ12935 fs, clone NT	2.5
	449311	AJ657014		gb:tl49a12.x1 NCL CGAP_G06 Homo sapiens	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
60	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.4
	421583	AA293333		gb:zd53c09.r1 Soares ovary tumor NbHOT H	2.4
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.4
	454437	AJ248173	Hs.191460	hypothetical protein MGC12936	2.4
	419187	AA234852	Hs.44693	ESTs	2.4
65	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	2.4
	405547				2.4
	454086	AW885909	Hs.6975	PRO1073 protein	2.4
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	2.4
	416277	W78765	Hs.180145	HSPC030 protein	2.4
70	420976	AJ924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.4
	406468				2.4
	408617	R61736	Hs.124128	ESTs	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
75	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	455328	AW896438		gb:PM1-NN0047-040400-001-d09 NN0047 Homo	2.4
	409500	U08098	Hs.54576	sulfotransferase, estrogen-prefering	2.4
	434138	AA625804		gb:zu86h01.s1 Soares testis_NHT Homo sap	2.4
	419511	AA429750	Hs.75113	general transcription factor IIA	2.4
80	437980	R50393	Hs.278436	KIAA1474 protein	2.4
	439999	AA115811	Hs.6838	ras homolog gene family, member E	2.4
	403501				2.4
	446845	AJ343645	Hs.156108	ESTs	2.4
	401775				2.4

	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411836	AW901879	Hs.314453	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
5	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypotheli	2.4
	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	428945	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse l	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
10	435255	AF193766	Hs.13872	cytokine-like protein C17	2.4
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.4
	458239	BE439877	Hs.283389	ESTs	2.4
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	2.4
	441262	AI809130	Hs.176906	ESTs	2.4
	402076				2.4
15	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.4
	400587				2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	411203	AW872430	Hs.273743	ESTs	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
20	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	424131	AA335714	Hs.199665	ESTs	2.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	2.4
	440385	AA884283	Hs.192136	ESTs	2.4
25	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.4
	447179	AW015633	Hs.157299	ESTs	2.4
	412977	AA125910	Hs.191461	ESTs	2.4
	436958	AA740322	Hs.293539	Homo sapiens mRNA for KIAA1758 protein,	2.4
	401361				2.4
	403891				2.4
30	408419	AW250092	Hs.305953	zinc finger protein 83 (HPF1)	2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	458570	AW971698	Hs.12627	TJ6 protein	2.4
35	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.4
	412114	AW893891	Hs.240833	ESTs, Weakly similar to I38022 hypotheli	2.4
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	2.4
40	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	2.4
	428268	AA424957	Hs.294132	ESTs	2.4
	450947	AI745400	Hs.204662	ESTs	2.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.4
	438142	T90309	Hs.269651	ESTs	2.4
45	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.4
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	401645				2.4
50	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.4
	453393	AW956392	Hs.110376	ESTs	2.4
	436054	AI076262	Hs.119813	ESTs	2.4
	425433	AA357471		gb:EST66274 LNCAP cells 1 Homo sapiens c	2.4
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.4
55	420839	AI683116	Hs.25328	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	453369	BE551550	Hs.232630	ESTs	2.4
	405017				2.4
	405385				2.4
	435633	AI248152	Hs.270047	ESTs	2.4
60	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	2.4
	434544	C05875	Hs.91575	ESTs	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	455219	AW879403		gb:PMO-OT0019-150300-002-d01 OT0019 Homo	2.4
65	458734	AI554946	Hs.158794	ESTs	2.4
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	2.4
	444313	AI140494	Hs.197855	KIAA0704 protein	2.4
	440448	AA885428	Hs.125646	ESTs	2.4
	441498	AI379248	Hs.58742	ESTs	2.4
70	438205	AA780365	Hs.122161	ESTs	2.4
	402615				2.4
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.4
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
75	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	449007	AI620433	Hs.193201	EST, Weakly similar to NIP2_HUMAN BCL2/A	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	2.4
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	2.4
80	458914	BE327696	Hs.280922	ESTs	2.4
	435061	AI651474	Hs.163944	ESTs	2.4
	416458	AA180511		gb:zp53f03.r1 Stratagene NT2 neuronal pr	2.4
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, l	2.4

	403003			2.4
	405347			2.4
	406091			2.4
5	428402	AW237531	Hs.326876 Homo sapiens SOX5 mRNA, complete cds	2.4
	438762	AW844412	Hs.65450 reticulon 4	2.4
	455780	BE088828	gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397546	ESTs	2.4
	404249			2.4
10	443921	AI091310	Hs.134848 ESTs	2.4
	407055	X89211	gb:H.sapiens DNA for endogenous retrovir	2.4
	417154	AI674701	Hs.21388 ESTs	2.4
	419720	AA249131	Hs.337778 hypothetical protein FLJ11068	2.4
	405230			2.4
	405935			2.4
15	436998	AA745625	Hs.291414 ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252 Human EST clone 22453 mariner transposon	2.4
	419233	AA458873	Hs.178306 ESTs	2.3
	414277	BE269910	gb:601186291F1 NIH_MGC_8 Homo sapiens cD	2.3
20	452092	BE245374	Hs.27842 hypothetical protein FLJ11210	2.3
	453738	AL118674	Hs.34871 zinc finger homeobox 1B	2.3
	410888	AW861207	gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.3
	434239	AF119910	Hs.283047 hypothetical protein PRO2964	2.3
	434098	AA625499	gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	2.3
25	414195	BE263293	Hs.89605 cholinergic receptor, nicotinic, alpha p	2.3
	445688	AI248205	Hs.153244 ESTs	2.3
	451655	BE327088	Hs.212752 ESTs	2.3
	423956	W28203	Hs.136169 Homo sapiens clone 25215 mRNA sequence,	2.3
	413445	BE141022	gb:MR0-HT0067-201099-002-d10 HT0067 Homo	2.3
30	436149	AI754308	Hs.159452 ESTs	2.3
	405629			2.3
	432702	AW973953	Hs.293744 ESTs	2.3
	433377	AI752713	Hs.43845 ESTs	2.3
	444711	AI188739	Hs.148488 ESTs	2.3
35	445621	AI733818	Hs.145549 ESTs	2.3
	456432	AW966931	Hs.179662 nucleosome assembly protein 1-like 1	2.3
	449236	AJ403126	Hs.26373 Homo sapiens cDNA: FLJ23449 fis, clone H	2.3
	459024	AA020799	Hs.262869 plasminogen-like	2.3
	441037	AA913360	Hs.126468 ESTs	2.3
40	431577	T34523	Hs.302040 Homo sapiens DNA sequence from PAC 43401	2.3
	438782	AA828380	Hs.126733 ESTs	2.3
	412329	AW937445	gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.3
	410999	AW813004	gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	429044	AI251490	Hs.145527 ESTs	2.3
45	431655	AW971119	gb:EST383206 MAGE resequences, MAGL Homo	2.3
	439642	W81441	Hs.153967 ESTs	2.3
	441721	AI288259	Hs.127652 ESTs	2.3
	443482	AW188093	Hs.250385 ESTs	2.3
	403416	AI744626	Hs.151385 KIAA0564 protein	2.3
50	416443	N69469	Hs.194225 ESTs	2.3
	419714	AA758751	Hs.98216 ESTs	2.3
	415511	AI732617	Hs.182362 ESTs	2.3
	412344	AW938384	Hs.264190 vacuolar protein sorting 35 (yeast homol	2.3
	449264	AI637649	Hs.196105 ESTs	2.3
55	451664	AA889081	Hs.153952 5' nucleotidase (CD73)	2.3
	441269	AW015206	Hs.178784 ESTs	2.3
	402333			2.3
	453849	Y07494	Hs.34114 ATPase, Na+/K+ transporting, alpha 2 (+)	2.3
	430680	AW138724	Hs.168974 ESTs, Highly similar to ALU7_HUMAN ALU S	2.3
60	404367			2.3
	403698			2.3
	441622	AW450957	Hs.224864 ESTs	2.3
	411004	AW813242	gb:MR3-ST0191-020200-207-g10 ST0191 Homo	2.3
	411093	BE067650	gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
65	428548	AA430058	Hs.98649 EST	2.3
	404059			2.3
	446861	AI696519	Hs.14427 Homo sapiens cDNA: FLJ21800 fis, clone H	2.3
	413640	BE158118	gb:MR2-HT0378-240200-205-d09 HT0378 Homo	2.3
	423554	M90516	Hs.1674 glutamine-fructose-6-phosphate transamin	2.3
70	435338	AA678071	Hs.194300 ESTs, Weakly similar to I38022 hypothe	2.3
	442710	AI015631	Hs.23210 ESTs	2.3
	444206	AW301017	Hs.146492 ESTs	2.3
	451250	AA491275	Hs.236940 hypothetical protein FLJ12542	2.3
	454784	AW820626	gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
75	458455	AV648310	Hs.213488 ESTs	2.3
	458521	AI651039	Hs.148559 ESTs	2.3
	407938	AA905097	Hs.85050 phospholamban	2.3
	439546	AF088056	gb:Homo sapiens full length insert cDNA	2.3
	441274	AW593781	Hs.131357 ESTs	2.3
80	454314	AW364844	gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.3
	409560	AW452065	Hs.258905 ESTs	2.3
	428532	AF157326	Hs.184786 TBP-interacting protein	2.3
	411384	AW842115	gb:RC0-CN0026-090200-031-e11 CN0026 Homo	2.3
	453687	T55674	Hs.283108 hemoglobin, gamma G	2.3

	410140	AL134435	Hs.22269	neurexin 3	2.3
	422443	NM_014707	Hs.116753	histone deacetylase 7B	2.3
	409071	AW316932	Hs.181982	ESTs	2.3
5	421253	AJ188102	Hs.31028	ESTs	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypothet	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.3
	443718	AJ083580	Hs.221373	ESTs	2.3
10	445568	H00918	Hs.268744	KIAA1796 protein	2.3
	400582				2.3
	411262	AW834480		gb:MR2-TT0014-151199-011-b07 TT0014 Homo	2.3
	401145				2.3
	407440	AF227135		gb:Homo sapiens candidate taste receptor	2.3
15	455121	BE156459		gb:QV0-HT0368-040100-082-006 HT0368 Homo	2.3
	459077	N20370	Hs.235883	ESTs	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	453331	AJ240665	Hs.6895	ESTs	2.3
	443751	AJ285839	Hs.153324	EST	2.3
20	402038				2.3
	402176				2.3
	456605	AJ827786	Hs.259044	ESTs	2.3
	432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B	2.3
	402527				2.3
25	449272	AW137656	Hs.197645	ESTs	2.3
	411024	BE062590		gb:QV1-BT0260-281099-023-005 BT0260 Homo	2.3
	455608	BE011437		gb:CM4-BN0220-080500-170-003 BN0220 Homo	2.3
	458818	AJ523857	Hs.232257	ESTs	2.3
	419875	AA853410	Hs.93557	proenkephalin	2.3
30	405521				2.3
	436517	BE080932	Hs.135225	ESTs	2.3
	456801	AW961886	Hs.138263	Homo sapiens clone 24528 mRNA sequence	2.3
	430444	AW296421	Hs.121035	ESTs	2.3
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.3
35	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothet	2.3
	454456	AW850984		gb:IL3-CT0220-150200-058-H08 CT0220 Homo	2.3
40	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	2.3
	457028	AW449838	Hs.97562	ESTs	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.3
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	2.3
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	2.3
	421227	R78581	Hs.266308	mosaic serine protease	2.3
	426902	AJ125334	Hs.97408	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	447475	AJ380797	Hs.158992	ESTs	2.3
50	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.3
	430712	AW044647	Hs.196284	ESTs	2.3
	458103	AW780192	Hs.267596	ESTs	2.3
	420959	AA282119	Hs.88975	ESTs	2.3
	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
55	445641	AJ245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	452294	AJ871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.3
	457653	AJ820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	459497	AA825742	Hs.87517	ESTs	2.3
60	412852	BE004117	Hs.37415	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	437539	AA974873	Hs.121419	ESTs	2.3
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien	2.3
	411994	R87298	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.3
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	2.3
65	452463	R36452	Hs.300817	ESTs	2.3
	404936				2.3
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.3
	440836	AW370882	Hs.222080	ESTs	2.3
	405120				2.3
70	400238				2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	441417	AJ733297	Hs.144474	ESTs	2.3
75	445117	AJ208754	Hs.147369	ESTs	2.3
	431162	AW971180		gb:EST383268 MAGE resequences, MAGL Homo	2.2
	437036	AJ571514	Hs.133022	ESTs	2.2
	455849	BE146866		gb:QV4-HT0222-211099-014-006 HT0222 Homo	2.2
	447624	AJ640326	Hs.62713	ESTs	2.2
80	439760	AL109688		gb:Homo sapiens mRNA full length insert	2.2
	405706				2.2
	447732	AJ758398	Hs.161318	ESTs	2.2
	440625	BE539853	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.2
	404257				2.2

	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypothel	2.2
	449133	AI631655	Hs.197919	ESTs	2.2
	456555	AW592167	Hs.293299	ESTs	2.2
5	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	436018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	446096	AI276454		gb:xl71a12.x1 Soares_NhHMPu_S1 Homo sapi	2.2
10	448106	AI800470	Hs.171941	ESTs	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	436134	AK000618	Hs.123784	ESTs	2.2
	448466	AI522109	Hs.171066	ESTs	2.2
	420678	AW593288	Hs.3530	TLS-associated serine-arginine protein 2	2.2
15	430692	X80240		gb:Hsapiens endogenous retrovirus HERV-	2.2
	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	423611	AB011163	Hs.129908	KIAA0591 protein	2.2
	444050	AW138295	Hs.135024	ESTs	2.2
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
20	422669	H12402	Hs.119122	ribosomal protein L13a	2.2
	403388				2.2
	403780				2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	424719	H90452		gb:yy01c03.r1 Soares fetal liver spleen	2.2
25	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.2
	427119	AW880562	Hs.114574	ESTs	2.2
30	400486				2.2
	448482	AW294078	Hs.171092	ESTs	2.2
	402621				2.2
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	2.2
	424584	H10692	Hs.13310	ESTs	2.2
35	445061	AI253094	Hs.145227	ESTs	2.2
	431065	AA491286	Hs.128792	ESTs	2.2
	411908	L27943	Hs.72924	cytidine deaminase	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
40	422677	AL046388	Hs.208206	hypothetical protein FLJ21162	2.2
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo	2.2
	400163				2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.2
45	410556	R32158		gb:yh67a07.s1 Soares placenta Nb2HP Homo	2.2
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	2.2
	439482	W70045	Hs.58089	ESTs	2.2
	447877	AI435184	Hs.164252	ESTs	2.2
	418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	2.2
50	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	414000	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.2
	432762	NM_014099	Hs.278924	PRO1768 protein	2.2
	437606	AA761594	Hs.122440	ESTs	2.2
55	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
60	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens c	2.2
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	454204	AW816498		gb:QV0-ST0236-171299-075-b02 ST0236 Homo	2.2
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.2
	432887	AI926047	Hs.162859	ESTs	2.2
65	448063	AI459108	Hs.159818	ESTs	2.2
	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.2
	433098	AW190593	Hs.151143	ESTs	2.2
	409781	AW812266	Hs.15220	zinc finger protein 106	2.2
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.2
70	423646	H02364		gb:yj35d06.r1 Soares placenta Nb2HP Homo	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
75	437334	AL353947	Hs.283780	hypothetical protein DKFZp761N1814	2.2
	431917	D16181	Hs.2868	peripheral myelin protein 2	2.2
	400843				2.2
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.2
80	449560	AA001767	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	408940	M58583	Hs.662	cerebellin 1 precursor	2.2
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.2
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.2
	459495	BE544158		gb:601078707F1 NIH_MGC_12 Homo sapiens c	2.2
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	2.2

	444547	AV650207	Hs.282437	ESTs, Weakly similar to I38022 hypotheti	2.2
	417156	N49476	Hs.166563	replication factor C (activator 1) 1 (14	2.2
	416761	H85422	Hs.108556	ESTs	2.2
5	408867	AA437199	Hs.656	cell division cycle 25C	2.2
	406748	AW339106	Hs.217493	annexin A2	2.2
	427443	AA402713	Hs.97872	ESTs	2.2
	452843	AI796769	Hs.208320	ESTs	2.2
	427473	AW274439	Hs.252709	ESTs	2.2
10	433919	AA746311		gb:aa56d12.r1 NCI_CGAP_GC81 Homo sapiens	2.2
	431058	AW968865		gb:EST380941 MAGE resequences, MAGJ Homo	2.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	2.2
	415250	F02614	Hs.27319	ESTs	2.2
	440253	AI651329	Hs.160289	ESTs	2.2
15	434470	AA634818	Hs.298138	ESTs	2.2
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.2
	432463	AA548518	Hs.186733	ESTs	2.2
	400861				2.2
	407287	AI678812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens	2.2
20	414817	AW902892	Hs.23782	hypothetical protein FLJ12847	2.2
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	2.2
	442952	AI743261	Hs.131860	ESTs	2.2
25	425187	AW014486	Hs.22509	ESTs	2.2
	408221	AA912183	Hs.47447	ESTs	2.2
	411480	AW848022		gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.2
	459681				2.2
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	2.2
30	442726	AW136066	Hs.19145	ESTs	2.2
	450433	AW444538	Hs.231863	ESTs	2.2
	437642	AL079309		gb:Homo sapiens mRNA full length insert	2.2
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
35	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	446534	AI307356	Hs.175225	ESTs	2.2
	403764				2.2
40	442735	R91949		gb:yq06h06.s1 Soares fetal liver spleen	2.2
	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.2
	405965				2.2
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recess)	2.2
	441679	BE502267	Hs.65996	ESTs	2.2
45	432781	NM_014133	Hs.278940	PRO0618 protein	2.2
	448470	AW026226	Hs.309479	ESTs	2.2
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.2
	443180	R15875	Hs.258576	claudin 12	2.2
	422213	AA306385	Hs.133160	ESTs	2.2
50	423119	AA322201	Hs.131976	ESTs	2.2
	450192	AA263143	Hs.24596	RAD51-interacting protein	2.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	2.2
	400734				2.2
	430499	AW969408	Hs.231991	ESTs	2.2
55	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
60	436640	AA724411	Hs.156065	ESTs	2.2
	436802	N34486	Hs.170504	ESTs	2.2
	443994	AI094805	Hs.135522	ESTs, Weakly similar to S38038 hypotheti	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	446412	AW135313	Hs.150098	ESTs	2.2
65	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
	412700	BE222433	Hs.201262	ESTs, Weakly similar to I38022 hypotheti	2.2
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
70	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.2
	452441	BE222078	Hs.113069	ESTs	2.2
	402395				2.2
	459659				2.2
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.2
75	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	2.2
	409446	AI561173	Hs.67688	ESTs	2.2
	408764	BE087164	Hs.302415	ESTs	2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
80	436992	AA741074	Hs.120750	ESTs	2.2
	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	444199	AI128931	Hs.260681	ESTs, Moderately similar to ALUF_HUMAN I	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	435510	BE143837		gb:MR0-HT0164-151299-012-b08 HT0164 Homo	2.1

	403691				2.1
	458333	A1000792	Hs.108209	ESTs	2.1
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo	2.1
5	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.1
	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protei	2.1
	406941	X58140		(NONE)	2.1
	445712	A1458246	Hs.167451	ESTs	2.1
10	451270	AW341392	Hs.235795	ESTs	2.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.1
	437073	A1885608	Hs.94122	ESTs	2.1
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.1
	430684	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.1
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.1
15	405233				2.1
	446512	H30351	Hs.207982	ESTs	2.1
	403188				2.1
	404443				2.1
20	433645	A1821746	Hs.190258	ESTs, Moderately similar to ALU6_HUMAN A	2.1
	414456	H74314		gb:yu56a10.r1 Soares fetal liver spleen	2.1
	433479	AW511459	Hs.249972	ESTs	2.1
	455482	AW948353		gb:RC0-MT0015-130400-031-d07 MT0015 Homo	2.1
	446364	AB006624	Hs.14912	KIAA0286 protein	2.1
	452004	A1827815	Hs.277359	ESTs	2.1
25	405059				2.1
	425457	AW964212		gb:EST376285 MAGE resequences, MAGH Homo	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
30	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	432774	AA564946	Hs.156280	ESTs	2.1
	436349	A1445255	Hs.115315	ESTs	2.1
	445532	BE138944	Hs.146200	ESTs	2.1
	456313	AA225741		gb:nc17b10.s1 NCLCGAP_Pr1 Homo sapiens	2.1
35	412818	NM_003337	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 h	2.1
	450271	A1693900	Hs.200920	ESTs	2.1
	401521				2.1
	422880	AF228704	Hs.121524	glutathione reductase	2.1
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hckr	2.1
40	449233	BE048401	Hs.196511	ESTs	2.1
	408217	A1433201	Hs.279860	tumor protein, translationally-controlled	2.1
	457003	S78234	Hs.172405	cell division cycle 27	2.1
	417448	AA203135	Hs.130186	ESTs	2.1
	402103				2.1
45	450579	AW136774	Hs.48614	ESTs	2.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.1
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	2.1
	415333	H24415	Hs.13273	KIAA0592 protein	2.1
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticot	2.1
50	434985	AA658229	Hs.291228	ESTs	2.1
	414729	BE466928	Hs.281901	ESTs	2.1
	400510				2.1
	420844	AA595522		gb:nh22c09.s1 NCLCGAP_Pr1 Homo sapiens	2.1
	427434	BE538374	Hs.301732	hypothetical protein MGC5306	2.1
55	432188	A1362952	Hs.2928	solute carrier family 7 (cationic amino	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
	453853	AL040600	Hs.188083	ESTs	2.1
	459108	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	2.1
	430118	A1377255	Hs.183287	ESTs	2.1
60	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.1
	437981	AA774445	Hs.192095	ESTs, Weakly similar to KIAA1397 protein	2.1
	439957	A1453184	Hs.66357	ESTs	2.1
	423734	H02217		gb:yj38d11.r1 Soares placenta Nb2HP Homo	2.1
	450721	A1732271	Hs.25567	ESTs	2.1
65	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	2.1
	429986	AF082047	Hs.227277	sine oculis homeobox (Drosophila) homolo	2.1
	432919	AL079800		gb:DKFZp43402330_r1 434 (synonym: htes3)	2.1
	434791	AA649235	Hs.116457	ESTs, Weakly similar to NIP3_HUMAN BCL2/	2.1
	445273	A1218441	Hs.153846	ESTs	2.1
	400514				2.1
70	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	439391	AW975638	Hs.293490	ESTs, Weakly similar to I38022 hypotheti	2.1
75	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.1
	429430	A1381837	Hs.155335	ESTs	2.1
	449689	AF228421	Hs.23889	DKFZP564A032 protein	2.1
	430909	AF034632	Hs.248126	G protein-coupled receptor 38	2.1
	453116	A1276680	Hs.146086	ESTs	2.1
80	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	2.1
	423019	A1640185	Hs.283626	ESTs	2.1
	414007	A1733895	Hs.103813	ESTs	2.1
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	2.1
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	2.1

	421279	AW664878	Hs.106645	ESTs	2.1
	443167	AI202009	Hs.132087	ESTs	2.1
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.1
5	448078	AI460117	Hs.170464	ESTs, Highly similar to A53933 myosin I	2.1
	436858	BE545498		gb:601070344F1 NIH_MGC_12 Homo sapiens c	2.1
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.1
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.1
	407401	AF029325		gb:Homo sapiens laminin beta-4 chain pre	2.1
10	426336	AA375802		gb:EST88135 HSC172 cells II Homo sapiens	2.1
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	2.1
	425541	AA359119		gb:EST58172 Fetal lung II Homo sapiens c	2.1
	406504				2.1
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	2.1
15	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.1
	416175	H24230	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	442095	AI733162	Hs.128470	ESTs	2.1
	451878	AI821027	Hs.8429	ESTs	2.1
20	449178	AI633748	Hs.197597	ESTs	2.1
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	2.1
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.1
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.1
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	2.1
25	441543	AI733014	Hs.269715	ESTs	2.1
	403065				2.1
	428811	AA436052	Hs.99487	ESTs	2.1
	451803	BE541174	Hs.252058	ESTs, Moderately similar to PC4259 ferri	2.1
	442906	AW296888	Hs.170939	ESTs	2.1
30	409171	R17126		gb:yg09c11.r1 Soares infant brain 1N18 H	2.1
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	2.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	2.1
	412039	AW887384		gb:RCO-OT0089-130300-021-d07 OT0089 Homo	2.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.1
35	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.1
	455022	AW850845		gb:IL3-CT0220-111199-028-D11 CT0220 Homo	2.1
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	2.1
	422942	AF054839	Hs.122540	tetraspan 2	2.1
	400451				2.1
40	406668	T62745	Hs.184411	albumin	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	404834				2.1
	448732	BE614063	Hs.334689	KIAA1838 protein	2.1
	423453	AW450737	Hs.128791	CGI-09 protein	2.1
45	421447	AB005216	Hs.104481	Nck, Ash and phospholipase C binding pro	2.1
	408774	AW270899	Hs.254569	ESTs, Weakly similar to B34087 hypothel	2.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.1
	405732				2.1
	417848	AA206581	Hs.39457	ESTs, Weakly similar to JC5314 CDC28/bdc	2.1
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.1
	420344	BE483721	Hs.97101	putative G protein-coupled receptor	2.1
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.1
	426953	AI769281	Hs.97439	ESTs	2.1
	440454	AI733037	Hs.129990	ESTs	2.1
55	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	2.1
	424872	AA347823		gb:EST54302 Fetal heart II Homo sapiens	2.1
	454658	AW812330	Hs.11123	DKFZP684G092 protein	2.1
	441963	AI733307	Hs.128002	ESTs	2.1
	439498	AA908731	Hs.58297	CLUL8 protein	2.1
60	456224	AW282905	Hs.128770	ESTs	2.1
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	2.1
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	2.1
	417787	R14948	Hs.23883	ESTs	2.1
	400612				2.1
65	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	451087	BE172186		gb:MR0-HT0559-110300-005-h11 HT0559 Homo	2.1
	455032	AI830890	Hs.192422	ESTs	2.1
70	417945	R29072		gb:F1-101D 22 week old human fetal liver	2.1
	438268	AA782163	Hs.293502	ESTs	2.1
	424754	R09692		gb:yc23b12.r1 Soares fetal liver spleen	2.1
	404599				2.1
	459655				2.1
	402455				2.1
75	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	2.1
	421987	AI133161	Hs.286131	CGI-101 protein	2.1
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
	438206	AA780385	Hs.187885	ESTs	2.1
80	458451	AW297181	Hs.195922	ESTs	2.1
	447534	AW953935	Hs.30837	ESTs	2.1
	417687	AI828596	Hs.250691	ESTs	2.1
	412717	W00973	Hs.334728	ESTs	2.1
	405759				2.1

406413				2.1
442081	AA401863	Hs.22380	ESTs	2.1
457938	AJ373638	Hs.133900	ESTs	2.1
420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fls, clone PL	2.1
428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
411421	BE272110	Hs.21177	ESTs	2.1
437825	AA769123	Hs.291947	ESTs	2.1
437083	AW082597	Hs.244862	ESTs	2.1
409466	AA436207	Hs.226666	ESTs, Moderately similar to I54374 gene	2.1
433523	H29882	Hs.162614	ESTs	2.1
446868	AV660737	Hs.135100	ESTs	2.1
445882	AJ948717	Hs.225155	ESTs, Weakly similar to A46302 PTB-assoc	2.1
438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
406817	AJ936028		gb:wo47a09.x1 NCL_CGAP_Gas4 Homo sapiens	2.1
410486	AW235094	Hs.69233	zinc finger protein	2.1
411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
412446	AJ768015	Hs.92127	ESTs	2.1
457289	AW573204	Hs.137078	ESTs	2.1
400335	Y13187	Hs.248067	Homo sapiens dmd gene, Intron 11	2.0
435959	AW296243	Hs.118375	ESTs	2.0
448188	AW001835	Hs.13323	hypothetical protein FLJ22059	2.0
418339	AA639902	Hs.104215	ESTs, Moderately similar to SPON_HUMAN S	2.0
420430	AJ703192		gb:wd92h04.x1 NCL_CGAP_Lu24 Homo sapiens	2.0
445717	AW664658	Hs.149332	ESTs	2.0
451862	H09260	Hs.32333	ESTs	2.0
459686				2.0
441996	BE349537	Hs.38383	ESTs	2.0
412194	AW900282	Hs.115412	hypothetical protein FLJ13881	2.0
444229	AV648613	Hs.282397	ESTs	2.0
441635	AJ908538	Hs.133000	ESTs, Weakly similar to S26689 hypothetical	2.0
421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	2.0
414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.0
428209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin I	2.0
443520	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	2.0
409248	AB033035	Hs.51965	KIAA1209 protein	2.0
444518	AI160278	Hs.146884	ESTs	2.0
422237	M13149	Hs.1498	histidine-rich glycoprotein	2.0
409316	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC	2.0
402725				2.0
413783	AA314337	Hs.301547	ribosomal protein S7	2.0
423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
425008	AW675764	Hs.174248	ESTs	2.0
427271	AW195922	Hs.188758	connexin 59	2.0
444102	AV647953	Hs.83077	Interleukin 18 (interferon-gamma-inducin	2.0
445829	AJ452457	Hs.145526	ESTs	2.0
452366	AK000464	Hs.29272	hypothetical protein FLJ20457	2.0
457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.0
429540	M85776		gb:EST02297 Fetal brain, Striatagene (cat	2.0
459456	AA486036	Hs.190124	ESTs	2.0
409840	AW502122		gb:UL-HF-BR0p-ajr-c-08-0-ULr1 NIH_MGC_5	2.0
441025	AA913880	Hs.176379	ESTs	2.0
457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.0
445627	AW818475	Hs.7363	ESTs	2.0
440299	AJ871778	Hs.250112	ESTs	2.0
401236	H24185	Hs.92918	hypothetical protein	2.0
429996	N90822	Hs.48969	ESTs	2.0
455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	2.0
411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	2.0
433449	AW772282		gb:hn71b05.x1 NCL_CGAP_J0d11 Homo sapien	2.0
454197	BE140966		gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
445297	BE544163	Hs.87128	hypothetical protein FLJ23309	2.0
403977				2.0
458948	AI695359	Hs.280943	ESTs	2.0
418663	AK001100	Hs.41690	desmocollin 3	2.0
411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.0
426536	AJ949749	Hs.44441	ESTs	2.0
442765	BE567353	Hs.99480	ESTs	2.0
400859				2.0
405829				2.0
411863	BE075244	Hs.12420	ESTs	2.0
415258	AW752247	Hs.293853	ESTs	2.0
416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	2.0
437733	AJ792574	Hs.122876	ESTs	2.0
453118	AW195849	Hs.252757	ESTs	2.0
457039	H29950	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
444292	AJ139794	Hs.146569	ESTs	2.0
431360	NM_000427	Hs.251680	lorixin	2.0
407644	D16815	Hs.37268	nuclear receptor subfamily 1, group D, m	2.0
412029	AW886238		gb:RCS-OT0078-280300-022-F01 OT0078 Homo	2.0
438522	AA809431	Hs.258886	ESTs	2.0
422634	NM_016010	Hs.118821	CGI-62 protein	2.0

	418790	H95693		gb:Y5d11.s1 Soares_pineal_gland_N3HPG	2.0
	442950	AI500417	Hs.46764	ESTs	2.0
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.0
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
5	402674				2.0
	408733	AW264812	Hs.254290	ESTs	2.0
	408767	AA057279	Hs.211928	ESTs	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
10	418205	L21715	Hs.83760	tropoin I, skeletal, fast	2.0
	404604				2.0
	413627	BE182082	Hs.245973	ESTs	2.0
	402341				2.0
	438090	AA777534	Hs.191992	ESTs	2.0
	421303	T06464		gb:EST04353 Fetal brain, Stratagene (cal	2.0
15	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cal	2.0
	417756	Z43058		gb:HSC12B021 normalized infant brain cDN	2.0
20	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
	433755	AW085934	Hs.120868	ESTs	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	435648	H24347	Hs.27524	ESTs	2.0
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	2.0
25	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothei	2.0
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.0
	447678	BE385257	Hs.336457	Homo sapiens dopamine receptor interact	2.0
	448150	AI472167	Hs.302739	ESTs	2.0
	453445	AL036532	Hs.91453	ESTs	2.0
30	444420	AI148157	Hs.146766	ESTs	2.0
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ111170 fis, clone PL	2.0
	413758	BE162391		gb:PM2-HT0451-090100-002-f04 HT0451 Homo	2.0
	428231	U17989	Hs.183105	nuclear autoantigen	2.0
35	455873	BE152239		gb:QV4-HT0316-091199-028-f12 HT0316 Homo	2.0
	430970	AI018210	Hs.144083	ESTs	2.0
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (G pr	2.0
	413025	AA805265	Hs.291646	ESTs	2.0
	424083	AF055018	Hs.139137	Homo sapiens clone 24442 mRNA sequence	2.0
40	427654	AA410183	Hs.137475	ESTs	2.0
	410483	BE163587		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.0
	423942	AF209704	Hs.135723	glycolipid transfer protein	2.0
	430340	AA476777		gb:zw94g11.r1 Soares_tetal_fetus_Nb2HF8_	2.0
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.0
45	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.0
	400285				2.0
	405966				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
50	415105	D60166		gb:HUM089G11B Clontech human fetal brain	2.0
	434531	AA642007	Hs.116369	ESTs	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447185	AW377092	Hs.99601	hypothetical protein FLJ12553	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
55	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
	400617	AF151064	Hs.36069	hypothetical protein	2.0
	418647	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	2.0
	401785				2.0
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	2.0
60	420777	AA280223	Hs.130865	ESTs	2.0
	439509	AF086332	Hs.58314	ESTs	2.0
	430203	L36140	Hs.235069	RecQ protein-like (DNA helicase Q1-like)	2.0
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	2.0
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	2.0
65	437620	AW976930	Hs.128760	ESTs	2.0
	407528	X84990		gb:H.sapiens mRNA HTPCRX16 for olfactory	2.0
	402048				2.0
	403623				2.0
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.0
70	417531	NM_003157	Hs.1087	serine/threonine kinase 2	2.0
	422600	BE143586	Hs.87	retinoblastoma-like 1 (p107)	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.0
	433153	AA578512		gb:nh22e11.s1 NCL_CGAP_Pr1 Homo sapiens	2.0
75	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	435373	AW665538	Hs.117689	ESTs	2.0
	442988	AI026130	Hs.131683	ESTs	2.0
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (tr	2.0
80	454423	AW603995		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0

Table 31B

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	409623	1144047_1	AW449185 AW449665 BE220971
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	410201	118365_1	AA126129 AA126033 AA082561
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	410556	1208157_1	R32158 AW754055 AW754054 AW754053 AW754045 AW857320
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	420430	193538_1	AI703192 AW901259 AA278523 AA262062
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	422977	223410_1	AA631498 AI017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510
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	454185	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 BE141749 AW177598
5	454190	1049996_1	AW177821 AW177896 AW177867
	454197	1050392_1	BE140956 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969 BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975 BE141657 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013 BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646 BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671 AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
10	454204	1050597_1	AW816498 AW808791 AW808515 AW808379 AW808532 AW808605 AW808977 AW808816 AW178676 AW178486 AW808514 AW178483 AW178485 AW809007 AW808524
15	454314	1108161_1	AW384844 AW364847 AW937534 AW937593 AW937659
	454352	1129567_1	AW389668 AW389657 AW609198 AW389649
	454423	1183079_1	AW603985 AW854350
	454447	1204995_1	BE163567 BE073589 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073571
	454456	1207088_1	AW850984 AW752836 M86124
	454482	1215087_1	BE147919 AW794884 BE147847
20	454560	1223940_1	AW807281 AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
	454564	1224407_1	AW807573 AW807566 AW807572
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956
25	454597	1226059_1	AW809648 AW809704 AW809643 AW809653 AW809709 AW809949 AW809939 AW810010 AW809705 AW809950 AW809822 AW809667 AW810093 AW810076 AW809573 AW810349 AW809895
30	454633	1227504_1	AW811380 AW811385
	454716	1230503_1	AW850684 AW850150
	454747	1233006_1	AW818535 AW818588 AW818651
	454754	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265 AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
35	454767	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202 AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784 AW820199 AW820434 BE174743
	454778	1234343_1	AW820626 AW820621 AW820608
	454784	1234630_1	AW820852 AW820773 AW821088
40	454790	1234752_1	AW833711 AW833620 AW833699
	454836	1236509_1	AW835775 AW845768 AW845764 AW845773 AW845757 AW845758 AW845780
	454854	1237929_1	AW846134 AW846467 AW846468 AW846386 AW846461 AW846211 AW846179 AW846205 AW846320 AW846379 AW846367 AW846561
	454938	1245635_1	AW846556
45	454962	1246750_1	AW847645 AW847791 AW854083 AW853945
	455022	1249160_1	AW850845 BE144010 AW855164
	455121	1254339_1	BE156459 BE156469 BE158468 AW857447
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455170	1256906_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860988 AW860925 AW860922 AW860986 AW860984 AW860989
50	455201	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
	455219	1261640_1	AW879403 AW867707
	455221	1261678_1	AW867751 AW867770 AW867763
	455236	1265662_1	AW875972 AW875983 AW875974 AW876000 AW875966 AW876050
	455252	1266222_1	AW876627 AW876630 AW876631 AW876625
55	455255	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	455275	1272255_1	AW977806 AW887923 AW886321
	455280	1272607_1	AW886156 AW887926 AW886324 AW886236 AW887906 AW886304
	455310	1278158_1	AW893961 AW893998 AW894034 AW894019
	455328	1280063_1	AW895438 AW896534 AW896500 AW896540 AW896446
	455484	1292643_1	AW983901 AW984485 AW947715
60	455482	1293183_1	AW948353 AW948351 AW948331 AW948303 AW948336 AW948305 AW948299 AW948346 AW948352
	455488	129372_1	AA102322
	455511	1321229_1	BE144762 AW979091
	455534	1322942_1	AW991925 AW991919
65	455540	1323701_1	BE080231 AW993284 AW993293 AW993000
	455556	1325658_1	AW995423 AW995373
	455571	1331885_1	BE003714 BE003721 BE003720 BE003716
	455587	1335046_1	BE007829 BE007815 BE007822 BE007995 BE007835 BE007837 BE007824 BE007836 BE007827
	455608	1337389_1	BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
70	455675	1349659_1	BE065984 BE065942 BE065955 BE066085
	455688	1350606_1	BE067238 BE067235 BE067240 BE067256 BE067263 BE067236 BE067260 BE067253 BE067248 BE067252
	455696	1351077_1	BE067870 BE067866 BE165133 BE165334 BE165329 BE165332
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
	455756	1358603_1	BE079307 BE079309
75	455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
	455780	1364580_1	BE088828
	455849	1375441_1	BE146866 BE146865 BE146867
	455851	1375451_1	BE146879 BE146914 BE146918
	455866	1377119_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152619 BE149030 BE149062 BE149023 BE149055
80	455873	1379498_1	BE152239 BE152242 BE152230
	455980	1380022_1	BE153208 BE153148 BE152981
	455935	1384144_1	BE158687 BE158688
	455964	1389912_1	BE166924 BE166921 BE166925 BE166915 BE166970 BE166968
	455992	1398552_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997

5 455993 1398655_1 BE179085 BE179084 BE179086 BE179264
 456186 1618618_1 W26642 H88394
 456313 177240_1 AA225741 AI734056 AI820965 AI732153 AA259201 AA225731
 456394 1843275_-2 W28506
 456407 184986_1 AW968614 AA243209 AA281411
 456476 191761_1 AA258753 AW628580
 457242 307984_1 AA457011 AI978850
 457824 41515_6 R84938 AL047151 AA310309 AW063200 AI569528 AI307823 N49975
 458804 75803_1 AL157625 N72696 BE622492
 10 458890 812733_2 AW865523 AW865128 AW865467 AW865127 AW865466
 459160 920051_1 AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
 459201 925883_1 AW391177 W45021

15

TABLE 31C

20 Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400451	8113550	Minus	82189-82320
400462	9929659	Minus	197610-197785
400486	8569385	Plus	181108-181605
400510	9796540	Minus	139633-139910, 140469-140979
400514	9796594	Minus	78844-79025, 80850-80991, 89754-89941, 93750-93891
400579	9887603	Plus	21323-21526
400582	9887609	Plus	88642-88728, 89716-89866
400587	9887626	Plus	25435-25588, 25668-25747
400608	9887666	Minus	96756-97558
400612	9929646	Minus	151513-151662
400613	9864507	Plus	92278-92472
400641	8117693	Plus	4785-4992
400643	8117693	Plus	12818-13016
400706	7249204	Minus	78299-78686
400734	8118979	Plus	122853-123971
400816	8569993	Plus	161221-162078
400843	9188605	Plus	5863-5970, 7653-7784, 8892-9023, 9673-9807, 10634-10789, 15254-15403, 23827-23958
400844	9188605	Plus	24746-24872, 25035-25204
400859	9757499	Minus	91888-92018, 98131-98294, 99474-99570
400861	9757506	Plus	163855-164016
400889	9958234	Minus	169782-170036
401078	3687273	Plus	105052-105171
401098	9965518	Minus	85632-86174
401132	8705350	Minus	85679-85795
401145	2547238	Plus	17599-17776
401189	9690246	Minus	90815-90929
401200	9743387	Minus	111586-111806, 114791-114916, 115419-115583, 116351-116446, 116847-116907, 122853-123067, 124982-125407
401344	9926411	Minus	82478-82602, 86952-87110
401361	9958052	Plus	153083-154106
401365	9796180	Minus	119572-119672
401449	8574316	Minus	144928-145030
401497	7381770	Plus	92607-92813
401521	7705251	Plus	9127-9234
401526	7705661	Plus	91570-93177
401602	7689983	Plus	101095-101253
401614	7839924	Plus	17350-17735
401645	7657839	Minus	34986-35133
401694	3540172	Minus	64056-64168
401775	9966311	Minus	110228-110340
401785	7249190	Minus	165776-165995, 166189-166314, 166408-166569, 167112-167268, 167387-167469, 168634-168942
401882	8139716	Plus	86466-87077
401887	7229981	Plus	93973-94120
401886	4406829	Minus	31137-31293
401992	4153858	Plus	31452-31649
402038	7684482	Minus	100751-100885
402048	8072512	Plus	43936-44078
402076	8117410	Plus	128316-128627
402103	7249203	Plus	14453-15414
402131	7704961	Minus	33114-33209, 33496-33678
402176	7543687	Minus	10-750
402230	9966312	Minus	29782-29932
402333	8844110	Minus	165693-165856
402341	7656696	Plus	22583-23699
402395	9929693	Minus	131016-131998
402429	9796372	Minus	57622-57793, 59282-59402, 59624-59827
402430	9796372	Minus	62382-62552
402455	9796753	Minus	139840-139779, 140568-140660
402527	9800806	Plus	4722-4916, 17858-18037, 19964-20140, 24423-24605, 26699-26881

	402615	9926801	Plus	131390-132157
	402621	9930950	Plus	130806-131036
	402674	8077108	Minus	39290-39502
5	402725	8979991	Plus	107231-107383
	402790	4835258	Minus	147744-147861
	402867	5596716	Plus	52806-53106,53500-53818
	402953	9408724	Minus	122603-122743
	403003	5441423	Minus	79403-79560,79712-80021
10	403011	6693597	Minus	3468-3623
	403065	8954197	Minus	71615-71773,73930-74144
	403188	9838289	Minus	157618-157755
	403271	7230852	Plus	134283-134485
	403273	8018055	Plus	133809-134099
15	403281	8072630	Minus	7521-7728
	403296	8096530	Minus	35913-36520
	403310	8139936	Minus	183883-184026
	403329	8518120	Plus	96450-96598
	403341	8569175	Plus	30699-30910
20	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
	403381	9438267	Minus	26009-26178
	403388	9438331	Plus	112733-113001,114599-114735
	403396	9438367	Minus	952-1160
25	403501	7534005	Minus	108903-110438
	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
	403534	8076917	Minus	46652-47332
	403549	8081591	Minus	137150-137362
30	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403619	8569810	Plus	62501-62653
	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
35	403637	8671936	Minus	142647-142771,145531-145762
	403667	6850483	Minus	1344-1442,1545-1697
	403677	7331617	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
	403698	3135242	Minus	143467-143634
40	403743	7652003	Minus	136463-136646
	403760	7712202	Minus	45910-46260,47563-47824
	403764	7717105	Minus	118692-118853
	403776	7770611	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
45	403786	8083636	Minus	73028-73217
	403891	7331467	Minus	191508-193220
	403895	7381715	Minus	3502-4002,4070-4308
	403977	7657840	Minus	115573-115820
	404043	9558573	Plus	29042-29135,46597-46699
50	404059	3548785	Plus	104326-106788
	404076	8931752	Minus	3848-3967
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
	404257	9367215	Plus	15262-16227
55	404285	2326514	Plus	32282-32416
	404288	2769644	Plus	3512-3691
	404367	9965011	Minus	114391-114628
	404443	7579073	Minus	87198-87441
	404453	7657714	Plus	27768-29179
60	404476	8080699	Plus	101841-102043
	404513	8151941	Minus	112837-113339
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404577	4020145	Plus	17991-18420
65	404588	6456726	Minus	40059-40210
	404599	8705107	Plus	110443-110733
	404604	8212537	Minus	72019-72509
	404638	9798751	Minus	99433-99528,100035-100161
	404767	7882827	Minus	23244-23759
70	404793	7232206	Minus	81087-81590
	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404845	7958980	Minus	47174-47326,52928-53146,53312-53602
	404898	7331420	Minus	177015-177328
75	404936	6850774	Plus	191519-191664
	404957	7407927	Plus	147512-148011
	405017	6532084	Plus	35551-35690
	405059	7656683	Plus	349-822
80	405090	8072525	Minus	38552-39202
	405093	8072575	Plus	95878-96020
	405120	8099940	Plus	140176-140340
	405170	9966524	Plus	37047-37198
	405229	7249019	Plus	51081-51701
	405230	7249032	Minus	97493-97682

5	405233	7249045	Plus	9588-10065
	405241	7249178	Minus	69927-70526
	405264	7329374	Plus	28556-28684
	405287	3928029	Plus	89802-89999
	405302	2078453	Minus	121688-121840
	405303	2078453	Minus	130607-130802
	405336	6094635	Plus	33267-33563
	405347	2979602	Minus	977-1116
10	405385	6552772	Plus	48332-48454
	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
15	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405547	1054740	Plus	124361-124520,124914-125050
	405605	5836195	Minus	117070-117270
	405608	5815499	Minus	66822-66925
	405629	4508116	Minus	101678-101866
20	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405706	4165003	Plus	44307-44431,49619-49802
	405720	9797144	Plus	13409-13861
25	405732	7534017	Plus	146981-147316
	405759	3288022	Minus	18283-18399
	405780	7248203	Minus	48204-48371
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
30	405869	6758731	Minus	89867-90358
	405935	6758795	Minus	163112-163652
	405959	6758815	Plus	1-642
	405965	8247786	Minus	179930-180373
	405966	8247788	Minus	51762-51978
35	405970	8247789	Minus	45795-46295
	405981	8247790	Plus	4771-5338
	406005	8247801	Minus	39912-40220
	406053	6758997	Plus	30921-31532
	406073	9119150	Plus	60495-60610
40	406091	9123919	Minus	197370-197935
	406092	9123919	Plus	251370-251797,252168-252882
	406298	5686278	Minus	30084-30770
	406327	9212407	Plus	168241-168492
	406333	9213235	Plus	64689-64798
45	406364	9256114	Minus	50715-50833
	406377	9256135	Plus	126826-126979,129755-129942
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406470	9795562	Minus	15532-15697
50	406504	7711360	Minus	107068-107277
	406506	7711374	Minus	6843-8077F
	406592	4567182	Plus	352560-352963

55 Table 32A lists about 969 genes upregulated in lung fibrosis relative to normal body tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

60 Table 33A lists about 800 genes upregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

65 Table 34A lists about 703 genes upregulated in idiopathic pulmonary fibrosis (IPF) relative to hypersensitivity pneumonitis (HP) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

70 Table 35A lists about 323 genes upregulated in hypersensitivity pneumonitis (HP) relative to idiopathic pulmonary fibrosis (IPF) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

75 Table 36A lists about 52 genes upregulated in non-specific interstitial pneumonitis (NSIP) relative to hypersensitivity pneumonitis (HP) or idiopathic pulmonary fibrosis (IPF). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

80 Table 37A lists about 206 genes downregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 38A lists about 207 genes upregulated in lung fibrosis relative to normal tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

TABLE 32A: About 969 genes upregulated in lung fibrosis relative to normal body tissues

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.
 R2: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

Pkey	ExAccn	UnigenID	Unigene Title	R1	R2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	22.45	28.63
406964	M21305		FGENES predicted novel secreted protein	16.10	7.65
431723	AW058350	Hs.16762	Homo sapiens mRNA: cDNA DKFZp564B2062 (f	15.83	14.86
442275	AW449467	Hs.54795	ESTs	15.74	21.96
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	13.83	34.53
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	12.40	7.38
431089	BE041395		ESTs, Weakly similar to unknown protein	12.38	6.05
421110	AJ250717	Hs.1355	cathepsin E	11.86	6.49
457200	U33749	Hs.197764	thyroid transcription factor 1	11.38	9.79
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	10.89	15.94
443709	AI082692	Hs.134662	ESTs	10.84	8.27
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	10.06	8.92
445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.96	5.43
432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	9.90	7.87
421798	N74880		N-acetylsphingosine amidohydrolase (acid c	9.38	8.35
400269			Eos Control	9.03	6.48
444325	AW152618	Hs.16757	ESTs	8.31	6.76
416402	NM_000715	Hs.1012	complement component 4-binding protein,	8.14	5.51
413048	M93221	Hs.75182	mannose receptor, C type 1	7.70	4.09
432985	T92363	Hs.178703	ESTs	7.56	7.83
443324	R44013	Hs.164225	ESTs	7.06	4.47
449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	6.90	2.89
408562	AA36323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88	4.00
449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56	4.25
421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46	4.47
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.30	13.57
409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	6.28	3.38
441835	AB036432	Hs.184	advanced glycosylation end product-speci	5.99	13.26
446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.88	4.10
415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.88	3.35
442652	AI005183	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	5.87	5.69
414812	X72755	Hs.77367	monokine induced by gamma interferon	5.84	3.34
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72	5.90
421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	5.59	6.89
436954	AA740151	Hs.130425	ESTs	5.58	4.72
446998	N99013	Hs.16762	Homo sapiens mRNA: cDNA DKFZp564B2062 (f	5.48	5.33
421340	F07783	Hs.1369	decay accelerating factor for complement	5.48	2.69
420656	AA279098	Hs.187636	ESTs	5.45	3.99
432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38	3.65
408380	AF123050	Hs.44532	ubiquitin	5.37	3.11
414998	NM_002543	Hs.77729	oxidized low density lipoprotein (lectin	5.30	3.98
446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.29	4.00
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.28	2.48
442832	AW208560	Hs.253569	ESTs	5.20	3.78
407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	5.11	3.81
433293	AF007835	Hs.32417	hypothetical protein MGC4309	5.11	2.88
424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.07	3.46
428043	T92248	Hs.2240	uteroglobin	5.06	9.48
431745	AW972448	Hs.163425	ESTs	5.04	4.16
444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04	3.68
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	5.02	4.26
419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	4.97	3.35
428927	AA441837	Hs.90250	ESTs	4.92	3.15
432222	AI204995		gbzn03c03.x1 Stratagene schizo brain S1	4.79	3.05
442994	AI026718	Hs.16954	ESTs	4.76	2.65
416030	H15261	Hs.21948	ESTs	4.76	4.26
438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.73	3.24
453142	AA033648	Hs.7473	ESTs	4.66	2.92
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64	4.88
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	4.60	2.60
432810	AA863400		ESTs	4.54	2.42
418259	AA215404		ESTs	4.54	2.54
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	4.48	4.86
424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.46	3.62
423575	C18863	Hs.163443	intron of perlestin(OSF-2os)	4.44	3.41
428667	AI375550	Hs.346868	nucleolar protein p40; homolog of yeast	4.42	3.41

	429228	AI553633		ESTs	4.32	2.98
	432435	BE218886	Hs.282070	ESTs	4.30	2.26
	446932	AA961459	Hs.125644	ESTs	4.30	2.81
5	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30	2.39
	409435	AI810721	Hs.95424	ESTs	4.30	2.60
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	4.29	2.48
	452561	AI692181	Hs.49169	KIAA1634 protein	4.23	2.26
	427698	AW972594	Hs.335499	ESTs	4.22	3.49
10	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	4.22	13.34
	446608	N75217	Hs.257846	ESTs	4.20	3.62
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18	3.14
	459702	AI204995		gb:an03c03.x1 Striatogene schizo brain S1	4.16	2.64
	445885	AI734009	Hs.127699	KIAA1603 protein	4.16	3.99
15	430280	AA361258	Hs.237868	interleukin 7 receptor	4.13	2.79
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12	2.19
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.12	3.02
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.08	3.13
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.08	3.48
20	432731	R31178	Hs.287820	fibronectin 1	4.06	2.66
	439398	AA284267	Hs.221504	ESTs	4.06	2.86
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.05	3.51
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04	2.44
	436120	AI248193	Hs.119860	ESTs	4.04	3.11
25	407910	AA550274	Hs.41296	fibronectin leucine rich transmembrane p	4.03	2.69
	421462	AF016495	Hs.104624	aquaporin 9	4.00	2.51
	443257	AI334040	Hs.11814	HSPC065 protein	4.00	2.61
	421659	NM_014459	Hs.106511	protocadherin 17	4.00	3.00
	424273	W40460	Hs.144442	phospholipase A2, group X	3.98	2.30
30	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.97	3.36
	450656	AA010539	Hs.18912	ESTs	3.96	4.37
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94	2.44
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	3.93	3.08
	413385	M34455	Hs.840	Indoleamine-pyrrole 2,3 dioxygenase	3.92	3.53
35	452416	AA026115	Hs.114777	ESTs	3.92	2.90
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	3.90	5.06
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90	2.00
	453204	R10799	Hs.191990	ESTs	3.90	2.22
	450695	AI654223	Hs.16026	hypothetical protein FLJ23191	3.81	3.82
40	422173	BE385828	Hs.250619	phorbol-like protein MDS019(CEM15)	3.80	2.23
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.78	2.86
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.78	3.70
	457411	AW085961	Hs.130093	iroquols-class homeobox protein IRX2	3.76	2.56
	432606	NM_002104	Hs.3068	granzyme K (serine protease, granzyme 3;	3.76	2.76
45	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74	2.83
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.72	2.55
	428820	AA436187	Hs.172631	Integrin, alpha M (complement component	3.71	2.25
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	3.70	2.26
	419555	U29615	Hs.91093	chitinase 1 (chitinobiosidase)	3.69	7.71
50	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68	2.17
	426174	AA547959	Hs.115838	ESTs	3.65	2.93
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	3.64	2.62
	435990	AI015882	Hs.131793	ESTs	3.62	2.27
	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	3.62	3.48
55	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	3.61	3.18
	419088	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.60	3.05
	426116	AA868729	Hs.144694	ESTs	3.60	2.80
	419235	AW470411	Hs.288433	neurotrophin	3.58	2.88
	424054	AA334511	Hs.26638	membrane-spanning 4-domains, subfamily A	3.56	2.58
60	422657	H25642		ESTs	3.55	2.44
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.54	3.98
	414142	AW368397	Hs.334485	hemiscentin(fibulin 6)	3.54	3.30
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.54	3.11
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	3.53	2.38
65	417318	AW953937	Hs.240845	ESTs	3.52	2.02
	458034	AW450979		gb:UH-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	3.50	3.21
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.48	2.35
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.48	2.13
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	3.47	2.83
70	424711	NM_005795	Hs.152176	calcitonin receptor-like	3.47	2.69
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.46	2.31
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	3.46	2.37
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.45	2.07
	447183	AI554733	Hs.173182	ESTs	3.42	2.01
75	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypothel	3.40	3.49
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40	2.42
	413714	AI580944	Hs.71428	ESTs	3.38	2.52
	407361	AA744622	Hs.292845	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.36	2.13
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36	2.41
80	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36	2.06
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.35	2.42
	410606	AW418779	Hs.114889	ESTs	3.35	2.39
	450726	AW204600		retinoic acid receptor, alpha	3.34	6.35
	430573	AA744550	Hs.136345	ESTs	3.33	1.94

	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2f	3.32	2.75
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.31	2.22
	454076	AW204712	Hs.61957	ESTs	3.31	1.95
	452039	AI922988	Hs.172510	ESTs	3.30	2.95
5	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30	2.37
	430414	AW365665	Hs.120388	ESTs	3.30	2.48
	417958	AA767382	Hs.193417	ESTs	3.30	2.04
	423001	AA320014	Hs.208603	ESTs	3.29	2.62
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28	2.35
10	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28	2.05
	424238	AA337401	Hs.137635	ESTs	3.28	2.45
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.27	2.63
	448869	AI792798	Hs.12495	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.26	2.67
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.26	2.04
15	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22	2.36
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22	3.87
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20	2.79
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20	2.30
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18	2.42
20	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18	2.12
	438568	R98865	Hs.11135	major histocompatibility complex, class	3.18	3.86
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	3.18	2.99
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.17	2.02
25	446094	AK001760	Hs.13801	KIAA1685 protein	3.17	2.42
	442048	AA974603		gb:rop34f05.s1 Soares_NFL_T_GBC_S1 Homo s	3.17	2.27
	406685	M18728		gb:Human nonspecific crossreacting antig	3.17	2.80
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16	1.95
	424943	AU077260	Hs.153924	death-associated protein kinase 1	3.16	2.18
30	436805	AA731533	Hs.270751	ESTs	3.16	1.95
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.15	3.63
	409789	D11928	Hs.76845	phosphoserine phosphatase-like	3.14	1.74
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.13	3.35
	420729	AW964897	Hs.290825	ESTs	3.12	2.09
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12	2.06
35	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12	2.58
	451820	AW058357	Hs.199248	ESTs	3.10	2.26
	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.10	3.01
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10	2.32
40	437866	AA156781		metallothionein 1E (functional)	3.10	1.80
	428513	BE220806	Hs.184697	plexin C1	3.10	2.11
	438607	AW080237	Hs.252884	ESTs	3.10	2.20
	445034	AW293376	Hs.143659	ESTs	3.08	2.81
	458332	AI000341		ESTs	3.08	1.87
45	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.08	1.87
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08	1.94
	407192	AA609200		gb:af12a02.s1 Soares_Jesitis_NHT Homo sap	3.07	2.12
	452960	AK001335	Hs.311137	protein tyrosine phosphatase, receptor 1	3.07	2.16
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06	2.75
50	431087	H12723	Hs.290791	ESTs	3.06	2.41
	452235	AL039743	Hs.28514	tastes development-related NYD-SP21	3.06	2.64
	449328	AI962493		ESTs	3.06	2.78
	422900	AA641201	Hs.222051	ESTs	3.05	1.87
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.05	1.99
55	430250	NM_016929	Hs.283021	chloride intracellular channel 5	3.05	2.49
	437527	AI241019	Hs.145644	ESTs	3.04	2.17
	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.04	1.78
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.02	2.43
	446495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	3.02	1.77
60	411252	AB018549	Hs.69328	MD-2 protein	3.02	1.95
	439991	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02	2.24
	420683	AA830168	Hs.271305	ESTs	3.01	2.14
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00	2.13
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00	2.60
65	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00	1.94
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.00	1.81
	435800	AI248285	Hs.118348	ESTs	3.00	1.89
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	3.00	2.08
70	449057	AB037784	Hs.22941	KIAA1363 protein	3.00	2.18
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.99	2.46
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	2.99	2.76
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.99	2.16
	444020	R92962	Hs.35052	ESTs	2.98	2.21
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.98	2.08
75	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	2.98	2.40
	457675	AF119917	Hs.306574	Homo sapiens PRO3098 mRNA, complete cds	2.96	2.03
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.95	1.74
	429950	AW081608	Hs.105053	ESTs	2.96	2.40
	420394	AB023161	Hs.97403	KIAA0944 protein	2.95	2.46
80	406698	X03068	Hs.73931	major histocompatibility complex, class	2.95	4.13
	419038	AW134924	Hs.190325	ESTs	2.94	1.72
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94	2.93
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	2.94	1.94
	400880			NM_000611: Homo sapiens CD59 antigen p18	2.94	1.74

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypol	2.94	2.12
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.93	2.25
	439335	AA742697	Hs.62492	NM_052863: Homo sapiens secretoglobin, fa	2.93	3.72
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.92	1.91
	419981	AA897581	Hs.128773	ESTs	2.92	2.18
10	400419	AF084545		Target	2.92	1.83
	435176	AA744875	Hs.189413	ESTs	2.91	2.15
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	2.90	2.25
	444339	T96555	Hs.31562	ESTs	2.90	3.16
	429272	W25140	Hs.110667	ESTs	2.90	2.43
15	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.90	2.29
	435080	AJ831760	Hs.155111	hypothetical protein FLJ14428	2.90	2.40
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	2.88	2.47
	421554	AW137676	Hs.97775	ESTs	2.88	3.37
	422770	AL117544	Hs.120021	DKFZP4341092 protein	2.88	2.00
20	434658	AJ624436	Hs.310286	ESTs	2.88	2.06
	440248	AA876138		ESTs	2.86	2.24
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.86	4.32
	430515	AA746503	Hs.283313	ESTs	2.86	2.96
	446063	AJ720140	Hs.151079	ESTs	2.86	2.47
25	438177	BE327015		ESTs	2.86	1.70
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.85	2.06
	417105	X60992	Hs.81225	CD6 antigen	2.85	3.00
	433230	AW136134	Hs.220277	ESTs	2.84	1.97
	438676	AA813745	Hs.123446	ESTs	2.84	2.62
30	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.82	4.33
	420252	AW270404	Hs.183161	ESTs	2.82	3.22
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82	1.78
	428055	AJ634046	Hs.157313	ESTs	2.81	2.47
	434340	AJ193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.81	2.67
35	451558	NM_001089	Hs.26530	ATP-binding cassette, sub-family A (ABC1	2.78	3.39
	435517	AA928626	Hs.130177	ESTs	2.78	2.36
	439883	AL358652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78	1.82
	434158	T86534	Hs.14372	ESTs	2.78	1.96
	428923	BE047698	Hs.188785	ESTs	2.78	2.07
40	413786	AW613780	Hs.13500	ESTs	2.78	1.97
	406387			Target Exon	2.77	4.22
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.76	3.24
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.76	2.11
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	2.76	1.94
45	417728	AW138437	Hs.24790	KIAA1573 protein	2.76	1.78
	435154	AA668764		ESTs	2.76	2.10
	429490	AJ971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.76	2.21
	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.76	2.36
	432060	AW971364	Hs.324775	ESTs	2.75	2.02
50	434164	AW207019	Hs.148135	serine/threonine kinase 33	2.74	2.48
	423706	U95218	Hs.131924	G protein-coupled receptor 65	2.74	1.93
	442703	AL044949	Hs.116298	ESTs	2.74	1.89
	450247	AF123303	Hs.24713	hypothetical protein	2.74	1.73
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.74	2.85
55	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.74	1.88
	409196	NM_001874	Hs.334873	carboxypeptidase M	2.73	1.86
	422389	AF240635	Hs.115897	protocadherin 12	2.72	2.26
	444324	AJ301330	Hs.143838	ESTs	2.72	1.74
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.72	2.40
60	428769	AW207175	Hs.106771	ESTs	2.72	2.19
	404277			NM_019111: Homo sapiens major histocompa	2.72	3.12
	409553	AW451693	Hs.220826	ESTs	2.72	2.62
	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.72	2.25
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.72	2.09
65	444381	BE387335	Hs.283713	hypothetical protein BC014245	2.71	2.26
	443547	AW271273		hypothetical protein FLJ12666	2.71	1.74
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.70	2.39
	402674			Target Exon	2.70	1.95
	438068	AJ927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.70	2.23
70	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	2.69	2.11
	444314	AJ140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.69	2.28
	428656	AB037788	Hs.188790	KIAA1377 protein	2.68	1.91
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.68	3.95
	443951	F13272		ferritin, light polypeptide	2.68	2.66
75	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.68	1.74
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	2.68	1.78
	446423	AW139655	Hs.150120	ESTs	2.68	2.29
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.67	2.07
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.67	3.00
80	458124	AW005548	Hs.124590	ESTs	2.67	3.78
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	2.66	1.64
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.66	1.64
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.65	1.92
	432231	AA339977	Hs.274127	CLST 11240 protein	2.64	4.23
	442200	AW590572	Hs.235768	ESTs	2.64	2.46
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	2.64	2.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.63	3.23

	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.63	2.48
	411213	AA676939	Hs.69285	neuropilin 1	2.62	1.73
	439737	A1751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.62	2.69
5	446570	AV659177	Hs.127160	ESTs	2.61	2.44
	411020	NM_005770	Hs.67726	macrophage receptor with collagenous str	2.60	3.39
	434792	AA649253	Hs.132458	ESTs	2.60	1.74
	426782	R14614	Hs.33845	ESTs	2.60	2.36
	425371	D49441	Hs.155981	mesothelin	2.60	6.97
10	447720	AL038765	Hs.161304	ESTs	2.59	3.06
	444623	A1183829	Hs.202111	ESTs	2.59	2.77
	433376	A1249361	Hs.74122	caspace 4, apoptosis-related cysteine pr	2.58	2.01
	444542	A1161293	Hs.280380	aminopeptidase	2.58	2.31
	439549	AW937885	Hs.137314	ESTs	2.58	2.37
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.58	2.56
15	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.56	2.47
	433308	AA582718	Hs.291650	ESTs	2.56	2.01
	443885	H91806	Hs.15284	ESTs	2.55	1.71
	408170	AW204516	Hs.31835	ESTs	2.55	1.59
20	456844	A1264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.54	1.63
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.54	2.98
	428791	AA435661	Hs.264750	ESTs	2.53	2.29
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.53	3.91
	447357	A1375922	Hs.159367	ESTs	2.52	2.83
25	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.52	1.90
	424105	A1142336	Hs.43977	Human DNA sequence from clone RP11-196N1	2.52	3.45
	403308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.52	1.98
	438698	AW297855		ESTs, Weakly similar to I38022 hypotheti	2.52	1.98
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	2.52	2.41
30	424049	AB014524	Hs.138380	KIAA0624 protein	2.51	2.19
	438543	AA810141	Hs.192182	ESTs	2.51	2.06
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	2.51	2.14
	424806	AA382523	Hs.105689	MSTP031 protein	2.51	2.11
	438580	AA811262	Hs.299202	ESTs	2.50	1.83
35	434445	A1349306	Hs.11782	ESTs	2.50	3.13
	444001	A1095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.50	1.76
	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.50	2.00
	421281	A1299139	Hs.17517	ESTs	2.50	2.40
	441384	AA447849	Hs.288660	retinoic acid induced 3	2.50	2.75
40	436772	AW975888		metallothionein 1E (functional)	2.49	1.80
	433102	A1343966	Hs.158528	ESTs	2.49	2.25
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.48	2.09
	445612	N94126	Hs.12969	hypothetical protein	2.48	2.28
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	2.48	1.87
45	433854	AA610649	Hs.333239	ESTs	2.48	2.09
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.48	2.75
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.48	2.01
	440694	AW445167	Hs.126036	ESTs	2.48	1.57
	450295	A1766732	Hs.210528	ESTs	2.48	1.99
50	431316	AA502663	Hs.145037	ESTs	2.48	1.80
	438564	AA381553	Hs.198253	major histocompatibility complex, class	2.48	2.80
	439593	BE073597	Hs.124863	ESTs	2.48	1.89
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	2.47	3.74
	453134	AA032211	Hs.118493	ESTs	2.46	2.72
55	417169	R13550	Hs.21388	ESTs	2.46	1.88
	434411	AA632649	Hs.201372	ESTs	2.46	1.95
	440381	AA917808	Hs.190495	ESTs	2.46	2.09
	448782	AL050295		KIAA0758 protein	2.46	2.69
	404240			NM_018950:Homo sapiens major histocompat	2.45	2.83
60	450843	A1741483	Hs.205383	ESTs	2.44	2.25
	434137	AA907734	Hs.124895	ESTs	2.44	2.55
	438315	R56795	Hs.82419	ESTs	2.44	1.94
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44	1.61
	439402	W02753	Hs.103002	ESTs	2.44	1.90
65	445903	A1347487	Hs.132781	class I cytokine receptor	2.44	2.32
	437323	AA371145	Hs.194397	leptin receptor	2.44	1.70
	433923	A1823453	Hs.146625	ESTs	2.44	1.58
	442201	AW516704	Hs.208726	ESTs	2.43	1.68
	437982	N93456	Hs.121764	ESTs, Weakly similar to testicular tekti	2.43	3.22
70	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.43	2.21
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	2.43	2.13
	406973	M34996	Hs.198253	major histocompatibility complex, class	2.43	2.68
	428055	AA420584	Hs.101760	ESTs	2.42	2.05
	426970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	2.42	2.79
75	433138	AB029496	Hs.59729	semaphorin sem2	2.42	1.68
	415757	AA830854	Hs.187810	ESTs	2.42	2.02
	438507	AA809052		ESTs	2.42	2.08
	450811	A1739486	Hs.245497	ESTs	2.42	1.97
	424027	AW337575	Hs.201591	ESTs	2.42	2.76
80	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.41	3.15
	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	2.41	2.08
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	2.40	1.76
	416370	N90470	Hs.203697	CD38 antigen (p45)	2.40	1.97
	415688	AA166963		gb:zo86d01.s1 Stratagene ovarian cancer	2.40	1.63

	445633	AM53386	Hs.17287	ESTs, Weakly similar to S26589 hypotheli	2.39	1.99
	431300	AA502346		gb:na26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.39	1.79
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	2.39	1.84
5	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.39	2.21
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.38	2.09
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheli	2.38	1.78
	437479	R61866	Hs.101277	ESTs	2.38	3.00
	445784	AI253155	Hs.146065	ESTs	2.38	1.61
10	418300	AJ433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.38	2.25
	413753	U17760	Hs.75517	laminin, beta 3 (niteln (125kD), kafinin	2.37	1.55
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.37	2.41
	416140	AJ918035	Hs.301198	roundabout (axon guidance receptor, Dros	2.37	1.61
	418262	Z38968		ESTs	2.37	2.05
15	420943	AJ718702	Hs.279930	major histocompatibility complex, class	2.37	2.00
	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.37	2.05
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.37	1.67
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.36	1.88
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TTT3 co	2.36	2.61
20	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	2.36	2.84
	427250	R35941	Hs.25418	ESTs	2.36	2.15
	452194	AI694413		olfactory receptor, family 2, subfamily	2.36	3.41
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	2.36	3.05
	407242	M18728		gb:Human nonspecific crossreacting anti	2.35	2.34
25	418875	W19971	Hs.233459	ESTs	2.35	1.95
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.35	1.85
	432608	AI492660	Hs.170935	ESTs	2.35	2.06
	408048	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2	2.35	1.91
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.35	2.34
30	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	2.35	2.13
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	2.34	1.73
	422099	AA156022	Hs.111518	hypothetical protein	2.34	1.80
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	2.34	2.24
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.33	2.62
35	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.32	2.52
	431848	AI378857	Hs.271605	ESTs, Highly similar to AF175283 1 zinc	2.32	2.50
	446354	AW449650		ESTs	2.32	2.21
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.32	4.34
	423961	D13665	Hs.136348	perlestin(OSF-2os)	2.31	2.19
40	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	2.31	2.34
	457250	AA811987	Hs.125779	ESTs	2.31	1.66
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	2.31	2.96
	425839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	2.30	2.12
	422746	NM_004484	Hs.119651	glypican 3	2.30	2.16
45	439920	H05430	Hs.288433	neurotrimin	2.30	4.06
	414942	C14898	Hs.192986	ESTs	2.30	2.02
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.29	3.08
	424878	H57111	Hs.221132	ESTs	2.29	1.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.29	2.76
50	411605	AW006831		ESTs	2.29	1.58
	416965	N26223	Hs.160436	ESTs	2.29	4.71
	428713	AA432067		ESTs, Moderately similar to CYA4 RAT ADE	2.29	1.73
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	2.28	1.90
55	420380	AA640891	Hs.102406	ESTs	2.28	2.82
	407137	T87307		gb:ye53h05.s1 Soares fetal liver spleen	2.28	1.52
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28	2.09
	447160	AA330310	Hs.24181	ESTs	2.28	1.71
	421114	AW975051	Hs.283156	ESTs, Weakly similar to I78885 serine/th	2.27	1.98
	453686	AL110328	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	2.27	1.91
60	452114	N22687	Hs.8236	ESTs	2.27	1.88
	417355	D13168	Hs.82002	endothelin receptor type B	2.26	1.63
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.26	1.84
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.26	1.86
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.26	1.72
65	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26	1.70
	409190	AJ076536	Hs.50984	sarcoma amplified sequence	2.26	1.56
	414221	AW450979		gb:UT-H-BI3-ata-a-12-Q-UI.s1 NCI_CGAP_Su	2.26	2.12
	435272	AA906415	Hs.110041	ESTs	2.25	2.15
	414991	C17698		gb:C17698 Human placenta cDNA (TFujwara	2.24	3.58
70	424623	AW963062	Hs.270737	ESTs	2.24	1.87
	424665	AW368576	Hs.139851	caveolin 2	2.24	2.15
	422426	W79117	Hs.58559	ESTs	2.22	3.33
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.22	2.39
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.22	3.28
75	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.22	1.59
	446142	AJ754693	Hs.145968	ESTs	2.22	1.88
	410503	AW975746	Hs.188662	KIAA1702 protein	2.22	1.56
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.22	2.49
	437629	AW574774	Hs.121692	ESTs	2.22	1.70
80	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	2.21	1.64
	430413	AWB42182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20	2.73
	447033	AJ357412	Hs.157601	Predicted gene: Ecos cloned; secreted w/V	2.20	2.58
	429496	AA453800	Hs.192793	ESTs	2.20	2.97
	425516	BE000707	Hs.29567	ESTs	2.20	1.58

	422404	AL133571	Hs.336189	Homo sapiens mRNA: cDNA DKFZp434F1135 (I	2.19	1.92
	423526	AB011086	Hs.129739	KIAA0514 gene product	2.19	2.85
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.19	2.01
5	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.19	2.53
	443441	AW291196	Hs.92195	ESTs	2.18	1.73
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	2.18	2.53
	408705	AA312135	Hs.46967	HSPCO34 protein	2.18	1.54
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.18	1.93
10	430915	AA488953	gb:aa55e05.r1 NCL_CGAP_GC81 Homo sapiens	2.18	1.57	
	418791	AA935633	Hs.194628	ESTs	2.17	2.05
	432620	AA777749	Hs.5978	LIM domain only 7	2.17	1.75
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kn	2.17	2.01
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.17	3.12
	424450	AL137526		dynein intermediate chain 2	2.17	4.14
15	426410	BE298448	Hs.305890	BCL2-like 1	2.16	2.19
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.16	1.70
	421077	AK000061	Hs.101590	hypothetical protein	2.16	1.60
	424563	AA446932	Hs.151428	ret finger protein 2	2.16	1.83
20	405102			C15001220*:g[4469558]gb[AA21311.1] (AF	2.16	1.78
	452438	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	2.15	1.87
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	2.15	1.65
	418067	AI127958	Hs.83393	cystatin E/M	2.15	2.40
	436372	AW972301	Hs.310286	ESTs	2.15	2.35
25	418728	AW970937	Hs.293843	ESTs	2.14	2.58
	450400	AI694722	Hs.279744	ESTs	2.14	2.06
	409031	AA376836		ESTs	2.14	2.14
	435143	R12375	Hs.194600	ESTs	2.14	1.69
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	2.14	2.03
30	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	2.14	1.57
	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GC81 Homo sapiens	2.14	1.68
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.14	2.04
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	2.13	1.72
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.13	1.68
35	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.13	2.47
	452353	C18825	Hs.29191	epithelial membrane protein 2	2.12	2.31
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	2.76
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.12	2.11
	437581	N59284	Hs.288010	ESTs	2.12	2.85
40	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.12	2.04
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.12	2.00
	423069	W15513	Hs.1613	adenosine A2a receptor	2.12	1.72
	432860	AW974077	Hs.283349	ESTs	2.12	1.75
	449509	AA001615	Hs.84561	ESTs	2.12	1.84
45	456062	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	2.11	4.42
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.11	1.65
	459680	H96982	Hs.42321	ESTs	2.11	2.20
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.10	2.12
50	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	2.10	2.48
	443021	AA368546	Hs.8904	Ig superfamily protein	2.10	2.42
	437838	AI307229		ESTs	2.10	1.67
	429421	AL031658		Human DNA sequence from clone RP1-310013	2.10	1.91
	407202	N58172	Hs.109370	ESTs	2.10	1.68
	443669	AI140462	Hs.134587	ESTs	2.10	1.64
55	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	2.10	1.71
	408410	AA447438	Hs.44697	ATPase, Class V, type 10C	2.10	2.05
	436293	AI601188	Hs.120910	ESTs	2.10	2.01
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	2.10	1.66
	427876	AI494291		ESTs	2.10	2.48
60	456672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.09	3.11
	434987	AW975114		ESTs	2.09	1.69
	433735	AA608955	Hs.109653	ESTs	2.09	1.78
	433226	AW503733	Hs.9414	KIAA1488 protein	2.09	1.62
	425787	AA363867	Hs.155029	ESTs	2.09	1.85
65	452304	AA025388	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.08	3.41
	442369	AI665071		ESTs	2.08	1.60
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	2.08	2.39
	434421	AI915927	Hs.34771	ESTs	2.08	1.66
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.08	1.72
70	431728	NM_007351	Hs.268107	multimerin	2.08	1.51
	444929	AI685841	Hs.161354	ESTs	2.08	3.14
	408873	AL046017		calmodulin 2 (phosphorylase kinase, delt	2.08	2.09
	437634	AW293046	Hs.255158	ESTs	2.08	1.66
	400277			Eos Control	2.08	1.46
75	443601	AI078554	Hs.42658	ESTs	2.08	1.87
	432212	AW137742		ESTs	2.08	2.84
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	2.07	1.48
	406122			Target Exon	2.06	2.75
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	2.06	1.66
80	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.06	1.70
	421057	T58283		Homo sapiens cDNA: FLJ22063 fis, clone H	2.06	1.78
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.06	2.30
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	2.06	2.31
	449444	AW818436		solute carrier family 16 (monocarboxylic	2.06	1.41

	421464	AA291553	Hs.190086	ESTs	2.06	2.61
	424831	H61453		ESTs	2.06	2.12
	434542	AA769310		hypothetical protein FLJ13164	2.06	1.44
5	418323	NM_002118	Hs.1162	major histocompatibility complex, class	2.05	2.61
	418836	AI655499	Hs.161712	ESTs	2.05	1.73
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	2.05	1.99
	400750			Target Exon	2.05	1.75
	406851	AA609784		major histocompatibility complex, class	2.05	3.94
10	414936	C14774		gb:C14774 Clontech human aorta polyA mRNA	2.05	2.41
	453459	BE047032	Hs.257789	ESTs	2.04	1.86
	443450	N66045	Hs.133529	ESTs	2.04	2.46
	430015	AW768399		ESTs	2.04	1.63
	425399	AA452244	Hs.16727	ESTs	2.04	1.51
15	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	2.04	1.73
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-static aci	2.04	1.46
	421757	Z20897	Hs.296259	paraoxonase 3	2.04	2.13
	441942	AF182645	Hs.8024	IK cytokine, down-regulator of HLA II	2.04	1.82
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.04	1.67
20	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	2.04	3.23
	414154	AW205314	Hs.323060	ESTs	2.03	2.96
	449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1.59
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.03	2.01
	406645	M57466	Hs.814	major histocompatibility complex, class	2.03	2.49
25	414516	AJ307802		ESTs, Weakly similar to T43458 hypotheti	2.02	1.56
	417032	AA192469	Hs.271838	ESTs	2.02	1.48
	414875	H42679	Hs.77522	major histocompatibility complex, class	2.02	2.79
	414522	AW518944	Hs.76325	immunoglobulin J chain	2.02	1.84
	410511	AA743475	Hs.285655	ESTs	2.02	1.87
30	423533	NM_014339	Hs.129751	Interleukin 17 receptor	2.02	2.26
	437259	AJ377755	Hs.120695	ESTs	2.02	2.34
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.02	1.86
	426722	U53823	Hs.171952	occludin	2.02	1.57
	421229	AJ056590	Hs.7086	hypothetical protein MGC12435	2.02	1.79
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.02	1.97
	447232	AW498334	Hs.327	Interleukin 10 receptor, alpha	2.02	2.09
	449317	AW293413	Hs.132908	19A24 protein	2.02	1.84
	439556	AI623752	Hs.163603	ESTs	2.02	1.62
	443031	AW134696	Hs.49418	ESTs	2.01	1.58
40	444838	AV651680	Hs.208558	ESTs	2.01	1.69
	453108	AJ311457	Hs.99472	ESTs	2.01	1.64
	432967	AA572949	Hs.207566	ESTs	2.01	1.83
	441390	AI692560	Hs.131175	ESTs	2.01	1.63
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.01	1.80
45	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.01	2.32
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.01	1.90
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.01	1.90
	415443	T07353	Hs.7948	ESTs	2.00	1.54
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	2.00	2.74
50	404394			ENSP00000241075:TRRAP PROTEIN.	2.00	2.99
	459557	N58315		gb:yy68g06.s1 Soares fetal liver spleen	2.00	1.89
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	2.00	1.46
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	2.00	1.37
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.00	1.51
55	431193	AW749505	Hs.296770	KIAA1719 protein	1.99	2.01
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	1.99	2.11
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.98	1.79
	417072	BE243915	Hs.81118	leukotriene A4 hydrolase	1.98	2.47
	429073	AA446167	Hs.47385	ESTs	1.98	1.92
60	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.98	2.94
	420838	AW118210	Hs.42321	ESTs	1.98	1.67
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	1.97	2.10
	430702	U56979	Hs.278568	H factor 1 (complement)	1.97	1.84
	456804	AJ421645	Hs.139851	caveolin 2	1.97	1.58
65	439195	H89360		gb:yy28d08.s1 Morion Fetal Cochlea Homo	1.97	1.93
	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	1.97	2.28
	413836	W92003	Hs.70614	ESTs	1.97	1.80
	400417	X72475		Target	1.97	1.75
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	1.96	1.46
70	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.96	2.18
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	1.96	2.06
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	1.96	2.21
	414572	AU077174	Hs.288181	cathepsin H	1.96	2.65
	433891	AA613792		gb:nc097h03.s1 NCL_CGAP_P12 Homo sapiens	1.95	1.71
75	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.95	2.88
	451609	AL046019	Hs.209276	ESTs	1.94	3.26
	447131	NM_004585	Hs.17456	retinoic acid receptor responder (tazaro	1.94	2.94
	430887	N66801	Hs.260287	KIAA1841 protein	1.94	1.62
	414700	H63202	Hs.38183	ESTs	1.94	1.72
80	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	1.94	1.56
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	1.93	2.22
	425252	AW391162		calreticulin	1.92	2.14
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	1.92	2.19
	425810	AI923627	Hs.31903	ESTs	1.92	1.76

	433618	AA602539	Hs.345494	ESTs	1.92	1.84
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.92	2.27
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.92	1.76
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	1.92	1.72
5	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	1.91	1.83
	426780	BE242284	Hs.172199	adenylate cyclase 7	1.91	1.67
	452386	R12499	Hs.20468	ESTs	1.91	2.64
	438670	AI275803	Hs.123428	ESTs	1.91	3.12
10	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.91	1.82
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.90	2.06
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.90	1.85
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	1.90	1.65
	428166	AA423849	Hs.79530	M5-14 protein	1.90	1.70
	428721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	1.89	3.22
15	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ111946 fis, clone HE	1.88	2.07
	436576	AI458213	Hs.77542	ESTs	1.88	2.25
	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.88	2.41
	449618	AI076459	Hs.15978	KIAA1272 protein	1.88	1.63
20	430634	AI860651	Hs.26585	calcyphosine	1.88	3.01
	440663	AW452976	Hs.247112	hypothetical protein FLJ10902	1.88	1.65
	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.88	1.78
	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.88	2.37
	444051	M48373	Hs.10247	activated leucocyte cell adhesion molecu	1.87	2.07
	414464	AI870175	Hs.13957	ESTs	1.87	2.68
25	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	1.87	2.25
	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity Iib, re	1.87	2.05
	430027	AB023197	Hs.227743	KIAA0980 protein	1.87	1.70
	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.87	2.18
30	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	1.86	2.27
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	1.86	2.31
	420361	N92054	Hs.194718	zinc finger protein 265	1.86	1.63
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.86	2.13
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor I	1.85	1.77
35	442434	AA995787	Hs.129583	ESTs	1.85	2.15
	422735	AA169685	Hs.119529	Niemann-Pick disease, type C2 gene	1.85	2.77
	444083	AI123195		gb:0017a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.84	1.73
	449679	AI823951	Hs.129700	toll-like 1	1.84	1.57
	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.84	2.02
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.84	1.72
	414803	X03100	Hs.914	Human mRNA for SB class II histocompatibi	1.84	2.47
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	1.84	2.29
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.84	1.69
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	1.83	2.12
45	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.83	1.59
	459247	N46243	Hs.110373	ESTs, Highly similar to T42628 secreted	1.83	1.57
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	1.83	1.45
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	1.83	2.18
	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	1.83	1.75
50	438596	AA829427	Hs.243081	ESTs	1.83	2.83
	436486	AA742221	Hs.120633	ESTs	1.82	2.14
	433365	AF026944	Hs.293797	ESTs	1.82	2.50
	449943	AF104266	Hs.24212	latrophilin	1.82	2.08
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.82	2.37
55	421563	NM_006433	Hs.105806	granulysin	1.82	2.48
	449161	NS3431	Hs.47647	ESTs, Weakly similar to T00057 hypotheti	1.81	2.81
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.81	2.66
	418371	M13560	Hs.84298	CD74 antigen (Invariant polypeptide of m	1.81	2.50
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.81	2.05
60	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	1.80	3.13
	428677	AI657119	Hs.120036	troponin I, cardiac	1.80	2.94
	409485	S60890	Hs.252136	ficollin (collagen/fibrinogen domain-cont	1.80	2.28
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.80	1.56
	425458	H89317	Hs.182889	ESTs	1.80	2.21
65	425390	AI092834	Hs.156114	protein tyrosine phosphatase, non-recept	1.80	1.41
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	1.80	2.20
	430570	AI417881	Hs.292464	ESTs	1.80	1.62
	439425	AF086244	Hs.114659	ESTs	1.80	2.37
	408688	AI634522	Hs.152925	KIAA1268 protein	1.80	2.13
70	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	1.80	1.80
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	1.79	1.57
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.79	2.18
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.79	1.68
	403421			NM_016369; Homo sapiens claudin 18 (CLDN	1.79	2.47
75	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical pro	1.79	2.92
	416384	AU076903	Hs.79283	selectin P ligand	1.79	1.87
	440638	AI376551		gb:tc64e10.x1 Soares_NFL_T_GBC_S1 Homo s	1.78	1.69
	422003	AA361760	Hs.296326	ESTs	1.78	2.05
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140	1.77	1.82
80	432987	AI864771	Hs.27964	CD86 antigen (CD28 antigen ligand 2, B7-	1.77	2.03
	411602	AI655043	Hs.133456	ESTs	1.77	2.01
	458194	AW383818		ESTs, Moderately similar to ALU2_HUMAN A	1.76	2.35
	432565	AA553477	Hs.152428	ESTs	1.76	2.63
	421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.75	2.59

	408989	AW361666	Hs.49500	KIAA0748 protein	1.75	1.66
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.75	1.54
	403903			C5001632:gil10645308[gb AA621430.1 AC00	1.75	3.20
5	421461	AW291023		ESTs, Weakly similar to A46010 X-linked	1.74	2.67
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	1.74	2.52
	424377	AF081675	Hs.146322	killer cell lectin-like receptor subfam1	1.74	2.15
	443884	N20617	Hs.194397	leptin receptor	1.74	1.51
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	1.74	1.63
10	448262	AW880830	Hs.186273	ESTs	1.73	2.57
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit	1.73	1.87
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	1.73	2.21
	412896	AW804157	Hs.308026	major histocompatibility complex, class	1.72	2.37
	407366	AF026942	Hs.17518	gb:Homo sapiens c133 mRNA, partial sequ	1.72	2.16
15	419407	AW410377	Hs.41502	hypothetical protein FLJ21278	1.72	1.52
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	1.71	1.55
	438606	NM_014859	Hs.6336	KIAA0672 gene product	1.71	1.57
	434795	BE620794	Hs.4147	translocating chain-associating membrane	1.71	2.21
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.71	1.46
20	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	1.71	2.49
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	1.71	1.57
	423857	N48902	Hs.133481	Homo sapiens mRNA; cDNA DKFZp564O0862 (f	1.71	1.56
	408393	AW015318	Hs.23165	ESTs	1.70	1.43
	432409	AA806538	Hs.130732	KIAA1575 protein	1.70	1.54
25	440817	AI341423	Hs.288433	neurotrophin	1.70	2.17
	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.69	2.54
	453691	H12235	Hs.226505	ESTs	1.69	2.07
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	1.68	1.54
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.68	2.29
30	434951	AF161442	Hs.191591	Homo sapiens HSPC324 mRNA, partial cds	1.68	2.24
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.68	1.44
	407775	NM_004914	Hs.38772	RAB38, member RAS oncogene family	1.68	2.03
	437119	AI379921	Hs.177043	ESTs	1.68	4.21
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.68	2.28
35	453498	BE181412	Hs.23245	hypothetical protein FLJ11767	1.68	2.76
	428289	M26301	Hs.2253	complement component 2	1.67	2.40
	404854			Target Exon	1.67	1.76
	450954	AI904740	Hs.25691	receptor (calcitonin) activity modifying	1.67	2.32
	410048	W76457	Hs.343874	proline oxidase homolog	1.67	3.03
40	407857	AI928445	Hs.92254	synaptotagmin-like 2	1.66	1.51
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.66	2.01
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	1.66	2.05
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	1.66	2.20
	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, clone A	1.66	2.11
45	417451	AW007280	Hs.115537	putative dipeptidase	1.65	2.11
	443791	N64458	Hs.143345	ESTs	1.65	2.11
	440475	AI807671	Hs.24040	potassium channel, subfamily K, member 3	1.65	2.04
	431743	AW972642	Hs.293055	ESTs	1.64	2.64
	400328	X87344		transporter 2, ATP-binding cassette, sub	1.64	2.43
50	451876	T63141		gb:gb99a12.s1 Stratagene lung (937210) H	1.64	2.02
	417321	N68722	Hs.191368	ESTs	1.64	2.53
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64	2.01
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.63	2.17
	432176	AW080386	Hs.112278	arrestin, beta 1	1.63	2.04
55	450708	AA376654		eukaryotic translation initiation factor	1.62	2.05
	429570	BE242256	Hs.2441	KIAA0022 gene product	1.62	1.39
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp584B076 (fr	1.62	1.57
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	1.62	1.44
	452424	AI964028	Hs.48353	ESTs	1.62	2.53
60	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.62	1.38
	416316	H58721	Hs.271628	ESTs	1.62	1.39
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam1	1.62	2.67
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.62	2.45
65	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a1	1.62	1.51
	438089	W05391		nuclear receptor subfamily 1, group I, m	1.61	1.45
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.61	1.52
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.61	2.40
	444009	AI380792	Hs.135104	ESTs	1.60	2.15
	436057	AJ004832	Hs.5038	neuropathy target esterase	1.60	2.60
70	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.60	2.57
	433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	1.60	3.30
	410494	M36564	Hs.64016	protein S (alpha)	1.59	1.42
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	1.59	2.02
	446618	R65984	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.59	2.52
75	419918	X80700	Hs.93728	pre-B-cell leukemia transcription factor	1.59	2.04
	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	1.59	1.98
	434308	N51517	Hs.47282	ESTs	1.58	2.29
	447341	AF106941	Hs.18142	arrestin, beta 2	1.58	2.09
	454315	AW373564	Hs.251928	BANP homolog, SMAR1 homolog	1.58	2.10
80	423281	AJ271684	Hs.126355	C-type (calcium dependent, carbohydrate-	1.57	1.75
	433671	AW138797	Hs.132906	19A24 protein	1.57	2.05
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	1.57	2.71
	436906	H95990	Hs.181244	major histocompatibility complex, class	1.57	2.24
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.57	1.43

	406825	AI982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.57	2.37
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.56	1.61
	423329	AF054910	Hs.127111	teklin 2 (testicular)	1.56	2.51
	424909	ST8187	Hs.153752	cell division cycle 25B	1.55	2.00
5	431921	N46466	Hs.58879	ESTs	1.54	3.04
	437400	AB011542	Hs.5559	EGF-like-domain, multiple 5	1.54	1.44
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily	1.54	3.04
	415078	AA311223	Hs.283091	found in inflammatory zone 3	1.53	2.61
10	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.53	2.18
	401854			Target Exon	1.53	2.08
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.52	1.52
	433815	AI696602	Hs.112757	ESTs	1.52	2.57
	431130	NM_006103	Hs.2719	HE4; epidermis-specific, whey-acidic pr	1.52	1.36
15	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	1.51	1.43
	414763	U97276	Hs.77266	quiescin Q6	1.50	2.07
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	1.50	1.46
	412870	N22788	Hs.82407	CXC chemokine ligand 16	1.50	2.83
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.50	2.04
20	432894	AW167668	Hs.279772	brain specific protein	1.50	2.25
	457941	AI004525	Hs.14587	ESTs, Weakly similar to AF151859 1 CGI-1	1.49	2.22
	442743	AI801351	Hs.302110	ESTs, Weakly similar to MUC2_HUMAN MUCIN	1.49	2.09
	419542	AA366037	Hs.90911	solute carrier family 16 (monocarboxylic	1.49	2.40
	433124	U51712	Hs.13775	hypothetical protein SMAP31	1.49	1.39
25	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.49	1.39
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.48	1.76
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.48	1.41
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	1.48	1.44
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.47	1.31
30	427872	AA835058		Human DNA sequence from clone RP1-261G23	1.47	2.50
	449853	AF006823	Hs.24040	potassium channel, subfamily K, member 3	1.47	2.21
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.47	1.50
	415149	X12451	Hs.78056	cathepsin L	1.46	1.84
	447217	BE465754	Hs.17778	neuropilin 2	1.46	1.40
35	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.46	2.16
	445672	AI907438	Hs.282862	ESTs	1.46	2.01
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.46	2.10
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	1.46	1.60
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.45	1.40
40	419577	L36531	Hs.91296	integrin, alpha 8	1.45	1.40
	439620	AA838727	Hs.124405	ESTs, Weakly similar to A46010 X-linked	1.45	1.57
	423804	AW403448	Hs.16725	interferon-stimulated transcription fact	1.45	2.10
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3)-glycoprotein beta-	1.44	2.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	1.44	1.45
	431573	AW971070	Hs.291160	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.44	1.40
45	409524	AW402151	Hs.54673	tumor necrosis factor (ligand) superfamily	1.43	2.01
	406787	AW090702	Hs.240615	tubulin alpha 1	1.42	1.86
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.42	1.95
	406422			Target Exon	1.41	2.02
50	421341	AJ243212		deleted in malignant brain tumors 1	1.41	1.47
	421195	BE464560	Hs.133017	ESTs	1.41	2.42
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	1.41	2.05
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.41	1.34
	451220	AF124251	Hs.26064	novel SH2-containing protein 3	1.40	2.10
55	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp584G112 (fr	1.40	3.64
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.40	3.24
	432133	AB033088	Hs.272567	KIAA1262 protein	1.40	2.78
	428833	AI928355		ESTs	1.40	2.02
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	1.39	1.55
60	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	1.39	2.09
	427732	NM_002980	Hs.2199	secretin receptor	1.38	2.44
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	1.38	1.85
	407568	AA740964	Hs.62699	ESTs	1.38	3.13
	422573	AW297985	Hs.295726	Integrin, alpha V (vitronectin receptor	1.38	1.38
65	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.37	1.12
	457918	AL359590	Hs.162504	hypothetical protein DKFZp762M186	1.36	2.01
	423696	Z92546	Hs.131819	Sushi domain (SCR repeat) containing	1.36	2.54
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.36	2.04
	407244	M10014		fibrinogen, gamma polypeptide	1.36	1.29
70	451109	F11876	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.35	1.34
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	1.35	2.47
	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	1.34	1.66
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	1.34	1.92
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	1.34	1.86
	427507	AF240467	Hs.179152	tail-like receptor 7	1.34	2.11
75	446967	AI699629	Hs.156781	ESTs	1.34	3.75
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.34	2.18
	456637	AW161450	Hs.109201	CGI-88 protein	1.33	1.78
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.33	1.95
80	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.32	2.05
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unnamed protein	1.32	2.08
	436986	AA740983	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.32	2.06
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	1.32	2.08
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	1.31	1.29

429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolactin)	1.30	1.25
413474	T85312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.30	1.92
406659	AA663985	Hs.277477	major histocompatibility complex, class	1.30	2.22
451049	AA013353		gb:za28h10.s1 Soares retina N2b4HR Homo	1.30	2.12
436494	AA720997	Hs.128295	ESTs	1.29	2.30
438374	AA321866	Hs.6193	hypothetical protein FLJ14590	1.28	2.34
417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	1.28	2.39
425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.28	1.69
428458	AA428820	Hs.251399	neurogranin (protein kinase C substrate,	1.27	2.00
443180	R15875	Hs.258576	claudin 12	1.26	1.25
421764	AI681535	Hs.148135	serine/threonine kinase 33	1.26	2.01
414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.26	1.21
433283	BE041135	Hs.175622	ESTs	1.24	3.05
426759	AI590401	Hs.21213	ESTs	1.23	1.20
436446	AW016809	Hs.119021	ESTs	1.23	1.20
421467	AA291590	Hs.97252	ESTs	1.22	1.54
431353	AA828032		ESTs	1.22	3.00
427403	AA402107	Hs.257146	ESTs, Moderately similar to I38022 hypot	1.22	1.91
453037	AA045175	Hs.17914	ESTs	1.22	2.40
437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.22	2.26
439941	AI392840	Hs.18272	amino acid transporter system A1	1.22	1.22
451385	AA017656		gb:za39h01.r1 Soares retina N2b4HR Homo	1.21	1.49
400495			ENSP00000224716*:GTP-binding protein SAR	1.20	1.25
409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	1.20	1.44
407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.19	2.06
426486	BE178285	Hs.170058	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.18	2.02
445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	1.17	1.14
439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	1.14	1.16
440555	D31292	Hs.6853	hypothetical protein FLJ22187	1.14	2.19
446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.13	1.12
432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.12	2.43
432798	AA565309	Hs.194015	ESTs	1.10	2.23
411274	NM_002776	Hs.69423	kallikrein 10	1.10	1.09
438856	N40027	Hs.7473	ESTs	1.09	1.52
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.09	1.07
448253	H25899	Hs.201591	ESTs	1.08	2.10
409718	D86640	Hs.56045	src homology three (SH3) and cysteine r	1.08	2.08
409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!	1.06	1.58
449321	AA001150	Hs.132937	ESTs	1.06	2.06
418693	AI750878	Hs.87409	thrombospondin 1	1.06	1.02
402333			Target Exon	1.03	1.03
421814	L12350	Hs.108623	thrombospondin 2	1.02	1.02
425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	2.36
458158	AW296778	Hs.144734	Human DNA sequence from clone RP3-416F21	1.00	2.73
406517			nel (chicken)-like 2	1.00	2.07
442526	AW277221		ESTs	1.00	2.21
446164	AW273539		hypothetical protein FLJ23577	1.00	2.52
449122	AI631310	Hs.196955	ESTs	1.00	2.23
438038	AI732629		ESTs, Weakly similar to TA2R HUMAN, BETA	1.00	2.04
429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	1.00	2.02
453672	U73531	Hs.34526	G protein-coupled receptor	1.00	2.57
436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	1.00	2.64
438909	AF085839		gb:Homo sapiens full length Insert cDNA	1.00	2.23
423609	AA328348	Hs.218289	ESTs	1.00	2.19
419261	X07876	Hs.89791	wingless-type MMTV integration site faml	1.00	2.28
436284	AA708016	Hs.190389	ESTs	1.00	2.22
440932	AI801509	Hs.182080	ESTs	1.00	1.66
403420			Target Exon	1.00	1.86
431169	AW971240		gb:EST383329 MAGL resequences, MAGL Homo	1.00	2.02
425918	NM_008786	Hs.162200	urotensin 2	1.00	2.11
419721	NM_001650		aquaporin 4	1.00	2.26
421761	AL120297	Hs.108043	Friend leukemia virus integration 1	1.00	1.88
425781	AF001622	Hs.159523	class-J MHC-restricted T cell associated	1.00	1.86
415094	D59513	Hs.330778	ESTs	1.00	2.32
434088	AF116677	Hs.249270	hypothetical protein PRO1968	1.00	2.26
420727	H75701	Hs.99886	complement component 4-binding protein,	1.00	1.84
430049	AW277085	Hs.99619	ESTs	1.00	1.87
446868	AV660737		ESTs	1.00	1.79
418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	1.00	1.44
436391	AJ227892	Hs.146274	ESTs	1.00	1.30
413059	BE151498		gb:RCO-HT0295-291199-031-E11 HT0295 Homo	1.00	1.42
427739	AW196755	Hs.98105	NYD-SP14 protein	1.00	2.41
452788	AW294571	Hs.135040	ESTs	1.00	2.23

75 TABLE 32B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826

5	421798	3042_4	B0017829 AW276646 A1984209 AA663933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329 T60644 T57747 BF852694 T92529 BG482852 BF883064 BF883056 N74880 AA829796 N90716
	400269	2726_1	X65018 B0022318 NM_003019 BE465060 A1732255 BF446634 A1820677 A1002217 A1924488 B1821373 B1770406 B1823937 B1820265 B1489632 BG482911 AA617783 A1807697 AW205576 T94427 AA487101 T94513 B1819407 B1822456 B1820618 B1824619 BG542824 BG537862
10	432222	539529_1	BG207209 BE166299 A1040995 BG199355 AW969908 AA528756 AW440776 B1044354
	432810	101919_1	BG292389 C06094 A1668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 A1810530 BF092924 AA34151 AA334725 D31302 R20723 AA263003 B1824635 A1276287 A1684428 A1524234 A1335035 AW014704 A1911443 AA972102 A1367512 A1126670 AW016017 A1286003 A147163 AA626033 A1539156 AA565542 A1094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 A1991439 R46187 BE929954 AA333976 D63102 BF744491
15	418259	133853_1	BM310925 AA426110 BM310529 BF434286 AW015091 BF475996 AW118867 BE675186 A1688568 A1453594 AW590589 A1652425 A1827969 BF056946 A1802866 A1393380 A1476224 AW590639 AW136271 A1458252 A1524726 AA843768 AA782158 A1336058 A1097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 A1493445 AW054729 A1221929 A1868744 AA215405 AA766713 AA821546 BF928317 BE464132 A1990909 AW271459 A1262051 AA215404 N74332 BG940151 BG952281 AA972115 W96315 AA689586 R69067 BF766886 BE769254 W05240
20	429228	215430_1	BG676155 BM009591 A1479075 A1025794 A1017967 AA448270 BE466812 AA853422 A1392649 BG952034 AA513384 BF840124 BE714620 AW969605 A1553633
	459702	539529_1	BG207209 BE166299 A1040995 BG199355 AW969908 AA528756 AW440776 B1044354
	422667	224778_1	A1758223 AW469334 BF940841 AW080348 A1270363 A1055892 BE464168 BF431797 BE350144 BF448739 A1693409 BF432999 D62848 AA398070 A1383375 AW611490
25	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	430709	1234627_1	AW969880 AA484613 AA501874 R34356
	450726	666520_1	A1732297 AW204600 T95017
	442048	750422_1	AW340495 A1984319 AA974603
	406685	0_0	M18728
	440028	598730_1	AW473675 A1190744 W69997 AW104913 A1221098 W69996 AA885487 AA851491
	437866	34267_1	U52054 AL581000 AA156850 AW293839 B1335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF445960 AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 A1866686 A1572124 AA687333 D20160 AA812489 A1852448 A186004 AA156781 A1536733 BM144850 A1471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 B1022546 B1021204 A1000341 A1766341 AW873274
30	458332	1139685_1	AA602964 AA609200
	407192	2200202_1	A1884781 A1652306 A1651694 A1638744 A1962493
	449328	3030726_1	AA534222 AA632632 T81234
	432340	1619980_1	AF119847 AA437261 AA436987 A1132965
	434194	62680_1	AK001125 AU120581 AU146612 AW301393
	436198	28277_1	AA876138 A1239602 A1698953
	440248	2616908_1	AW975183 AA973583 A1365103 A1699495 A1301787
	442006	1239046_1	AK024965 AU158033 AA978370 R79120 BE327015 AA778740 R79121
	438177	9337_12	AW972063 AA668764 AA804491 AW665688 AA765069
	435154	126605_1	L13288 AA928785 A1608912 AW872978 AA565655 A1022915 A1304920 A1564366 A1668793 A1094557 T60038 R72302 H45409 AA508805 R46356
	423387	2612_2	AA418798 BM129553 BM129126 BM129292 BM128865 A1808418 A1689932 A1806573 BF431808 AW872985 AW166269 H73241 T16182 A1264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 A1797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 B1022902 B1763932 B1910138 AV645808 AA701657 AW271273 A1796734 A1472316 A1017531 A1061178 BF109098 AA548964 N83805 AA131648 AA156589 BE708349 AW952494 D30877 AV684717 Z24837 F00167 BF576150 T63841 R78995 N87474
35	444314	1027984_1	AW749625 AW749628 AW749644 A1140497
	443951	MH1768_18	A1334106 R63583 A1028079 A1140098 A1911625 A1890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520
40	432639	1237887_1	AW973785 H60163 AA557608
	438698	598828_1	AW975851 A1911033 A1540093 AA932284 AW297855 AA829228 AA814442 AW105017
	413638	1525406_1	H71252 BE154642 BE154668
	436772	1239464_1	AA156151 Z25109 C05177 AW976688 AA731063 N67084
	448782	34980_1	AB018301 AL050295 BF513128 AW385080 AL551708 A1352542 A1829703 A1819388 AW629019 AW073189 AW273857 AW118768 A1453845 A1452494 AA886341 A1057144 AA904647 A1423547 AW263913 A1094774 A1434419 A1039546 A1002491 A1240412 Z25099 AA995178 AW050649 AW026140 A1796309 A1584012 BE166666 A1767991 A1309041 AA724059 A1695284 A1245095 T63971 Z40627 BE166681 BG570071 BF921915 B1562702 BG506502 AV658068 R48378 AA121543 A1096938 AA618131 H40993 R48277 A1352281 BG540263 BG538901 N95226 A1365752 A1221152 Z28777 R16574 AW966449 AA044116 AW797518 B1010405 AA044288 A1093508 BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 A1096437 AA384077 BF941499 T93764 BG003285
45	438507	2729_4	BG698329 A1417878 A1080171 A1190332 A1092344 A1357100 AA744522 AA412653 AA977007 BF438628 AA743264 AA365279 AW073197 B1493198 AA169355 B1493197 A1283051 BF436642 AA809052 A1833263
50	415688	1235745_1	AW971218 AA493942 AA166963
	431300	1529181_1	BE159863 AA502346 AU186097 R86267 H71358
	418262	5824_2	AK055180 AA490810 A1420925 A1473832 AA127397 AA127409 AW820078 A1214567 AA876961 AA283985 A1904240 D20426 BC015835 N28408 Z42826 A1927925 AW590850 AW195643 A1675823 W84675 AA767204 AW207335 A1051690 A134786 A1051699 A1139875 BF195790 A1250256 A1767042 A1521899 AA829382 AA526451 A1971192 R08173 N20059 AA215409 Z38968 H13200 H01182 R82482 AW972928 BF242637 H01273 H13567 R82532
55	452194	90339_1	A1694413 AW994700 A1912946 N73548 A1082035 AW271652 W24189 W24182 A1719718 AA024658 AW810120 AW015394 T79755 AA988043 A1709339
60	446354	831448_1	A1701583 A1291038 AW449650
	406687	0_0	M31126
	411605	10026_3	BG256892 H10532 N46614 R52610 AW977698 BM460488 W56819 B1042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 B1838226 BF034269 AA429173 BE741829 AW867495 A123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 A1533815 BF921562 AA094230 BE092587 W86151 AA526153 A1672156 BF914496 R12579 BF652352 AA699780 T57386 BF903022 R09933 AA678298
65	428713	21322_7	AA432067 AW572442
	414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA482073 BE168945
	414991	1785136_1	D78831 C17898 D78863
	447197	2176805_1	R36075 R36167 A1366546
	430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
	424450	1674_1	NM_023036 A1295276 AF250288 AL137526 AW517074 A1870459 A1215420
	409031	9531_1	BF036043 AW190446 BG194731 AW662036 A1445021 BE937550 AW818972 AW393132 AA834685 BF112068 AV721682 H16423 A1270167 A1857345 AA937302 AW818444 BE929780 BG498678 BF155010 B1598271 B1599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 A1018009 N42850 AW573242 AA17258

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AA453483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553
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 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW357006 BF358697
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 D53502 AW373300 AL118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 AI496876 AI264159 BM128481 AI624657
 AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797
 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752
 AW373305 AW373299 AW373302
 BE883520 BI057842 AA215702 AA215703 AA368006 BE006876 BE066555
 AA002232 T99209 AA002071
 AI308202 AI307229 AA769348
 AW341668 AI201382 AW104364 AA648367 AA897604 AW977914 AA811957 AI352198 AL040620
 BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823
 AI494291 AI582807 AA417018 AA608841
 AW975114 AI096634 AI767001 AA658364 AW517542
 AA993566 AI521958 AI565071 AI864217
 AL046017 AW504804 AA532433 AI634701 AI126421 AW151275 AA620782 AA933047 AI828223 AI624555 AI624489 AV749032 BI495751
 AI672289 AA342944 AV748076 AV747586 AA058597 H56073 W87367 R71630 H84499 AI866297 D25918 AV746788 N78995 H63752 H82985
 R46600 BE786692 R71128 AA608909 R29728 BG534018
 Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 AL555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656
 AI371816 AA292474 AA375747 AA308414 BM454544 BI333370 BM049921 BI451428 BI465007 BI223401 BE856245 AW821164 BF914775
 BF914761 AI125835 BI222678 BI091137 BF340536 BM462798 BI224452 BG707915 AL569160 AA443815 AW572857 AW363410 BF735268
 BG010283 BI013120 BF818845 BF763468 AA305165 AI303370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587
 BG166574 BI869342 BE562482 BE539637 AA165089 AL579118 AL553699 BE044054 AW117440 AI520674 BF435417 AW245648 AI952404
 T29534 AU153459 AU152168 AW591591 AU146918 AI393187 AA478013 AU148143 AI224471 AI640728 AI871537 AW264752 N93787 AI189357
 AV756134 AI471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 AI799771 F04407 AI285530
 AI914543 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 AI923594 BF439180 BI770936 BF032438 AU154884 AA682793
 AW072992 AU158815 AI884444 AL048031 AU158922 AU152546 AI695187 AL048033 AI245550 AU148507 AW687451 BE536868 BF913001
 BF062707 AL573082 AW067993 AA523354 BE886727 AI890705 AU159092 AI982693 AI817553 AA236729 BI687858 BI613677 AI524675
 AI678155 AA127100 AI762661 AU159718 AA469720 AA483627 AW131696 R26868 AI199885 AW875614 AW938694 AW578974 BI763988
 BG819168 BE874767 BG978292 BE162948 AL554483 AW189719 T56783 AI018819 AI476552 BI492837 AI284440 BG996262 AA932887 AI380726
 R79530 AA622108 AI262575 T56782 R27437 BE784153 AW129649 AI675567 AI866759 BG987935
 AW972351 AW182936 AI478370 AA528309 BG997292 AW137742 AI632006 AA775020 AA961625 W86628 BF112014 AI275423 AI680786
 BE222349 AA830545 BF224127 H99396 N81017 N81016 AI525205 T58283
 U59185 NM_004696 AV734324 AI245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU136895
 AU158158 AU155762 R73608 R65751 R23756 N74630 AW078687 BE439761 BE785351 R68994 BE785857 AW297502 AW297553 BG431545
 AW814843 BF382644 BG429539 BE929862 BF811258
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 AF392454 AK023074 AI884890 AI814455 AW966220 BF736545 AA026021 AA286843 AA251918 BG197710 AA026294 AA337356 BC010422
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 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399
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 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593
 AI918399 AI537650 AA491103 AW008188 R07703 AA899120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893
 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591
 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818
 C15161 D60184 D60656
 AK057782 AI146454 BG703115 AI765980 AI948611 AA889263 AA947457 BG547193 H11947 Z38147 F10426 BF447329 H11946 T74968 F06195
 BG548563 AI004988 AA148735 AI307802 AI439791 BE041453 AI984904 AA148734 F12823
 BG623239 N58315 AI524952
 AL110216 AI816283 AI688476 AA928351 AW157672 AI288740 BE468242 AI452476 AI291665 AW192364 BE503635 AW592872 AA857393
 AW162770 AI680660 AI879565 AI347717 BF880800 AI266646 AA834381 AI291667 AI264567 Z38449 T03352 AI929432 BE673697 AI124770
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 AI914323 AI684406 AA932348 BE670597 AA932080
 AF086037 H89360 H89546
 AW182329 AA613792 T05304 AW858385
 AK056513 AL553942 AL553941 BG924307 BE879339 AA576941 BG054674 BF431361 BE467806 BF445874 BE138798 AA425029 BF084265
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 BE146525 BE146515 AW295699 BE146518 BE146516 BF349828 AL520587 AW803944 BE931092 BF375188 BG676709 BF832746 BG696737
 AW391179 AI582980 AW582217 AW814484 BE77215 AW391162 AW814336 AW814302 AW814444 AL520586 AI333134 AI378333 AW243412
 BE350482 AI628661 AI925481 AI246159 AW593633 AI273558 AI494388 AA806280 AW005606 BE048135 AW341024 AA969419 AA912778
 AA621100 AA479920 AI867584 AI290391 BE348490 BF340755 AI225038 AI857592 BG113588 AI566808 AW196841 BF087184 AA353524
 AW957546 BF340833 BF037221 BE146523
 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722
 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762
 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
 AW978786 AA767373 AW173343 AA836163 N27563 AA905328 R97032

5	444083	10908_12	B1836699 A1123195
	455508	1239880_1	AW976165 C04000
	417086	1154_2	AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA184350 BC005933 BC017866 AA196396 Z24810 AA181361 AA193115 AA086465 F25194 F30130 AA180013 AJ346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28506 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW449825 A1620346 BG986374 BE706521 C02691 A1596834 F31902 F26078 AA670099 BF475555 F30818 F37524 AJ346558 F28050 F17933 F31637 C03413 A1092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546
10	409208	10117_2	AK074047 AJ144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 A1824838 A1963970 A1637671 AW196330 BG427526 BM148789 BF893644 BF881946
	440638	371165_1	BG009500 A1376551 AA897445 T87714
	458194	506272_1	A1692525 AW005307 AW383618 A1689861 A1342712 AA906899
15	421461	128918_1	AA291529 A1629027 A1890447 AA677465 BF001179 A1301102 AW452003 AA704419 AA706883 T68871 AW291023
	430850	296806_1	BE144152 AA487799 BF916865 AA937952
	400328		
20	451876	2328579_1	T63141 A1821021 BF370092 BF370127 BF370060 T62998
	450708	12745_1	AK055196 AW952031 A1694545 A1742403 AW874431 AW204731 A1887383 BE220997 AA011287 AA115112 A1306385 AW571707 BF433009 AW197042 AJ367086 H23002 H11743 R37085 Z39208 A1002267 H10206 T23948 W74801 R51633 R37677 R59986 H10833 BG012000 R13817 H22794 Z43122 H10257 BG984543 H10875 BG984542 AA318232 BF849799 W76357 AA376654 R18795 AA114979 AA303838 AW139819 A1674165 A1686172 W94102 R67170 H11820 BG015023
	452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 B1823519 B1770023 AL554969 B1489908 A1304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 A1569694 AW073296 A1361433 AA564644 AA487429 BE858232 AA838610 A1539114 A1719375 A1829129 BG057675 A1423422 AU158860 BE300655 AW107777 AA586956 AL571889 AL556850 AL576404 AL562800 B1256544 BF342301 BG875994 AA054458 AA353161 A1940434 BE816522 AL577636 A1479650 AW150377 AU154395 AW951271 A1032220 A1819778 A1346733 AW771150 AW512525 A1249904 AA279809 A1352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 B1819184 AV660190 AL556475 A1620020 AW089888 AW079179 Z21518 AA687601 F04651 A1783961 T57198 A1433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 A1266514 A1538823 A1475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 A1682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW356685 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 B1560216 B1753586 BM475665 BE644917 W7707089 AW952971 N64863 BM263259 A1224545 A1184866 N69114 AW518902 A1440169 AA809472 AV654440 AA281642 AU185230 AW337382 A1872923 A1537113 N73882 T83378 H63731 BF671764 AW697824 A1811204 AA344546 BE009112 BG6989664 H91240 R60548 N41701
25	427872	4983_5	B1826340 B1868674 R12615 AW887767 BF439409 A1424995 BG059893 AA417003 A1202270 AA418740 A190974 Z39070 AA742556 AA835058 AA694436 R20520 AA418795 BG460307 B1560147
	458208	45807_4	A1990640 A1380016 BM273298 BM273060
	421341	1407_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 A1492875 A1796676 A1749838 AA918144 A1814590 A1923531 BF513992 A1720725 A150879 A1279072 AW612904 A1492104 A1284510 A1141231 AA613554 AW662148 AW769047 AA565985 AW612888 A1100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311 BE088101 T05990 AW872477
30	411880	1139083_1	A1928355 A1709178 AA436447 A1431274 BF946000
	428833	317753_1	BE091833 BE091874 BE091871
	455797	1511159_1	
35	407244		
	451049	83923_1	W92422 AA013353
	431353	1241126_1	AW977507 AA503803 AA767137 AA828032 AA828033
40	451385	85022_1	AA019761 AA017656 AA017374
	442526	450370_1	AF150283 AW182000 AW277221 AV735848
	446164	41648_2	AK026817 A1559708 AW273539 AW892986
45	438038	2523501_1	A1732629 A1732831 AA776249
	438909	4045_1	AF085839 R69254 R69137 AW188788
	431169	1235760_1	AW971240 AA493723 AA493843
50	419721	40816_1	AK026728 AL138138 BF059437 A1657037 AL600872 C15206 C14676 AA001003 AL157562 BG706081 H24162 BF841047 H15952 Z45355 AL157565 AV721762 AW953127 AA324171 BF476417 R52508 N54211 R46734 BG485659 BF810747 BE766227 AL538364 R19964 T15657 AW197333 R16235 R40826 BG152309 AV729035 R45066 AA016969 BE504976 BF593783 N51085 R61284 BE702264 A1216994 Z41068 N72577 R37645 AW237014 AW197630 A1359402 AA707806 AL119885 H23480 T16037 A1950756 T62597 T91664 R40195 D60186 H23014 T89715 H05749 H24054 AA001565 H15041 C15205 D59987 R13787 R61283 H23479 H07874 R14070 R52555 R21139 H05858 AA348655 AL120460 T62525 AV725241 AA046875 A1361912 H13341 BG150488 AL119338 Z42792 F05895 H07966 F06492 R59866 D31594 H09436 R35726 B1917845 BG704196 BF735198 AL036526 BG569879 AW195713 R55867 AA016968 H09087 BE841173 AW893631
	446868	15525_1	AK074473 BC017997 B1831060 BF971101 A1886394 A1082824 AV708785 W86073 W07772 AV660737 A1816793 R52250 BG183529 AA633473 A191256 R44763 R19947 BF571345 W86257
	413059	1488711_1	BE063078 BE151503 BE151498

TABLE 32C:

65	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
70	NL_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand
	400880	9931121	Plus
75	402474	7547175	Minus
	406387	9256180	Plus
	404277	1834458	Minus
80	402674	8077108	Minus
	404240	5002624	Minus
	405102	8076881	Minus
85	406122	9144087	Minus
	400750	8119067	Plus
	404394	3135305	Minus
90	403421	9655041	Minus
	403903	7710671	Minus
	404854	7143420	Plus

5	401854	7770538	Plus	151483-151637,151902-152008,152146-15231
	406422	9256411	Plus	163003-163311
	400496	9743564	Plus	41515-41695
	402333	8844110	Minus	165693-165856
	406517	7711431	Plus	7151-7402
	403420	9664969	Plus	159835-159938

10 TABLE 33A: About 800 genes upregulated in lung fibrosis relative to normal lung

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal lung AIs, where the minimum value for the numerator and denominator was set to 50

	Pkey	ExAccon	UnigeneID	Unigene Title	R1
20	406964	M21305		FGENES predicted novel secreted protein	16.10
	431089	BE041395		ESTs, Weakly similar to unknown protein	12.38
	421110	AJ250717	Hs.1355	cathepsin E	11.86
25	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.62
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.90
	444381	BE387335	Hs.283713	hypothetical protein BC014245	8.58
30	406850	AI624300	Hs.172928	collagen, type I, alpha 1	8.26
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	8.24
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.72
35	408380	AF123050	Hs.44532	diubiquitin	7.24
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	7.15
	456034	AW450979		gb:U1-H-BI3-ala-a-12-0-U1.s1 NCL CGAP_Su	7.12
40	453355	AW295374	Hs.31412	myopodin	6.96
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.83
45	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.72
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.72
	438089	W05391		nuclear receptor subfamily 1, group 1, m	6.62
50	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46
	417433	BE270268	Hs.82128	5T4 oncofetal trophoblast glycoprotein	6.32
55	439195	H89360		gb:yyw28d08.s1 Morton Fetal Cochlea Homo	6.29
	444301	AK000136	Hs.10760	asporin (LRR class 1)	6.28
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	6.13
60	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	6.11
	430702	U56979	Hs.278568	H factor 1 (complement)	6.10
	424878	H57111	Hs.221132	ESTs	6.00
65	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fls, clone H	6.00
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fls, clone L	5.94
	408491	AJ088063	Hs.7882	ESTs	5.94
70	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	5.92
	432222	AI204995		gb:an03c03.x1 Strelagene schizo brain S1	5.92
	407857	AI928445	Hs.92254	synaptotagmin-like 2	5.90
75	433230	AW136134	Hs.220277	ESTs	5.86
	412719	AW016510	Hs.816	ESTs	5.86
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.82
80	426759	AI590401	Hs.21213	ESTs	5.72
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72
	421814	L12350	Hs.108623	thrombospondin 2	5.71
85	430887	N66801	Hs.260287	KIAA1841 protein	5.70
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fls, clone L	5.62
	436954	AA740151	Hs.130425	ESTs	5.58
90	411573	AB029000	Hs.70823	KIAA1077 protein	5.55
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38
	410608	AW418779	Hs.114889	ESTs	5.38
95	410800	BE280421	Hs.94499	ESTs	5.32
	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	5.28
	406687	M31126		matrix metalloproteinase 11 (stromelysin	5.26
100	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	5.22
	412622	AW664708	Hs.171959	ESTs	5.22
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.18
105	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	5.15
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	5.13
	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	5.12
110	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	5.11
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04
	452239	AW379378		protein tyrosine phosphatase, receptor t	4.97
115	453874	AW591783	Hs.36131	collagen, type XV, alpha 1 (undulin)	4.96
	443884	N20617	Hs.194397	leptin receptor	4.94
	444040	AF204231	Hs.182982	golgin-87	4.94
120	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	4.93
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	4.92
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	4.92
	432435	BE218886	Hs.282070	ESTs	4.92

5	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	4.90
	430655	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	4.90
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.90
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.82
	430027	AB023197	Hs.227743	KIAA0980 protein	4.78
	408393	AW015318	Hs.23165	ESTs	4.76
	449509	AA001615	Hs.84561	ESTs	4.72
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	4.72
10	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	4.72
	433226	AW503733	Hs.9414	KIAA1488 protein	4.68
	444745	AF117754	Hs.11881	thyroid hormone receptor-associated prot	4.68
	442994	AJ026718	Hs.16954	ESTs	4.66
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.66
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.66
15	418005	AJ186220	Hs.83164	collagen, type XV, alpha 1	4.65
	433586	T85301		gbcyd78d06.s1 Soares fetal liver spleen	4.64
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64
	424408	AI754813	Hs.145428	collagen, type V, alpha 1	4.64
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	4.62
20	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	4.62
	450086	AW016343	Hs.233301	ESTs	4.61
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	4.60
	442652	AJ005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	4.59
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.58
25	418259	AA215404		ESTs	4.54
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.54
	432810	AA863400		ESTs	4.54
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.53
30	436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.52
	412652	AI801777		ESTs	4.52
	438899	AF085833	Hs.135624	ESTs	4.52
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	4.52
	436252	AJ539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	4.52
35	443324	R44013	Hs.164225	ESTs	4.51
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	4.51
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.51
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	4.50
	431843	AA518420		ESTs, Weakly similar to I38022 hypotheti	4.50
40	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.46
	452561	AI692181	Hs.49169	KIAA1634 protein	4.46
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	4.45
	442048	AA974603		gbxp34f05.s1 Soares_NFL_T_GBC_S1 Homo s	4.44
	436120	AJ248193	Hs.119860	ESTs	4.44
45	423575	C18883	Hs.163443	Intron of perlestin (OSF-2os)	4.44
	429697	AW296451	Hs.24605	ESTs	4.44
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	4.43
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	4.43
	414462	BE622743	Hs.301064	arfaplin 1	4.42
50	428698	AA652773	Hs.334838	KIAA1866 protein	4.42
	420838	AW118210	Hs.42321	ESTs	4.41
	458584	AF217518	Hs.8360	PTD012 protein	4.40
	434340	AI93043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	4.40
	400076			Eos Control	4.38
55	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	4.38
	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (f	4.36
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.36
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.36
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.34
60	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.34
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4.33
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	4.33
	429228	AI553833		ESTs	4.32
	426458	D83032	Hs.169984	nuclear protein	4.30
65	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30
	432476	T94344	Hs.326263	ESTs	4.29
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.28
	435446	AW016809	Hs.119021	ESTs	4.27
	439556	AI623752	Hs.163603	ESTs	4.26
70	428179	AI127772	Hs.279695	serum/glucocorticoid regulated kinase-II	4.26
	428411	AW291464	Hs.10338	ESTs	4.26
	434936	AI285970	Hs.183817	ESTs	4.23
	413048	M93221	Hs.75182	mannose receptor, C type 1	4.23
	432606	NM_002104	Hs.3068	granzyme K (serine protease, granzyme 3;	4.22
75	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	4.22
	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	4.22
	441297	AW403084	Hs.7765	ubiquitin-conjugating enzyme E2E 1 (homo	4.21
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	4.20
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.20
80	423578	AW960454	Hs.222830	ESTs	4.20
	446608	N75217	Hs.257846	ESTs	4.20
	424238	AA337401	Hs.137635	ESTs	4.19
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	4.18
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.18

	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18
	439593	BE073597	Hs.124863	ESTs	4.17
	442369	AJ565071		ESTs	4.16
5	445885	AI734009	Hs.127699	KIAA1603 protein	4.16
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	4.16
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	4.15
	407347	AA829847		gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens	4.14
10	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.13
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.12
	451184	T87943		transcription factor 7-like 2 (T-cell sp	4.12
	426174	AA547959	Hs.115838	ESTs	4.12
	431562	AI884334	Hs.11637	ESTs	4.12
15	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.12
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12
	449437	AJ702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	4.12
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	4.10
	444020	R92962	Hs.35052	ESTs	4.10
20	439424	AI478667	Hs.118183	hypothetical protein FLJ22833	4.10
	416987	D86957	Hs.80712	KIAA0202 protein	4.10
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.09
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.08
25	431193	AW749505	Hs.296770	KIAA1719 protein	4.08
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.08
	433308	AA582718	Hs.291650	ESTs	4.08
	445756	AA290690	Hs.300776	ESTs	4.08
	431745	AW972448	Hs.163425	ESTs	4.08
30	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	4.07
	440099	AL080058	Hs.6909	DKFZP564G202 protein	4.06
	439398	AA284267	Hs.221504	ESTs	4.06
	432731	R31178	Hs.287820	fibronectin 1	4.06
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	4.05
35	433626	AF078859	Hs.86347	hypothetical protein	4.05
	428055	AA420584	Hs.101760	ESTs	4.04
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04
	413243	AA769266	Hs.193657	ESTs	4.02
	431214	AA294921	Hs.348024	v-rel simian leukemia viral oncogene hom	4.02
40	453753	BE252983	Hs.35086	ubiquitin specific protease 1	4.02
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	4.02
	434404	AW445034	Hs.256578	ESTs	4.02
	407604	AW191962		collagen, type VIII, alpha 2	4.02
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.02
45	436772	AW975688		metallothionein 1E (functional)	4.00
	443257	AI334040	Hs.11614	HSPC065 protein	4.00
	450187	AA736788	Hs.78521	KIAA1717 protein	3.98
	433913	AI694106	Hs.72325	ESTs, Weakly similar to I38022 hypotheti	3.98
	415050	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	3.98
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	3.98
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.98
	426818	AA554827	Hs.292996	DKFZp434A0131 protein	3.98
	440118	AB040893	Hs.6968	KIAA1460 protein	3.98
	413836	W92003	Hs.70614	ESTs	3.97
55	442647	AL038436	Hs.31388	ESTs	3.96
	449188	AW072939	Hs.347187	myotubularin related protein 1	3.96
	450656	AA010539	Hs.18912	ESTs	3.96
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	3.94
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94
60	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti	3.94
	407879	AA045464	Hs.6557	zinc finger protein 161	3.93
	438146	Z36842	Hs.57548	ESTs	3.93
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.93
	429355	AW973253	Hs.292689	ESTs	3.92
65	437210	AA311443	Hs.293563	Homo sapiens mRNA; cDNA DKFZp586E2317 (f	3.92
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	3.92
	452416	AA026115	Hs.114777	ESTs	3.92
	413873	AI310151	Hs.173524	ESTs	3.91
	400196			Eos Control	3.91
70	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.90
	453204	R10799	Hs.191990	ESTs	3.90
	454076	AW204712	Hs.61957	ESTs	3.90
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.90
	437158	AW090198		KIAA1150 protein	3.90
75	443970	AI280341	Hs.166571	ESTs	3.90
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.90
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90
	444057	AA316896	Hs.257267	FYVE and coiled-coil domain containing 1	3.89
	411495	AF000893	Hs.70359	KIAA0136 protein	3.88
80	438452	AJ220911	Hs.288959	hypothetical protein FLJ20920	3.88
	410297	AA148710		lumican	3.88
	427698	AW972594	Hs.335499	ESTs	3.88
	436769	AA748675		ESTs	3.86
	417819	AJ253112	Hs.133540	ESTs	3.86

5	445800	AA126419	Hs.32944	Inositol polyphosphate-4-phosphatase, ty	3.86
	425838	NM_014071	Hs.159813	nuclear receptor coactivator RAP250; per	3.86
	422173	BE385828	Hs.250619	phorbolIn-like protein MDS019 (CEM15)	3.86
	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell	3.85
	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	3.85
10	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	3.85
	412636	NM_004415		desmoplakin (DPI, DPII)	3.84
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	3.84
	418876	AA740616		gb:ny97111.s1 NCI_CGAP_GC81 Homo sapiens	3.84
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothe	3.84
15	430317	AB020645	Hs.239189	glutaminase	3.84
	442806	AW294522	Hs.149991	ESTs	3.84
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.82
	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	3.82
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.82
20	430573	AA744550	Hs.136345	ESTs	3.82
	453394	AW960474	Hs.40289	ESTs	3.81
	431266	AW149321	Hs.105411	ESTs	3.80
	434987	AW975114		ESTs	3.80
	452685	AB34651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	3.79
25	435176	AA744875	Hs.189413	ESTs	3.78
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	3.77
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.77
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.76
	441989	AA306207	Hs.285241	protein kinase, cAMP-dependent, regulato	3.76
30	417228	AL134324	Hs.7312	ESTs	3.76
	418546	AA224827		gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	3.76
	450779	AW204145	Hs.156044	ESTs	3.75
	412408	D51103	Hs.73851	ATP synthase, H transporting, mitochondr	3.75
	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	3.75
35	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.75
	429494	AA769365	Hs.126058	ESTs	3.75
	447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro	3.75
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	3.74
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	3.74
40	448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	3.74
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.73
	414883	AA926960		CDC28 protein kinase 1	3.72
	416178	AB08527	Hs.192822	serologically defined breast cancer anti	3.72
45	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	3.72
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.72
	438807	AW080237	Hs.252884	ESTs	3.72
	408221	AA912183	Hs.47447	ESTs	3.72
	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.70
50	419900	AB699860	Hs.170698	ESTs	3.70
	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.70
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	3.70
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.70
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	3.70
55	447846	AA324057	Hs.77955	Homo sapiens cDNA: FLJ23527 fis, clone L	3.70
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	3.70
	418300	AB433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.69
	408495	W68796	Hs.237731	ESTs	3.69
	424452	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothe	3.68
60	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	3.68
	431974	AW972689	Hs.200934	ESTs	3.68
	416354	NM_000633	Hs.79241	B-cell CLL/lymphoma 2 (BCL2)	3.68
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	3.67
65	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	3.67
	419111	AA234172	Hs.137418	ESTs	3.67
	423979	AF229181	Hs.136644	CS box-containing WD protein	3.66
	418875	W19971	Hs.233459	ESTs	3.66
	451690	AW451469	Hs.209990	ESTs	3.66
70	423032	AB84746	Hs.119274	RAS p21 protein activator (GTPase activa	3.66
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.66
	428347	AB264161	Hs.183773	golgi autoantigen, golgin subfamily a, 4	3.66
	426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypothe	3.66
	435335	AB693150	Hs.137928	ESTs	3.66
75	410577	X91911	Hs.64639	glioma pathogenesis-related protein	3.66
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	3.65
	429105	D87077	Hs.196275	KIAA0240 protein	3.64
	407813	AL120247	Hs.40109	KIAA0872 protein	3.64
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	3.64
80	451678	AA374181	Hs.26799	DKFZP564D0764 protein	3.64
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.64
	452408	AA306477	Hs.29379	hypothetical protein FLJ10687	3.64
	441466	AW673081	Hs.54828	ESTs	3.63
	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.62
	420056	AW043684	Hs.99804	ESTs	3.62
	424886	H88584	Hs.96900	hypothetical protein; KIAA1830 protein	3.62
	431774	BE348813	Hs.268561	hypothetical protein FLJ10726	3.62

	435990	AI015862	Hs.131793	ESTs	3.62
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	3.62
	414715	AA587891	Hs.904	amylase-1,6-glucosidase, 4-alpha-glucanotransferase	3.62
5	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	3.62
	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	3.62
	413823	AI341417	Hs.29406	ESTs	3.61
	435354	AA678267	Hs.117115	ESTs	3.60
	427832	AF038362	Hs.180930	TBP-associated factor 172	3.60
10	427846	AW499770	Hs.180948	KIAA0729 protein	3.60
	426116	AA868729	Hs.144694	ESTs	3.60
	457635	AV660976	Hs.3569	hypothetical protein	3.60
	443998	AI620661	Hs.296276	ESTs	3.60
	417867	AW952547	Hs.194603	ESTs, Moderately similar to I38022 hypothetical	3.58
15	418182	AW016405	Hs.16648	ESTs	3.58
	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	3.58
	424831	H61453		ESTs	3.58
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.58
	421823	N40850	Hs.28625	ESTs	3.58
20	414781	D50917	Hs.77293	KIAA0127 gene product	3.57
	427393	AB029018	Hs.177635	KIAA1095 protein	3.57
	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	3.56
	425465	L18964	Hs.1904	protein kinase C, iota	3.56
	417124	BE122762	Hs.25338	ESTs	3.56
25	416502	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	3.56
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymphocyte	3.55
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.55
	410390	AA876905	Hs.125286	ESTs	3.54
	442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	3.54
30	435266	AK001942	Hs.4853	hypothetical protein DKFZp566A1524	3.54
	441499	AW298235	Hs.101689	ESTs	3.54
	453256	AI565587	Hs.32556	KIAA0379 protein	3.54
	414142	AW368397	Hs.334485	hemocytin (fibulin 6)	3.54
	438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	3.54
35	412245	AI952669	Hs.22883	ESTs, Weakly similar to I38022 hypothetical	3.54
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.53
	446682	AW205632	Hs.211198	ESTs	3.52
	431392	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	3.52
	433430	AI863735		ESTs	3.52
40	420394	AB023161	Hs.97403	KIAA0944 protein	3.52
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like	3.52
	443547	AW271273		hypothetical protein FLJ12668	3.52
	420676	AI434780	Hs.4248	vav 2 oncogene	3.51
	410690	AA322979	Hs.130266	ESTs	3.50
45	459645	AA074346		ESTs	3.50
	401403			Target Exon	3.50
	451166	T98171	Hs.185675	ESTs	3.50
	418836	AI655499	Hs.161712	ESTs	3.50
50	421462	AF016495	Hs.104624	aquaporin 9	3.50
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	3.50
	432401	NM_013330	Hs.274479	NME7	3.49
	408392	U28831	Hs.44566	KIAA1641 protein	3.49
	425836	AW955696	Hs.90960	ESTs	3.48
	452327	AK000196	Hs.29052	hypothetical protein FLJ20189	3.48
55	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalytic	3.48
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	3.48
	422960	AW890487		cadherin 13, H-cadherin (heart)	3.48
	430570	AI417881	Hs.292464	ESTs	3.48
	406387			Target Exon	3.47
60	416585	X54162	Hs.79386	telomodulin 1, smooth muscle (LMOD1) (Thy	3.46
	432340	AA534222		gb:n121d02.s1 NCI_CGAP_AA1 Homo sapiens	3.46
	412240	H72176		hypothetical protein FLJ13159	3.46
	450937	R49131	Hs.26267	ATP-dependant Interferon response protein	3.46
	443634	H73972	Hs.134460	ESTs	3.46
65	422963	M79141	Hs.13234	ESTs	3.46
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.46
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine protease	3.46
	425100	AF051850	Hs.154567	supervillin	3.45
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.45
70	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	3.44
	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	3.44
	447764	NM_003776	Hs.19500	nuclear localization signal deleted in v	3.44
	411251	R19774	Hs.22835	HHGP protein	3.44
	432648	AA557952		gb:n176d05.s1 NCI_CGAP_HSC1 Homo sapiens	3.44
75	428708	NM_014897	Hs.190386	KIAA0924 protein	3.44
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	3.43
	451743	AW074266	Hs.23071	ESTs	3.42
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	3.42
	448705	H05072	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	3.42
80	414489	AI620677	Hs.73105	ESTs	3.42
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 domain)	3.41
	435841	R28522	Hs.186937	ESTs	3.41
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	3.40
	451198	AW984541		hypothetical protein FLJ21127	3.40

	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	3.40
	435023	T81819	Hs.302251	ESTs	3.40
	449656	AA002008	Hs.188633	ESTs	3.40
5	437739	AW579216	Hs.264610	ESTs, Moderately similar to Ibd1 (H.sapi	3.40
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	3.40
	448474	AJ792014	Hs.13809	hypothetical protein FLJ10648	3.40
	456505	AA504595		ESTs	3.40
	439867	AA847510	Hs.161292	ESTs	3.40
10	442113	BE622187		ESTs, Weakly similar to I38022 hypotheti	3.40
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40
	435299	AJ745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40
	421263	AB020638	Hs.103000	KIAA0831 protein	3.40
	410300	AW903988	Hs.62119	hypothetical protein FLJ14800	3.39
15	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.39
	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	3.38
	432572	AJ660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN IIII	3.38
	442426	AJ373062	Hs.332938	hypothetical protein MGC5370	3.38
	428412	AA428240	Hs.126083	ESTs	3.38
20	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.38
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.38
	413714	AJ560944	Hs.71428	ESTs	3.38
	415663	AW296841	Hs.313332	ESTs	3.38
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	3.37
25	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.37
	440214	AA247118	Hs.7049	hypothetical protein FLJ11305	3.37
	440980	AL042005	Hs.11117	tripeptidyl peptidase II	3.36
	411975	AI916058	Hs.144583	ESTs	3.36
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36
30	414783	AW069569		inactive progesterone receptor, 23 kD	3.36
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.36
	411213	AA676939	Hs.69285	neuroligin 1	3.36
	420613	AI873871	Hs.7041	ESTs, Weakly similar to A47582 B-cell gr	3.35
35	417534	NM_004998	Hs.82251	myosin IE	3.35
	431698	AI492369		ESTs	3.35
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.35
	441623	AA315805		desmoglein 2	3.34
	420729	AW964897	Hs.290825	ESTs	3.34
40	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	3.34
	448369	AW268962	Hs.111335	ESTs	3.34
	452820	N46161	Hs.35274	ESTs	3.34
	453271	AA903424	Hs.6786	ESTs	3.34
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.34
45	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.34
	443291	AA325633	Hs.136102	KIAA0853 protein	3.33
	418720	AI381687	Hs.39526	ESTs	3.33
	452107	AB020681	Hs.27973	KIAA0874 protein	3.33
	439943	AW083789	Hs.124620	ESTs	3.33
50	433282	BE539101		hypothetical protein	3.33
	410344	AW978436	Hs.62515	KIAA0494 gene product	3.33
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.32
	434210	AA665612		ESTs	3.32
55	431923	AJ741770	Hs.292690	ESTs, Weakly similar to I38022 hypotheti	3.32
	453199	AI336266	Hs.32353	mitogen-activated protein kinase kinase	3.32
	419534	AA443691	Hs.90858	Homo sapiens clone 25023 mRNA sequence	3.32
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	3.32
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	3.32
60	422092	AB007883	Hs.111373	KIAA0423 protein	3.32
	412262	W28406		seven in absentia (Drosophila) homolog 1	3.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.32
	446094	AK001760	Hs.13801	KIAA1685 protein	3.32
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.32
65	420339	AW968259	Hs.186647	ESTs	3.31
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.31
	432331	W37862	Hs.274368	MSTP032 protein	3.31
	433697	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.31
	419231	AL046284	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	3.31
70	430950	AA489525		ESTs	3.30
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	3.30
	417958	AA767382	Hs.193417	ESTs	3.30
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.30
	419543	AA244170		gb:nc05h02.s1 NCL_GGAP_Pr1 Homo sapiens	3.30
75	454024	AA933527	Hs.293907	hypothetical protein FLJ23403	3.30
	452039	AI922988	Hs.172510	ESTs	3.30
	443798	R07848	Hs.188522	ESTs	3.29
	449378	AW664026	Hs.59892	ESTs	3.29
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	3.28
80	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	3.28
	444291	AI598022	Hs.193989	TAR DNA binding protein	3.28
	424084	AJ940675	Hs.20914	hypothetical protein FLJ23056	3.28
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	3.28
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28

	425657	T89839	Hs.119471	ESTs	3.28
	406672	M26041	Hs.198253	major histocompatibility complex, class	3.28
	419905	AW248229	Hs.93659	protein disulfide isomerase related prot	3.27
5	425332	AA633306	Hs.127279	ESTs	3.27
	418529	AW005695	Hs.250897	TRK-fused gene	3.27
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.27
	433618	AA602539	Hs.345494	ESTs	3.27
	408630	AA748009	Hs.173328	ESTs	3.26
10	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	3.26
	415102	M31899	Hs.77929	excision repair cross-complementing roda	3.26
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	3.26
	429493	AL134708	Hs.145998	ESTs	3.26
	445860	AA332145	Hs.13392	lathering factor SEC34	3.26
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	3.26
15	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.26
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	3.26
	448412	AJ219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.26
	436758	AW977167	Hs.155272	ESTs	3.25
20	438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.26
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	3.25
	426860	U04953	Hs.172801	isoleucine-tRNA synthetase	3.25
	437830	AB020658	Hs.5867	KIAA0851 protein; suppressor of actin 1	3.25
	453368	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE	3.25
25	409939	AA463437	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	3.25
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	3.24
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	3.24
	418283	S78995	Hs.83942	cathepsin K (pseudodysostosis)	3.24
	414405	AJ362533		KIAA0306 protein	3.24
30	445893	AI610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.24
	434423	NM_006769	Hs.3844	LIM domain only 4	3.24
	408951	AW407227	Hs.227591	hypothetical protein FLJ11088	3.24
	408949	AF189011	Hs.49163	putative ribonuclease III	3.24
	410337	M83822	Hs.62354	cell division cycle 4-like	3.24
35	409010	AI648675		Homo sapiens, Similar to RIKEN cDNA 1700	3.24
	400419	AF084545		Target	3.24
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.24
	422461	NM_003417	Hs.117077	zinc finger protein 264	3.24
	441604	AI683049	Hs.201282	ESTs	3.24
40	411960	R77776	Hs.18103	ESTs	3.23
	414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	3.23
	430522	N75750	Hs.242271	KIAA0471 gene product	3.23
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23
	405268			ENSP00000223174:KIAA0783 PROTEIN.	3.23
45	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.22
	427196	AW967522	Hs.191593	ESTs	3.22
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length Insert cDN	3.22
	417727	AL133623	Hs.82501	similar to mouse Xn1 / Dhmd protein	3.22
	410853	H04588	Hs.30469	ESTs	3.22
50	411962	AA099050		gb:zk85d12.r1 Soares_pregnantLuterus_NbH	3.22
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22
	440452	AI925138	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22
	427480	BE148769	Hs.334477	hypothetical protein FLJ11328	3.22
	444623	AI183829	Hs.202111	ESTs	3.21
55	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	3.21
	435874	AA686688	Hs.93102	ESTs	3.20
	443801	AW206942	Hs.253594	intron of: trichorhinophalangae syndro	3.20
	434982	AW975084		gb:EST387190 MAGE resequences, MAGN Homo	3.20
	430929	AA489166	Hs.156933	ESTs	3.20
60	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced transl	3.20
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20
	451119	AA805417	Hs.64753	ESTs	3.20
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	3.20
65	432676	AI187366		gb:ql29c01.x1 Soares_testis_NHT Homo sap	3.19
	428820	AA436187	Hs.172631	integrin, alpha M (complement component	3.19
	422040	AA172106	Hs.110950	Rag C protein	3.18
	437838	AI307229		ESTs	3.18
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18
70	420789	AI670057	Hs.199882	ESTs	3.18
	419135	R61448	Hs.106728	ESTs, Weakly similar to KIAA1353 protein	3.18
	446019	AI382520		histone deacetylase 3	3.18
	430848	AW021726	Hs.345490	gb:d127e02.y1 Morton Fetal Cochlea Homo	3.18
	425375	AA631977	Hs.155995	KIAA0643 protein	3.18
75	424075	AI807320	Hs.227530	RE1-silencing transcription factor	3.18
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18
	453111	AB014598	Hs.31720	hephaestin	3.18
	454042	H22570		hypothetical protein FLJ20093	3.18
80	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.18
	447183	AI554733	Hs.173182	ESTs	3.18
	437446	AA788948	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.18
	431831	AW023204	Hs.302743	ESTs	3.18
	420664	AI681270	Hs.99824	BCE-1 protein	3.18
	451582	AI963026	Hs.289958	ESTs, Weakly similar to putative p150 JH	3.17

	432954	AI076345	ESTs	3.17
	444990	AJ912410	Hs.27475	3.17
	427373	AB007972	Hs.130760	3.17
5	408832	AW085690	Hs.63428	3.17
	441889	AI090455	Hs.268371	3.17
	416959	D28459	Hs.80612	3.17
	445525	BE149866	Hs.14831	3.16
	420623	BE245485	Hs.99437	3.16
10	451475	T19093	Hs.26450	3.16
	452066	AA772149	Hs.16979	3.16
	429556	AW139399	Hs.98988	3.16
	448514	AB020626	Hs.301866	3.16
	443732	AI188803	Hs.153944	3.16
15	436805	AA731533	Hs.270751	3.16
	430057	AW450303	Hs.2534	3.16
	417511	AL049176	Hs.82223	3.16
	423595	R82826	Hs.220702	3.16
	445837	AI261700	Hs.145544	3.16
20	418068	AW971155	Hs.293902	3.16
	430253	AK001514	Hs.236844	3.16
	414183	AW957446	Hs.301711	3.16
	433194	AB040883	Hs.83243	3.16
	453915	AA588721	Hs.286218	3.15
25	407725	BE388094	Hs.21857	3.15
	437412	BE069288	Hs.34744	3.14
	440937	AF207224	Hs.7531	3.14
	449057	AB037784	Hs.22941	3.14
	446126	AW085909	Hs.140237	3.14
30	407204	R41933	Hs.140237	3.14
	419145	N99638	Hs.140237	3.14
	418757	AJ864193	Hs.169728	3.14
	430000	AW205931	Hs.99588	3.14
	437286	AA350994	Hs.20281	3.14
35	441381	H22195	Hs.31874	3.14
	457250	AA811987	Hs.125779	3.14
	422900	AA641201	Hs.222051	3.14
	442787	W93048	Hs.250723	3.14
40	430589	AJ002744	Hs.246315	3.14
	419355	AA428520	Hs.90061	3.14
	409509	AL036923	Hs.322710	3.14
	417308	H60720	Hs.81892	3.14
	409799	D11928	Hs.76845	3.14
	429160	AW663083	Hs.144469	3.14
45	452679	Z42387	Hs.83883	3.14
	451107	AA235108	Hs.17639	3.14
	444034	AL161957	Hs.10177	3.14
	451518	AW340925	Hs.174918	3.14
	435702	AI033647	Hs.121001	3.13
50	439208	AK000299	Hs.180952	3.13
	451838	AW005866	Hs.193969	3.13
	426369	AF134157	Hs.169487	3.13
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	453920	AI133148	Hs.36602	3.13
55	411529	AA430348	Hs.317596	3.13
	417105	X60992	Hs.81226	3.12
	433854	AA610649	Hs.333239	3.12
	408089	H59799	Hs.42644	3.12
	453688	AL110326	Hs.304679	3.12
60	426167	AF039023	Hs.167496	3.12
	452195	AA94712	Hs.116878	3.12
	416580	T61572	Hs.79385	3.12
	419839	U24577	Hs.93304	3.12
	424001	W67883	Hs.137476	3.12
65	434584	D57341	Hs.188361	3.12
	433401	AF039698	Hs.284217	3.12
	409245	AA361037	Hs.284217	3.12
	414290	AI568801	Hs.71721	3.12
	400294	N95796	Hs.278695	3.12
70	429819	AL133011	Hs.225108	3.11
	448873	NM_003677	Hs.22393	3.11
	428471	X57348	Hs.184510	3.11
	436288	AI381722	Hs.192410	3.10
	433376	AI249361	Hs.74122	3.10
75	416051	AA835868	Hs.25253	3.10
	453468	W00712	Hs.32990	3.10
	412340	AA101809	Hs.182685	3.10
	438716	AA814903	Hs.155113	3.10
	419440	AB020689	Hs.90419	3.10
80	433017	Y15067	Hs.279914	3.10
	428513	BE220806	Hs.184697	3.10
	437866	AA156781	Hs.184697	3.10
	451027	AW519204	Hs.40808	3.10
	448030	N30714	Hs.325960	3.10

	435445	AA737345	Hs.294041	ESTs	3.10
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	3.09
	449924	W30581	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	3.09
5	406122			Target Exon	3.09
	435272	AA906415	Hs.110041	ESTs	3.09
	410726	AI623859	Hs.15936	ESTs	3.09
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein)	3.08
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.08
10	417538	AW050865	Hs.275711	hypothetical protein MGC2452	3.08
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	3.08
	434733	AI334367	Hs.159337	ESTs	3.08
	434421	AI915927	Hs.34771	ESTs	3.08
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08
15	424939	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.08
	458332	AI000341		ESTs	3.08
	445034	AW293376	Hs.143659	ESTs	3.08
	446570	AV659177	Hs.127160	ESTs	3.08
	429920	AW473208	Hs.115572	ESTs, Weakly similar to I38022 hypotheti	3.08
20	459513	AI032946		gb:ox05g09.s1 Soares_fetal_liver_spleen_	3.05
	419038	AW134924	Hs.190325	ESTs	3.06
	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	3.06
	417386	AL037228	Hs.82043	D123 gene product	3.06
	453108	AI311457	Hs.99472	ESTs	3.06
25	449328	AI962493		ESTs	3.06
	428656	AB037798	Hs.188790	KIAA1377 protein	3.06
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06
	447957	NM_014821	Hs.20126	KIAA0317 gene product	3.06
	417226	AW505054	Hs.4283	ESTs	3.05
30	452248	AA039368	Hs.28578	muscleblind (Drosophila)-like	3.05
	426279	AI648520	Hs.169084	tubby like protein 3	3.05
	433814	AA609738	Hs.16525	ESTs	3.05
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.05
	431341	AA307211	Hs.251531	prolaserone (prosome, macropain) subunit,	3.04
35	441789	D52059	Hs.7972	KIAA0871 protein	3.04
	456437	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.04
	438771	NM_016289	Hs.6406	MO25 protein	3.04
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.04
	416240	NM_001981	Hs.79095	epidermal growth factor receptor pathway	3.04
40	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.04
	424776	AI867931	Hs.164595	ESTs	3.03
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.03
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.03
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	3.03
45	431625	AW750627	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.03
	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	3.02
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.02
	408683	R58655	Hs.46847	TRAF and TNF receptor-associated protein	3.02
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (3.02
50	440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	3.02
	415443	T07353	Hs.7948	ESTs	3.02
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02
	406685	M18728		gb:Human nonspecific crossreacting antig	3.02
55	446013	AI360167	Hs.152774	ESTs	3.02
	433902	AW292820	Hs.144906	ESTs	3.02
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.02
	432505	AW274526	Hs.277721	KIAA0049	3.01
	440040	BE219431	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.01
60	433255	AI274270	Hs.96840	KIAA1527 protein	3.01
	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.01
	417258	N58885		gb:yy60a09.s1 Soares_multiple_sclerosis_	3.00
	435800	AI248285	Hs.118348	ESTs	3.00
	444838	AV651680	Hs.208558	ESTs	3.00
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	3.00
65	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	3.00
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.00
	436396	AI683487	Hs.162213	wingless-type MMTV integration site fami	3.00
	410434	AF051152	Hs.63668	toil-like receptor 2	3.00
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00
70	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.98
	450247	AF123303	Hs.24713	hypothetical protein	2.98
	417865	AW086059	Hs.6529	ESTs, Weakly similar to I78885 serine/th	2.98
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.98
	438543	AA810141	Hs.192182	ESTs	2.98
75	415503	U36601	Hs.78473	N-acetylase/N-sulfotransferase (hepara	2.98
	429138	AB020657	Hs.197298	NS1-binding protein	2.98
	447881	BE620886		GCN1 (general control of amino-acid synt	2.96
	425481	AW978162		ESTs	2.96
	453315	BE544203	Hs.24831	ESTs	2.96
80	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	2.95
	433208	AW002834	Hs.24095	ESTs	2.95
	442495	AI184717		ESTs	2.94
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.94
	408170	AW204516	Hs.31835	ESTs	2.94

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.94
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.93
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 ts, clone OV	2.93
	449458	AI805078	Hs.208261	ESTs	2.93
	449317	AW283413	Hs.132906	19A24 protein	2.92
	411118	N27944	Hs.221476	ESTs, Weakly similar to AF108460 1 ubinu	2.92
10	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 ts, clone L	2.91
	416311	D80529		gb:HUM081H058 Human fetal brain (TFujjwa	2.91
	433068	NM_006456	Hs.288215	slalytransferase	2.90
	429272	W25140	Hs.110667	ESTs	2.90
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUA S-100 pro	2.90
15	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.88
	426782	R14614	Hs.33846	ESTs	2.88
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 ts, clone HE	2.88
	413882	AA132973	Hs.184492	ESTs	2.88
	421554	AW137676	Hs.97775	ESTs	2.88
20	446488	AB037782	Hs.15119	KIAA1361 protein	2.84
	421391	AW304350	Hs.191958	Immunoglobulin superfamily receptor tran	2.84
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	2.82
	419284	AW820869	Hs.215658	ESTs, Moderately similar to ZN91_HUMAN Z	2.82
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82
25	448481	W15284	Hs.74832	ESTs	2.82
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.80
	443441	AW281196	Hs.92195	ESTs	2.80
	422725	AA315703	Hs.199993	ESTs, Weakly similar to ALU8_HUMAN IIII	2.80
	431926	AW972724		gb:EST384816 MAGI resequences, MAGL Homo	2.80
30	420405	AA741024	Hs.88378	ESTs	2.79
	437678	AA829860	Hs.122834	ESTs	2.78
	440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.78
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.77
35	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.76
	435154	AA668764		ESTs	2.76
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.75
	442703	AL044949	Hs.116298	ESTs	2.74
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
40	435861	AF254956	Hs.16608	candidate tumor suppressor protein	2.72
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.70
	438441	AW684960	Hs.205319	ESTs	2.70
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.67
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-li	2.66
45	416239	AL038450	Hs.48948	ESTs	2.62
	434792	AA649253	Hs.132458	ESTs	2.60
	424852	AI222779	Hs.144848	ESTs	2.58
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.57
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.56
50	450571	AF158240	Hs.60397	ESTs	2.56
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypotheti	2.56
	424148	BE242274	Hs.1741	integrin, beta 7	2.56
	445784	AI253155	Hs.148065	ESTs	2.53
	408072	BE005566	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	2.52
55	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.52
	450295	AI766732	Hs.210628	ESTs	2.48
	440381	AA917808	Hs.190495	ESTs	2.46
	433923	AI823453	Hs.148826	ESTs	2.44
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44
60	429670	L01087	Hs.211593	protein kinase C, theta	2.44
	437908	AI082424		ESTs	2.43
	438676	AA813745	Hs.123446	ESTs	2.37
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28
	444969	AI203334	Hs.160628	ESTs	2.28
65	446423	AW139655	Hs.150120	ESTs	2.27
	435517	AA928626	Hs.130177	ESTs	2.27
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.00
	426073	AA446167	Hs.47385	ESTs	1.98
70	433834	AA620742	Hs.130786	ESTs	1.72
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.52
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	1.30
	402550			Target Exon	1.09

TABLE 33B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	431089	125941_2	BC940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	456034	685586_1	AA136653 AA136656 AW450979 AA584358 AA809054 AW238038 AA920773 BE168945
	407192	2200202_1	AA602964 AA609200

438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AJ224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AJ872923 AJ537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344546 BE009112 BG899664 H91240 R60548 N41701
5	439195 432222 406687 444314 452239	21979_1 539529_1 0_0 1027984_1 10116_4
10	433586 418259	32908_1 133853_1
15	432810	101919_1
20	412652	18858_2
25	431843 442048 429228	445334_1 750422_1 215430_1
30	442369 459702 407347 451184	2691713_1 539529_1 810943_1 1531_4
35	444610 407604	2145292_1 43771_1
40	436772 437158	1239464_1 59575_1
50	410297	2990_1
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60	436769 412638	1239572_1 1438_1
65	70	
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431698 6468_7

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A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1686869 A1568892 A1915596 AW105614 A1887259 A1538577 BE926474
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BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 B1040941 AA337270 AW384371 AW847442
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BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365156 AW365154 AW606653
BF783109 BE931637 BE167181 BE713879 BF354008 BF678728 H90899 AW365145 W38382 A1498487
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AW975114 A1095634 A1767001 AA658364 AW517542
AW969880 AA484613 AA501874 R34356
T59708 AA224827 T59843 BE156903
AF274943 BG494894 A1719075 AA908783 A1935150 A1422691 AA910644 AA583187 BM272167 A1828996 AA527373 AW972459 A1831360
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AA130992 AW969537 AA503835
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AA961586 A1863735 AA588325
AV645808 AA701657 AW271273 A1796734 A1472316 A1017531 A1061178 BF109096 AA548964 N83805 AA131648 AA156589 BE708349
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BF090249 AW954947 AW890487 A1305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 A1350279 AA879119
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AA534222 AA632632 T81234
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A1831296 R53451 A1453440 AA983739 AW470873 A1348290 BE857670 D55901 Z43908 T34429 F07305 A23908 A1538118 BG201484 A1334192
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N69071 A1910707 BE219038 A1918036 BE670589 BM193515 A1338497 AA805525 AA487625 AA830336 AA749368 AW104323 A1628055 A1322332
A1272788 A1536849 AW162414 AW161823 T23854 AA610763 AA912188 AW339028 Z39946 T10224 F03171 A1205478 A1638791 F02580 F01551
AW207551 AA421030 BE246012 B1034937 B1035373 BF939581 H19984 BE867247 H26777 N55988 BF957332 H18615 R16442 BF956229
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AA677593 AA818150 AA557952
AK024780 NM_024549 AW440385 AW965502 BF477855 A1149742 BE669424 BE349941 A1376717 AA977493 AW592564 AA884111 AA865463
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AK074156 A1401548 BE002083 BE002085 BE002084 BG113650 AW580909 AA632959 BG610861 BG436183 BF438017 A1568508 A1095503
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AA975373 A1288904 A1984583 AA890325 N32562 A1358102 AW241694 A1038448 A1672071 A1018389 AA576391 AA977874 AW189392 W37448
AA612894 A1277548 H89551 A1699774 H89365 A1315805 AW579186 BC014584 BC014581 AW780125 A1672414 BE328145 AW600919 BF031308
AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW365504 BM129522
BM129822 A1127670 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 A1373653 R75904 BF979185 BF691393 BG495595
B1094458 BE706702 BG496559 BF248373 BG494800
BC015150 BM471660 BM478941 B1759769 B1094332 BE005819 BE005834 BM023432 BE179013 BE675522 A1680275 AA515794 AA256503
F01634 AF002990 BG288697 A1091615 AW002917 A1631085 AW182664 BE501232 A1922188 BF838783 A1631078 BE464544 A1376986 AW503774
AA424131 AW511849 AA872189 BF084885 A1432024 A1491908 BF197906 AA580599 A1274418 AW269225 AW058288 A1611346 AA236200
C00417 BE669699 A1468149 BM460137 A1685282 A1902714 BG990066 BF894391 T83393 T84298 BF809721 BE925494 AV755948 BF928512
BF894494 BF808842 AA256710 BF894347 BE928708 H06072 AA199607 B1859300 A1983233 A1521122 BE168896 BE302846 X76770 BC000927
NM_032632 BG707103 BG913857 BG613824 BG613257 BM431307 B1561132 B1461428 BE389811 BE391509 BE164646 AA746371 AV750611
BE175813 AA332040 BG200997 BG485576 AL043706 AV716994 BF903156 AW820369 A132824 BF941136 BE543211 AA521432 AW837568
BF809623 AW814570 AU129338 AW880782 AA371070 BG615427 B1667976 B1598706 B1599341 BE869166 BG502432 NM_020144 AF218840
B1461108 B1562235 B1462594 B1458753 BF195581 BF832738 BE890146 A1678629 A135238 AU129571 AW500045 AA382478 AW502738
B1561031 BE280153 BF087226 BM480024 AW804395 BE707050 R72668 BF038881 BF895070 BG036594 BE551809 BF326901 BG286526
AW962888 BE544939 AW363399
AK057015 A1026834 BE857936 AA149091 A1742972 AW439172 A1253168 AA255613 BF513175 A1005006 T03406 AW338149 AA836442
AA420630 R88566 A1611672 AA433916 AA442855 BF063008 AA812568 A1889706 AA715313 AA768539 AA767620 AA665471 AA404380
AA656512 BF056442 AA706388 A1650676 AA627448 A1141769 H78227 AW901852 H78221 BE701982 BF689273 AA397464 N33072 R60218
AW968247 H14833 AA768305 AA043348 R56470 BF739832 R51827 A474963 BG494574 AA149090 BF238154 A1082210 BE000129 BF734513
R41964 H21055 R85253 R17705 R40844 BF790218 BG388356 BF003037 AA703138 AA377348 W24822
AK056051 A1971258 A1681134 AU146134 A1803300 AA917325 AA923663 BF895058 A1304442 A167464 A1284188 AA054272 AA829262 A1351910
T90930 A1886230 U70056 AU119916 BF446537 BE503207 BE502849 A1698102 AA258553 AV718529 AV719917 BF724133 B1438668 A1804000
BE349103 A1912294 BE645117 AA227954 AA446520 AA879147 AA281770 AW135872 AA807907 A1435989 A1339526 A1383274 AA418512
BE771804 BF894509 AA455093 A1379061 A1150855 BF769906 R17298 AU138740 BF808607 BE674533 AV700132 AA227789 AA253099
AW975199 AA935418 T74315 F12666 AA022923 T89028 AA258606 W26406 BE838620 AV700706 AA101321 R41382 H14479 AA253044 R54810
R42784 R44804 R41278
A1525877 AA489525 AW088177

5	419543	251903_1	AJ018087 AA244170 AA244355
	455657	1490185_1	BE065209 BE065364 BE065110 BE065111
	414405	112689_1	AL047596 AA393792 AJ670731 AJ037957 AW874364 AJ038137 N62286 AJ241379 BE501096 AW090696 AJ927369 AJ669226 AJ369437 AJ317075
			AW612409 AJ686711 AJ183289 AA477717 AJ076122 AA635190 AA700984 AA781508 D81020 BF575223 AJ356183 D79312 AJ375558 H61111
			BG283489 BE090666 BE090664 BE090662 H26545
	409010	10331_1	AL575207 AL551714 BM014781 BG542863 BG771232 AA249722 AJ377511 AJ770155 AA716665 BG003427 AA810811 AA442760 AA128610
			AA059411 AJ796263 AJ494075 AJ572127 AA420992 BF436083 AJ648675 AA878813 BJ488614 BG700886 AA128609 AV702879 AA731146
			AJ580336 AJ373224 AA919169 AJ758175 AA976350 BG701414 BF057794 AW135598 AA062583 BJ549631 AJ185077 AA933879 AW024454
10			AA193289 AA045194 BG928396 BE856883 BF435859 AA186423 AW237471 R99289 D61992 BE856637 BF368270 AA194235 N51319 AA383499
			N63065 BG548812 BF027898 BG779448
	411962	2307710_1	AA099050 AA099526 T47733
	434982	121871_1	AW975084 T90204 AA658177
	432676	3503_22	AJ187366 AA618478 AA558869
	437838	2512601_1	AJ308202 AJ307229 AA769348
15	446019	658727_1	AJ362520 D25917 AJ707084 AJ742347 AW269789 AJ270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214
			AW362225 AW362228 AL119827
	454042	30254_1	AJ420458 AJ018523 AA708886 BF949633 AL119553 BF945960 AJ081305 AA041432 AJ921013 AJ684910 AJ654847 AW874199 AJ206120
			AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BJ040435 BF931989 BJ600000 AV722350
			V27787 H45331 BJ549761 R53955 BJ549855 BG991583 BJ491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199
20			AJ431587 BE858679 AW292267 AJ421678 AA041195 BE466753 AJ243913 AJ358894 AW137298 AJ366468 N64350 AA779107 AW025969 R49056
			AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BM93714 AJ880103 AW771447 AJ202561 AA788851 AJ944436 BF856114 H22570
	432954	2159612_1	AJ076345 AJ887648 AA572691
	446126	610_2	BF946219 BF946218 BF851494 AL536879 AA457150 AJ590194 AJ582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322
			AA336407 AA337222 AA319240 BJ026817 BJ027058 AL536880 AJ693827 AA651730 AJ701013 BM068789 AW339506 AA293021 BF891108
25			AJ458885 AW361203 AW974652 AJ761251 AJ655763 AA628063 BE047125 AW085916 AJ129587 N52070 AW172361 AA052951 AW085909
			AJ000008 AA962570 AJ371342 AJ364207 AA464514 AJ962506 AJ824603 AW376300 AA058439 AW361192 AV656660 N50282 BF820514 BF891008
			H40784 BF891112 BE708029 AW043567 AA055762
	419145	248375_1	BM456602 AV706711 BF379357 H90994 AA234435 AA558020 BF351723 AA328271 R94815 N99638 BG223375 AW973750 N59599
30	409245	3199_2	AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA381037 AA321632 N45608 AV752798 AV657116 AA296632 AJ137857
			AW467027 AJ742080 AJ624350 H58206 AA478518 AW439997 AW393556 AW393523 AJ559753 AJ808732 R66856 H01374 BJ257369 BJ259830
			AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG050578 AV654024
			BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BJ254209 BG499543 H42946 BJ059780 BJ086741 H87896 H87599 BF691752
			BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF809744 AW966003 AV714014 BJ492868 BJ495144 AA921845
35			AJ693426 AJ652147 AJ435449 N47325 AJ434429 AA573137 AJ183429 AJ829962 AJ332526 BF513937 AJ189561 AJ221962 AJ378034 AW118897
			AW665247 AW340077 N41605 AA478519 AA463875 AJ858260 AA463379 AJ292305 BE045947 AA971089 AJ125820 BG940947 AJ080245
			AA884954 AJ125702 AJ382934 AA931835 AJ358631 AW439905 AJ027833 AJ399648 AJ014533 AA347851 AA738261 N67374 N69081 AJ768667
			AA948472 AJ189214 AA293133 AJ186725 AA889214 AJ222635 BJ495143 N29605 N48812 AA769041 AJ492769 D56771 AA095911 BE222062
			D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BJ255749 BJ492848
40	437866	34267_1	H16217 H21980 H22651 H88179 H87354 H44052 H25165 H4412B
			U52054 AL581000 AA156850 AW239389 BJ358865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161
			BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960
			AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AJ866686 AJ572124 AA687333 D20160 AA812489 AU185248 AU186004
			AA158781 AJ536733 BM144850 AJ471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BJ022546 BJ021204
	458332	1139685_1	AJ000341 AJ765341 AW873274
45	459513	417837_1	AV704062 BE162284 AJ032946 BF360636
	449328	3030726_1	AJ884781 AJ652308 AJ651694 AJ638744 AJ962493
	406685	0_0	M18728
	417258	400835_1	BG116781 BJ914326 BJ030196 N58885 N63406 AV683374 N58892 BG110501 AA333708 AA359583 AW963123 N95562 N95696 N95587
50	447881	44623_1	AK074291 AW293424 BE676135 AJ832125 BE019146 BE465019 AJ761124 AA617778 AJ279232 AW575897 AJ672039 F28618 BF924261
			AA722184 BF934174 BE004328 AV749301 BE880282 BJ019798 BJ019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119
			AW814195 BE879126 AJ697926 BF594155 BE205787 BF063513 N35828 AJ948557 AJ433839 AJ379679 BG056182 AJ589094 N23123 AA588805
			AW316581 AJ080272 AJ421980 AJ493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BJ035539 BF747723
			BF171066 W01350 H05495 AJ243785 Z39622 AA887432 AJ350659 R46102
55	425481	334120_2	AL520496 AW978162 AJ610475 AJ688990 AW470054 AA609426 AJ167391 AA815231 AA368241
	440638	371165_1	BG009500 AJ376551 AA897445 T87714
	442495	928718_1	AJ184717 AW518883 AF121173
	416311	1280744_1	AA179446 AA357784 D81719 D80529 C1833
	431926	1237041_1	AW972724 AA877998 AA522631 AU185388
60	435154	126805_1	AW972063 AA668764 AA804491 AW665688 AA765069
	437908	13268_11	AJ740586 AA771806 BE500996 AW204531 AJ082424 AJ033879 BF093176 AA771764 D38676

TABLE 33C:

65

Pkey:
Ref:

Strand:
Nt_position:

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

70

Pkey	Ref	Strand	Nt_position
401403	7710966	Plus	146180-146294
408387	9256180	Plus	116229-116371,117512-117651
405268	4156151	Minus	24404-24521
406122	9144087	Minus	30940-31386
402550	7652009	Minus	80413-80673

75

80 TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific interstitial pneumonitis

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number		Unigene Title: Unigene gene title			
R1: 90th percentile of IPF AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50					
R2: 90th percentile of IPF AIs divided by 90th percentile of NSIP AIs, where the minimum value for the numerator and denominator was set to 50					
5	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
10	405443			Target Exon	9.66 7.50
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.23 3.66
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.63 3.03
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.84 2.81
15	406964	M21305		FGENES predicted novel secreted protein	4.73 5.69
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.34 4.34
	407244	M10014		fibrinogen, gamma polypeptide	4.14 5.88
	421823	N40850	Hs.28625	ESTs	4.12 1.80
20	419875	AA853410	Hs.93557	proenkephalin	3.90 2.01
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.88 2.90
	418310	AA814100	Hs.86693	ESTs	3.66 2.84
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	3.60 3.13
25	438315	R56795	Hs.82419	ESTs	3.49 3.70
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.47 1.38
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.46 3.46
	434233	AF119903	Hs.138453	hypothetical protein PRO2834	3.28 2.51
30	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.26 3.26
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	3.19 2.12
	420185	AL044056	Hs.251385	ESTs	3.18 3.01
	420195	N44348		Homo sapiens cDNA FLJ11177 fis, clone PL	3.16 3.16
35	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.08 3.18
	408221	AA912183	Hs.47447	ESTs	3.07 1.98
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.02 2.35
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.98 1.72
40	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.87 1.48
	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (f	2.80 2.66
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.78 1.65
	407938	AA905097	Hs.85050	phospholamban	2.78 2.46
45	423575	C18863	Hs.163443	intron of periostin (OSF-2os)	2.78 1.55
	446659	AI335361	Hs.226376	ESTs	2.74 1.56
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like	2.74 1.85
	437620	AW976930		ESTs	2.72 2.72
50	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.67 2.05
	416585	X54162	Hs.79386	leiomodulin 1, smooth muscle (LMOD1) (Thy	2.66 1.47
	425707	AF115402	Hs.11713	E74-like factor 5 (els domain transcript	2.66 2.66
	430712	AW044647		ESTs	2.62 2.62
55	453111	AB014598	Hs.31720	hephaestin	2.61 1.72
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.59 1.27
	414290	AI568801	Hs.71721	ESTs	2.59 1.23
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.58 2.58
60	412639	AW961284	Hs.203838	ESTs	2.58 2.29
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.57 1.74
	429757	AW452355	Hs.256037	ESTs	2.57 1.60
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57 1.00
65	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.56 1.12
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.56 1.25
	411880	AW872477		gb:hm30703.x1 NCL_CGAP_Thy4 Homo sapiens	2.54 2.54
	401645			C16001440:gb 12330704 gb AA652890.1 AF3	2.53 3.38
70	401673			C16001416:gb 12743112 ref XP_010131.2	2.47 2.83
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.46 1.18
	416316	H58721	Hs.271628	ESTs	2.42 3.44
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.40 1.69
75	451149	AL047585		RNA binding motif protein 8B	2.40 1.95
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.40 1.61
	410036	R57171	Hs.57975	caldesmon 2 (cardiac muscle)	2.40 2.40
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.39 1.27
80	405120			C4001445:gb 12697999 dbj BAB21818.1 (AB	2.38 2.38
	432224	AW189460	Hs.208358	ESTs	2.38 2.00
	418663	AK001100	Hs.41690	desmocollin 3	2.38 2.38
	412622	AW664708	Hs.171959	ESTs	2.37 1.63
85	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.37 1.52
	442767	AI017208	Hs.131149	ESTs	2.36 1.22
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.35 1.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.35 1.18
90	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.34 2.34
	444009	AI380792	Hs.135104	ESTs	2.34 2.07
	435143	R12375	Hs.194600	ESTs	2.33 1.68
	402333			Target Exon	2.33 3.15
95	429609	AF002246	Hs.210853	cell adhesion molecule with homology to	2.33 1.10
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.32 1.30
	452242	R50956	Hs.159933	glycosyltransferase	2.32 1.45
	418693	AI750878	Hs.87409	thrombospondin 1	2.32 2.32
100	428411	AW291464	Hs.10338	ESTs	2.32 1.54
	459702	AI204995		gb:an03c03.x1 StrataGene schizo brain S1	2.31 1.98
	428839	AI767758	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.31 2.49
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.31 1.32

5	422353	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.30	2.30
	456535	AW135986	Hs.257859	ESTs	2.28	2.28
	428166	AA423849	Hs.79530	M5-14 protein	2.27	1.88
	456936	M81349	Hs.1955	serum amyloid A4, constitutive	2.25	2.16
	417728	AW138437	Hs.24790	KIAA1573 protein	2.25	1.37
	453070	AK001465	Hs.31575	SEC53, endoplasmic reticulum translocon	2.24	2.42
	409159	AW673312	Hs.50848	hypothetical protein FLJ20331	2.24	2.24
	404942			splicing factor, arginine/serine-rich 9	2.24	2.64
10	410286	AI739159	Hs.51898	DKFZP586N2124 protein	2.24	2.46
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.24	1.94
	421574	AJ000152	Hs.105924	defensin, beta 2	2.23	1.36
	418005	AI185220	Hs.83164	collagen, type XV, alpha 1	2.22	1.37
	421948	L42583	Hs.334309	keratin 6A	2.20	2.20
15	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.19	1.61
	417563	AA203701		gb:zx52a10.r1 Soares fetal_liver_spleen_	2.18	2.40
	431089	BE041395		ESTs, Weakly similar to unknown protein	2.16	2.46
	447333	BE090580	Hs.70704	hypothetical protein dJ61688.3	2.16	2.00
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.16	1.26
20	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.16	1.99
	403362			NM_001615: Homo sapiens actin, gamma 2,	2.16	1.61
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11345 fis, clone PL	2.15	2.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.15	2.24
	402641			C1002296: g 5677817 ref NP_033126.1 rep	2.14	2.14
25	418236	AW994005	Hs.337534	ESTs	2.14	2.14
	413059	BE151498		gb:RCO-HT0295-291199-031-E11 HT0295 Homo	2.14	2.14
	423437	W07088	Hs.293685	ESTs	2.14	2.14
	426398	AI249368	Hs.98558	ESTs	2.14	2.14
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.12	1.43
30	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	2.12	1.93
	436391	AJ227892	Hs.146274	ESTs	2.12	2.12
	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.11	2.17
	407443	AF227138		gb:Homo sapiens candidate taste receptor	2.11	2.36
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.10	1.29
35	409432	D49372	Hs.64460	small Inducible cytokine subfamily A (Cy	2.10	2.10
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	2.10	2.00
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.10	1.37
	450271	AI693900	Hs.200920	ESTs	2.09	2.34
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.09	1.40
40	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	2.08	2.00
	405600			C12001673: g 9631264 ref NP_048045.1 or	2.07	1.97
	434654	AI826942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	2.07	2.52
	439261	AI126020	Hs.145674	basic transcription factor 3	2.05	1.45
	421515	Y11339	Hs.105352	GaNAc alpha-2, 6-sialyltransferase I, I	2.04	2.04
45	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.04	2.04
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	2.02	1.33
	412505	AA974491	Hs.21734	ESTs	2.02	2.02
	443180	R15875	Hs.258576	claudin 12	2.02	2.02
	431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.02	2.02
50	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	2.02	2.17
	452571	W31518	Hs.34665	ESTs	2.02	2.09
	405061			Target Exon	2.01	2.52
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.01	2.41
	402327			Target Exon	2.00	2.44
55	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.00	2.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.00	2.00
	438634	AW340400	Hs.126728	ESTs	1.99	2.43
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	1.97	1.41
	423961	D13666	Hs.136348	perlestin(GSF-2os)	1.96	1.48
60	430397	AI924533	Hs.105607	bicarbonate transporter related protein	1.96	1.31
	411010	AW813339		gb:MR3-ST0192-101299-013-c05 ST0192 Homo	1.96	2.73
	439628	W81007	Hs.58628	ESTs	1.96	1.28
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.96	1.58
	431726	NM_015361	Hs.258053	KIAA0029 protein	1.95	1.72
65	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.95	1.87
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	1.95	1.06
	417562	AW888754	Hs.134126	crystallin, gamma S	1.95	2.14
	424480	AA341442	Hs.205299	ESTs	1.94	1.94
	404342			C7002192: g 7299207 gb AAF54404.1 (AE0	1.92	1.32
70	443320	AI051607	Hs.16335	ESTs	1.91	2.18
	449780	AA443241		ribosomal protein L44	1.90	1.76
	423337	NM_004655	Hs.127337	xdn 2 (conductin, axil)	1.89	2.16
	434416	AA805903	Hs.59498	cell division cycle 2-like 5 (cholineste	1.89	2.04
	457505	AL044659	Hs.43791	ESTs	1.89	2.34
75	425912	AL137629	Hs.162189	serine/threonine kinase with Dbl- and pl	1.88	1.26
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	1.88	1.88
	428231	U17989	Hs.183105	nuclear autoantigen	1.88	1.88
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	1.88	1.88
	404429			Target Exon	1.88	2.18
80	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	1.88	3.04
	406641	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	1.86	2.57
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.86	1.48
	454565	BE141231		gb:MR0-HT0075-081199-003-a09 HT0075 Homo	1.86	1.21
	415115	AA214228	Hs.127751	hypothetical protein	1.85	1.23

5	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	1.85	1.45
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	1.84	1.44
	403344			NM_000341: Homo sapiens solute carrier fa	1.84	1.84
	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	1.84	2.33
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.84	2.02
10	401593			Target Exon	1.83	2.34
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	1.83	2.12
	406461			hypothetical protein, clone 24751	1.83	2.01
	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.83	1.26
	400609			C10001147:gil12698926[gb]AAK01739.1[AF33	1.82	2.08
15	422095	A1868872	Hs.282804	hypothetical protein FLJ22704	1.81	1.14
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.81	1.22
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	1.81	2.10
	426521	AF161445	Hs.170219	hypothetical protein	1.81	2.08
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.81	1.64
20	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	1.80	1.34
	439606	W79123	Hs.58551	G protein-coupled receptor 87	1.80	1.80
	459189	AI909090		gb:IL-BT198-010499-007 BT198 Homo sapien	1.80	1.80
	412429	AV650262	Hs.75765	GRO2 oncogene	1.80	2.55
	402674			Target Exon	1.80	3.41
25	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.79	1.57
	454824	AW833646		gb:QV4-TT0008-161199-033-d09 TT0008 Homo	1.78	1.94
	401677			BAI1-associated protein 3	1.78	2.28
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	1.78	1.53
	430028	BE564110	Hs.227750	Target CAT	1.78	1.59
30	445988	BE007663	Hs.13503	inactivation escape 2	1.78	2.10
	452272	AW292249	Hs.252739	hypothetical protein DKFZp434P0316	1.78	2.08
	418205	L21715	Hs.83760	troponin I, skeletal, fast	1.78	2.70
	400425	AY004252	Hs.287385	PR domain containing 12	1.77	2.02
	400419	AF084545		Target	1.77	2.67
35	447169	AJ989803	Hs.157289	ESTs	1.77	2.21
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	1.77	2.12
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1.76	2.54
	432808	NM_015985	Hs.278973	angiopoietin-3	1.76	1.76
	437400	AB011542	Hs.5599	EGF-like-domain, multiple 5	1.75	2.00
40	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.75	1.47
	444986	AJ204197		ESTs	1.75	2.48
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	1.74	1.69
	413524	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.74	1.74
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	1.74	2.26
45	405579			C22000151:gil16806921[ref]NP_004165.1[so	1.74	2.12
	405797			CX001015:gil11322384[emb]CAC16687.1[(AJ	1.73	2.66
	405159			ENSP00000243337*:C DNA FLJ13984 fis, clone	1.73	2.01
	450569	AW192334	Hs.38218	ESTs	1.73	2.08
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.73	1.24
50	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	1.73	2.52
	454231	AW450669	Hs.45068	hypothetical protein DKFZp434I143	1.73	1.64
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxin)	1.72	1.37
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.72	1.72
	456034	AW450979		gb:UL-H-B13-ala-a-12-0-UL.s1 NCI_CGAP_Su	1.72	1.34
55	451862	H09260	Hs.32333	ESTs	1.71	2.16
	403520			Target Exon	1.71	1.39
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	1.71	2.26
	426603	AA382291		gb:EST95683 Testis 1 Homo sapiens cDNA 5	1.70	1.70
	418387	R18085	Hs.22279	gb:yg16b12.r1 Soares infant brain 1N1B H	1.70	1.70
60	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 6830	1.70	1.87
	402538			C1001634:gil12621136[ref]NP_075245.1[Ba	1.69	1.57
	414844	AA296874	Hs.77494	deoxyguanosine kinase	1.69	2.06
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.69	1.63
	446553	AB021179	Hs.15299	HMBA-inducible	1.68	2.02
65	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	1.68	2.12
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	1.68	2.03
	433930	AA620338		ESTs	1.68	2.28
	404151			Target Exon	1.68	1.80
	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	1.67	2.18
70	430070	AF197927	Hs.231967	ALL 1 fused gene from 5q31	1.66	2.16
	400496			ENSP00000224716*:GTP-binding protein SAR	1.66	2.13
	413464	AL121500		ESTs	1.66	2.03
	411188	BE161168		gb:PM0-HT0425-170100-002-a10 HT0425 Homo	1.66	2.12
	446281	H69416	Hs.14606	hypothetical protein FLJ20271	1.65	2.28
75	443282	T47764	Hs.132917	ESTs	1.65	2.04
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.65	1.67
	453355	AW295374	Hs.31412	myopodin	1.65	1.66
	432375	BE538069	Hs.2952	S100 calcium-binding protein P	1.65	1.54
	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	1.65	2.04
80	410295	AA741357		nidogen (enactin)	1.64	2.30
	437767	AA830103	Hs.293331	ESTs	1.64	1.26
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	1.64	3.38
	450795	AW173371	Hs.60435	ESTs	1.64	1.64
	421847	NM_014717	Hs.108884	KIAA0390 gene product	1.64	2.75
	403010			C21000152:gil16226483[sp]Q52118[MO3_ERWS	1.64	2.03
	406387			Target Exon	1.64	1.78
	440423	AW293995	Hs.192277	ESTs	1.63	2.05

	444381	BE387335	Hs.283713	hypothetical protein BC014245	1.63	2.07
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.63	1.65
	442424	AI342715	Hs.129569	ESTs, Moderately similar to B34037 hypot	1.62	2.40
5	402885			Target Exon	1.62	1.18
	408788	AA773187	Hs.294027	ESTs	1.62	1.59
	448719	AA033627	Hs.21858	trinucleotide repeat containing 3	1.62	1.63
	414584	AW630023	Hs.76893	3-hydroxybutyrate dehydrogenase (heart,	1.62	2.10
	406838	AA827569	Hs.153	ribosomal protein L7	1.61	1.41
10	441600	AA939347	Hs.127223	Homo sapiens cysteine knot protein (ZSIG	1.61	2.32
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	1.60	2.37
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.60	1.23
	432331	W37862	Hs.274368	MSTP032 protein	1.60	1.23
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.60	1.69
	400279			NM_004581"Homo sapiens Rab geranylgeran	1.60	1.56
15	437865	AI472305	Hs.19565	ESTs	1.60	2.42
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	1.60	1.29
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	1.60	2.11
	410684	AA088500	Hs.170298	ESTs	1.59	1.46
20	433149	BE257672	Hs.42949	hypothetical protein HES6	1.59	2.22
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	1.59	1.41
	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.59	1.26
	427654	AA410183	Hs.137475	ESTs	1.59	2.83
	411662	D60541	Hs.285519	Homo sapiens cDNA FLJ11904 fis, clone HE	1.59	2.18
25	440383	AA884208	Hs.30484	ESTs	1.58	2.19
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.58	1.58
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.58	1.47
	407857	AI928445	Hs.92254	synaptotagmin-like 2	1.58	1.51
	411573	AB029000	Hs.70823	KIAA1077 protein	1.57	1.29
30	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	1.57	1.17
	428471	X57348	Hs.184510	stratifin	1.57	1.55
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	1.57	1.19
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.57	2.12
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.57	1.05
35	430469	AW603667	Hs.288742	Homo sapiens cDNA: FLJ22712 fis, clone H	1.56	1.56
	445511	AA846512		Homo sapiens cDNA FLJ14459 fis, clone HE	1.55	2.08
	404501			nucleoside phosphorylase	1.55	2.54
	429107	AI470451	Hs.99075	ESTs	1.55	2.05
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.55	1.45
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.54	2.61
	458091	AF150286		gb:AF150286 Human mRNA from cd34 stem ce	1.54	1.54
	439280	AI125436	Hs.123654	ESTs	1.54	2.06
	428096	AW291771	Hs.42239	Homo sapiens, clone IMAGE:3868989, mRNA,	1.53	1.55
	414221	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NCL_CGAP_Su	1.53	1.39
45	451712	AA019290	Hs.110489	ESTs	1.53	1.99
	402487			Target Exon	1.53	2.02
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.53	1.29
	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.53	1.21
	410253	T51823		ESTs	1.52	2.03
50	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	1.52	1.37
	432985	T92363	Hs.178703	ESTs	1.51	1.48
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.51	1.15
	429259	AA420450	Hs.292911	Plakophilin	1.51	1.31
	429289	AI400746	Hs.62187	phosphatidylinositol glycan, class K	1.51	1.19
55	441457	AW996651	Hs.43838	ESTs	1.51	2.08
	433365	AF026944	Hs.293797	ESTs	1.51	2.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.51	1.21
	424386	BE146577	Hs.285132	ESTs	1.50	1.53
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	1.50	1.29
60	442391	AW450544	Hs.220751	ESTs	1.50	1.65
	414341	D80004	Hs.75909	KIAA0182 protein	1.50	2.10
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	1.50	2.16
	442264	AI276777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	1.50
	443878	AW292499	Hs.139709	hypothetical protein FLJ12572	1.50	1.37
65	430152	AB001325	Hs.234642	aquaporin 3	1.50	1.43
	447752	M73700	Hs.105938	lactotransferrin	1.49	0.91
	404455			opitoid receptor, kappa 1	1.49	1.36
	424106	AA412442	Hs.98132	ESTs	1.49	1.30
	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	1.49	2.02
70	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.48	1.50
	456256	AB000450	Hs.82771	vaccinia related kinase 2	1.48	1.42
	439310	AF086120	Hs.102793	ESTs	1.48	1.48
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	1.48	1.15
	437981	AA774445	Hs.145365	ESTs, Weakly similar to KIAA1397 protein	1.48	2.36
75	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.47	1.21
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.47	1.25
	453864	AW021407	Hs.21068	hypothetical protein	1.47	2.18
	401067			ENSP00000252105::CDNA FLJ12240 fis, clon	1.47	1.81
	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens c	1.47	1.99
80	402324			C19001982:gi3043638[dbj]BAA25483.1[AB	1.47	2.03
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	1.47	1.29
	457734	BE394365	Hs.38750	hypothetical protein FLJ11526	1.47	2.26
	402013			Target Exon	1.46	2.42
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	1.46	2.09

5	430920	U96402	Hs.248132	goosecoid-like	1.46	2.46
	409368	AA071059		gb:zms56a10.r1 Stratogene neuroepithelium	1.46	2.02
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.46	1.43
	427719	AJ393122	Hs.134726	ESTs	1.46	1.46
	433430	AJ863735		ESTs	1.46	1.15
10	423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	1.46	2.36
	444083	AJ123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.45	2.29
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypothe	1.45	1.50
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	1.45	1.17
	456664	AW963354	Hs.334409	metallothionein 1G	1.45	2.20
15	438158	AJ796556	Hs.187884	ESTs	1.45	1.18
	409883	AW452419	Hs.295098	ESTs	1.45	2.00
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.45	1.27
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.45	1.36
	457462	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	1.45	2.08
20	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	1.44	1.28
	401116			Target Exon	1.44	2.19
	419618	AA528295		gb:nh26e06.s1 NCI_CGAP_Py3 Homo sapiens	1.44	2.30
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	1.44	2.03
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.43	1.48
25	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.43	1.51
	418742	AW451197	Hs.113418	ESTs	1.43	1.24
	418335	R63267	Hs.28399	ESTs	1.43	1.14
	408404	AW192518		gb:cd45h08.x1 NCI_CGAP_Pan1 Homo sapiens	1.43	2.08
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	1.43	2.29
30	431846	BE019924	Hs.271580	uroplakin 1B	1.43	2.12
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	1.43	2.00
	449925	AJ342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	1.43	1.33
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (1.43	1.10
	454843	AW834536	Hs.258549	gb:MF2-TT0014-241199-012-06 TT0014 Homo	1.43	1.55
35	410281	AF076612	Hs.166186	Homo sapiens clone Z3928 mRNA sequence	1.43	1.38
	402998			NM_002463*:Homo sapiens myxovirus (Influ	1.42	2.16
	443709	AJ082692	Hs.134662	ESTs	1.42	2.22
	435259	AA152106	Hs.4859	cyclin L ania-5a	1.42	2.01
	454407	AW578420	Hs.118843	gb:RC1-CT0249-120100-022-b04 CT0249 Homo	1.42	1.76
40	453359	AA448787	Hs.24872	ESTs	1.42	1.33
	434126	AJ138589	Hs.118205	ESTs	1.41	2.06
	417944	AJ077196	Hs.82985	collagen, type V, alpha 2	1.41	1.46
	442316	Z75331	Hs.8217	stromal antigen 2	1.41	2.20
	438330	AW450572	Hs.257316	ESTs	1.41	2.20
45	410935	BE067395	Hs.66881	dynlcn, cytoplasmic, intermediate polype	1.41	2.02
	455885	BE153524		gb:PMO-HT0339-241199-002-C03 HT0339 Homo	1.41	1.33
	405550			C7001981*:gil565157[gb]AAB31881.1 T-cel	1.41	1.24
	451385	AA017656		gb:za39h01.r1 Soares retina N2b4HR Homo	1.41	1.99
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	1.40	2.64
50	431022	AA490815	Hs.208351	ESTs	1.40	1.26
	439781	AB845538		glial cells missing (Drosophila) homolog	1.40	2.72
	429379	NM_014840	Hs.200598	KIAA0537 gene product	1.40	1.05
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	1.40	1.26
	430702	U56979	Hs.278568	H factor 1 (complement)	1.39	1.18
55	451331	AK002039		Homo sapiens cDNA FLJ11177 fis, clone PL	1.39	1.26
	459198	AJ086347	Hs.151138	ESTs	1.39	1.22
	442344	AJ022925	Hs.79368	epithelial membrane protein 1	1.39	1.35
	402917			ENSP00000202587*:Bicarbonate transporter	1.39	1.44
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	1.39	2.08
60	437158	AW090198		KIAA1150 protein	1.38	2.07
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	1.38	1.24
	433911	AJ923092	Hs.8899	ESTs	1.38	2.15
	402504			C1003823*:gil4826521[emb]CAB42853.1 (AL	1.38	1.38
	409465	AW393810	Hs.78054	gb:QV4-TT0008-251099-016-e11 TT0008 Homo	1.37	2.22
65	449426	T92251	Hs.198882	ESTs	1.37	2.38
	405491			Target Exon	1.37	2.74
	406685	M18728		gb:Human nonspecific crossreacting antig	1.37	1.34
	442410	AW996503	Hs.197680	ESTs	1.37	1.56
	407701	AW375009	Hs.164407	ESTs	1.36	2.02
70	400818			Target Exon	1.36	2.10
	406475			C15000508*:gil2558825[gb]AAC53387.1 (AF	1.36	2.78
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.36	1.41
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	1.36	2.20
	444195	AB002351	Hs.10587	KIAA0353 protein	1.35	0.94
75	447918	AJ129320	Hs.115175	ESTs, Highly similar to JCS818 gamma-act	1.35	1.22
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	1.35	1.40
	412992	AJ423369	Hs.75111	protease, serine, 11 (IGF binding)	1.35	1.24
	401025			NM_004055*:Homo sapiens catpain 5 (CAPN5	1.35	1.30
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	1.34	2.12
80	425308	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.34	1.02
	402308			Target Exon	1.34	1.21
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	1.34	1.40
	407242	M18728		gb:Human nonspecific crossreacting antig	1.34	1.22
	410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.34	2.05
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretogloblin, fa	1.34	1.12
	431254	NM_006069	Hs.251385	murine retrovirus integration site 1 hom	1.33	1.21
	405213			Target Exon	1.33	2.03

5	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.33	1.05
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	1.33	2.09
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.33	1.32
	443604	C03577	Hs.5615	myosin regulatory light chain 2, smooth	1.33	1.18
	430385	AA113437		N-myc downstream-regulated gene 3	1.32	1.48
10	447731	AA373527	Hs.19385	CGI-58 protein	1.32	2.22
	400740			hypothetical protein FLJ14280	1.32	2.01
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	1.32	1.32
	440274	R24595	Hs.7122	scrapie responsive protein 1	1.32	1.32
	406867	AA157857	Hs.182265	keratin 19	1.32	1.42
15	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosophila)	1.32	2.30
	443144	BE245335		hypothetical protein MGC14797	1.32	2.03
	432810	AA863400		ESTs	1.32	4.01
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	1.31	1.24
	424075	AI807320	Hs.227830	RE1-silencing transcription factor	1.31	2.17
20	440099	AL080058	Hs.6909	DKFZP584G202 protein	1.31	1.53
	426957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	1.31	1.31
	438874	H02780		gbv41a11.1 r1 Soares placenta Nb2HP Homo	1.31	2.03
	402825			Target Exon	1.31	1.24
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos)	1.31	1.45
25	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.31	1.19
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	1.31	1.12
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse l	1.30	2.06
	407409	AF060168		gb:Homo sapiens AS10 protein mRNA, partial	1.30	2.16
	400221			NM_002082:Homo sapiens G protein-coupled	1.30	2.02
30	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.30	2.44
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	1.30	1.19
	441591	AF055992	Hs.183	Duffy blood group	1.29	1.03
	405973			Target Exon	1.29	1.32
	424604	AW865388	Hs.151076	KIAA1243 protein	1.29	0.92
35	410899	AW809716		gb:MR4-ST0124-241199-025-h09 ST0124 Homo	1.29	2.06
	405818			CX001073.gi 4176497 emb CAA20116.1 (AL0	1.29	2.05
	402621			Target Exon	1.29	3.06
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	1.28	2.35
	431890	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subunit)	1.28	1.44
40	453331	AI240865		ESTs	1.28	2.36
	439791	H77774	Hs.35755	ESTs	1.28	2.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.28	3.00
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	1.28	1.28
	446526	H89616		Homo sapiens cDNA FLJ13357 fis, clone PL	1.28	1.28
45	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	1.28	1.28
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.28	2.10
	407711	AI085846	Hs.25522	KIAA1808 protein	1.28	1.23
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	1.28	1.19
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	1.27	1.24
50	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.27	2.08
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	1.27	2.05
	444418	AL034417	Hs.11169	Gene 33/Mig-6	1.27	1.98
	427809	M26380	Hs.180878	lipoprotein lipase	1.27	1.09
	414690	BE410103	Hs.12313	hypothetical protein FLJ14566	1.27	1.36
55	439919	AA970710	Hs.128064	ESTs	1.27	2.28
	401311			Target Exon	1.27	2.05
	444235	AW207346	Hs.143202	ESTs	1.27	2.00
	430858	AF007190		Homo sapiens SIB 297 intestinal mucin (M	1.26	1.23
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	1.26	2.40
60	400161			Eos Control	1.26	1.33
	444239	R57988	Hs.10706	epithelial protein lost in neoplasm beta	1.26	1.20
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptide	1.26	1.26
	441944	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA	1.26	1.12
	431142	AA852596	Hs.250641	tropomyosin 4	1.26	1.23
65	434229	R56378	Hs.181223	hypothetical protein PRO2801	1.26	2.04
	406733	AA976565	Hs.297753	vimentin	1.26	1.29
	422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.25	1.16
	424137	AA335769	Hs.16262	ESTs	1.25	1.27
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	1.24	1.50
70	424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.24	1.29
	433750	H15448	Hs.31330	Homo sapiens clone HQ0319	1.24	1.27
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.24	1.13
	438357	AI042101	Hs.294107	ESTs	1.24	2.04
	409959	BE349470		mucin 6, gastric	1.23	2.22
75	439897	NM_015310	Hs.6763	KIAA0942 protein	1.23	2.44
	421982	AF206019	Hs.110347	REV1 (yeast homolog)-like	1.23	2.14
	407207	T03651	Hs.336780	tubulin, beta polypeptide	1.23	1.32
	416956	AA810664	Hs.101660	hypothetical protein MGC5391	1.23	2.39
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev1n)	1.23	1.06
80	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	1.23	1.51
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.23	1.01
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.22	1.41
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.22	1.17
	421341	AJ243212		deleted in malignant brain tumors 1	1.22	1.09
	408850	AI624300	Hs.172928	collagen, type I, alpha 1	1.22	1.52
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	1.22	2.55
	423189	M59371	Hs.171596	EphA2	1.22	1.15

	401899		Target Exon	1.22	1.22
	403579		Target Exon	1.22	2.34
	415954	AA171850	Hs.42251	ESTs	1.22
5	429171	A1743173	Hs.169095	ESTs, Weakly similar to ARL2_HUMAN ADP-R	1.21
	444071	A1627808	Hs.110524	ESTs	1.21
	424344	AF036973	Hs.145477	HCGIV-6 protein	1.21
	434051	AF116622		gb:Homo sapiens clone FLB4217 mRNA sequ	1.21
	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.21
10	404600		Target Exon	1.21	1.29
	429751	M55210	Hs.214982	laminin, gamma 1 (formerly LAMB2)	1.21
	430392	NM_000627	Hs.241257	latent transforming growth factor beta b	1.21
	422687	AW068823	Hs.119206	insulin-like growth factor binding prote	1.21
	424855	AW204725	Hs.25560	ESTs	1.20
	416890	AA232134	Hs.190028	ESTs	1.20
15	413232	BE073258	Hs.133988	hypothetical protein FKSG28	1.20
	414154	AW205314	Hs.323060	ESTs	1.20
	416784	AA334592	Hs.79914	lumican	1.20
	410933	C15974		gb:C15974 Clontech human aorta polyA mRN	1.19
	415388	AF018081	Hs.78409	collagen, type XVIII, alpha 1	1.19
20	406731	A1559131		gb:tg31g07.x1 NCL_CGAP_U11 Homo sapiens	1.19
	447563	BE536115	Hs.160983	EST	1.19
	405531		Target Exon	1.19	2.02
	400363	NM_001403		eukaryotic translation elongation factor	1.19
25	426611	BE178050	Hs.171271	calenin (cadherin-associated protein), b	1.19
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	1.18
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.18
	413856	D13639	Hs.75586	cyclin D2	1.18
	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	1.18
30	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	1.18
	412758	Y07818	Hs.74566	dihydropyrimidinase-like 3(UU1P)	1.18
	446868	AV660737		ESTs	1.18
	417613	AV654351	Hs.82306	desmin (actin depolymerizing factor)	1.18
	405542		Target Exon	1.18	1.98
35	419908	AW971327	Hs.293315	ESTs	1.17
	434095	AA011117	Hs.3745	milk fat globule-EGF factor 8 protein	1.17
	407230	AA157857	Hs.182265	keratin 19	1.17
	448413	A1745379	Hs.42911	ESTs	1.17
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.17
40	424572	M19550	Hs.179600	2',3'-cyclic nucleotide 3' phosphodiester	1.17
	440109	AK001138	Hs.333149	hypothetical protein FLJ10276	1.17
	405131			C1002509:gi9338010(ref NP_064684.1) odo	1.17
	422354	U20982	Hs.1516	insulin-like growth factor-binding prote	1.17
	442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 fis, clone PL	1.17
45	400080		Eos Control	1.16	2.53
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	1.16
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	1.16
	429207	AA447941	Hs.123423	ESTs	1.16
	415149	X12451	Hs.78056	cathepsin L	1.16
50	400231		Eos Control	1.16	1.17
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	1.16
	422813	AV656571	Hs.121068	transmembrane 4 superfamily member 6	1.16
	439318	AW837048	Hs.6527	G protein-coupled receptor 56	1.16
	422424	A1186431	Hs.296638	prostate differentiation factor	1.16
55	432745	A1821926		gb:m178105.x5 NCL_CGAP_Pr3 Homo sapiens	1.15
	412477	AA150864		microsomal glutathione S-transferase 1	1.15
	430361	A1033965	Hs.239926	sterol-C4-methyl oxidase-like	1.15
	424512	X53002	Hs.149846	integrin, beta 5	1.15
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	1.15
60	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	1.15
	456076	BE243877		ATPase, Na ⁺ transporting, beta 3 polypep	1.15
	403028		Target Exon	1.15	2.00
	422545	X02761	Hs.287820	fibronectin 1	1.15
	412719	AW016610	Hs.816	ESTs	1.15
65	421848	X15880	Hs.108885	collagen, type VI, alpha 1	1.15
	422087	X58968	Hs.111301	matrix metalloproteinase 2 (gelatinase A	1.15
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	1.14
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	1.14
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	1.14
70	418806	AA485970	Hs.191718	ESTs	1.14
	424017	AA333789		gb:EST37925 Embryo, 9 week Homo sapiens	1.14
	422003	AA361760	Hs.296326	ESTs	1.14
	437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.14
	438367	N79688	Hs.204354	ras homolog gene family, member B	1.14
75	453152	AK001933	Hs.31945	hypothetical protein FLJ11071	1.13
	406849	AA454809	Hs.172928	collagen, type I, alpha 1	1.13
	422110	A1376736	Hs.111779	secreted protein, acidic, cysteine-rich	1.13
	425335	BE394327	Hs.296267	folistatin-like 1	1.13
	434785	BE620784	Hs.4147	translocating chain-associating membrane	1.13
80	417426	NM_002291	Hs.82124	laminin, beta 1	1.13
	452924	AW580939	Hs.97199	complement component C1q receptor	1.13
	416379	N38857	Hs.34145	ESTs	1.12
	421464	AA291553	Hs.190086	ESTs	1.12
	442420	A1024834	Hs.131729	ESTs	1.12

	405369			NM_005569*:Homo sapiens LIM domain kinas	1.12	1.99
	421730	AW449808	Hs.334534	glucosamine (N-acetyl)-6-sulfatase (Sanf	1.12	2.08
	405932			C15000305:gi 3806122 gb AAC69198.1 (AF0	1.11	2.01
5	453542	AW836724		Homo sapiens mRNA expressed only in plac	1.11	2.00
	437585	AW976857		ESTs	1.11	2.01
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.11	1.05
	449931	AW875786	Hs.25734	ESTs, Weakly similar to BING1 (H.sapiens	1.11	1.03
	407085	Z70759		gb:H.sapiens mitochondrial 16S rRNA gene	1.10	1.12
10	447191	NM_014521	Hs.17657	SH3-domain binding protein 4	1.10	1.04
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.10	1.07
	432675	A1791855	Hs.105884	ESTs	1.10	2.30
	432731	R31178	Hs.287820	fibronectin 1	1.09	2.12
	430763	AA485468		DNA fragmentation factor, 45 kD, alpha p	1.09	2.10
15	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	1.09	1.04
	405156			NM_003213*:Homo sapiens TEA domain famil	1.09	2.19
	409031	AA376836		ESTs	1.09	2.22
	422608	AW160644	Hs.118695	potassium voltage-gated channel, subfam	1.09	2.26
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.09	1.28
20	410577	X91911	Hs.64639	glioma pathogenesis-related protein	1.08	2.64
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.07	1.02
	452219	AA024860	Hs.61224	ESTs	1.07	2.08
	430108	AA465294		ESTs	1.07	2.11
	402174			Target Exon	1.07	2.11
25	416952	A1767736	Hs.290070	gelsolin (amyloidosis, Finnish type)	1.07	1.00
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	1.07	1.13
	442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.07	2.21
	442310	AF033199	Hs.8198	zinc finger protein 204	1.06	2.04
	405538			NM_005805:Homo sapiens 26S proteasome-as	1.06	2.20
30	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.06	1.06
	423017	AW18761	Hs.227948	serine (or cysteine) proteinase inhibito	1.06	1.06
	425371	D49441	Hs.155981	mesothelin	1.06	1.27
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	1.06	2.37
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.06	1.05
35	409407	AW987370	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.05	2.00
	406109			Target Exon	1.05	2.04
	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.05	2.67
	403162			C2000231*:gi 9802031 gb AAF99597.1 AF239	1.05	2.07
40	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	1.05	1.07
	407225	J04617		eukaryotic translation elongation factor	1.05	1.02
	416955	AW889150	Hs.80595	NM_004552*:Homo sapiens NADH dehydrogena	1.05	1.10
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	1.04	2.12
	410276	A1554545		angiopoietin-2	1.04	1.04
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.04	1.04
45	406712	M31212	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.03	1.05
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	1.03	1.10
	452082	N51905	Hs.125133	hypothetical protein FLJ22501	1.03	2.01
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	1.03	2.24
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	1.02	1.00
50	408339	R97502	Hs.30443	sentrin/SUMO-specific protease	1.02	2.19
	400247			Eos Control	1.02	2.04
	430030	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	1.01	1.01
	442275	AW449467	Hs.54795	ESTs	1.01	1.04
	406786	AW161678	Hs.111334	ferritin, light polypeptide	1.01	1.06
55	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!	1.01	2.11
	428043	T92248	Hs.2240	uteroglobin	1.00	1.06
	408722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.02
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	2.16
	450724	R55428		gb:J79505.r1 Soares breast 2NblBst Homo	1.00	0.99
60	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	1.00	1.08
	432077	AL134685		gb:DKFZp547M126_r1 547 (synonym: hibr1)	1.00	2.05
	427687	AW003887	Hs.1570	histamine receptor H1	1.00	1.00
	435256	AF193766	Hs.13872	cytokine-like protein C17	1.00	1.00
	420026	A1831190	Hs.166676	ESTs	1.00	1.00
65	455128	AW861555	Hs.314372	EST	1.00	1.00
	410685	AA497117	Hs.58893	ESTs, Moderately similar to ALU1_HUMAN A	1.00	1.00
	401404			Target Exon	1.00	1.00
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	1.00	1.00
70	443458	R05385	Hs.143509	hypothetical protein FLJ21924	1.00	1.00
	452744	A1267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	1.00	1.00
	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	1.00	1.00
	447947	N33033	Hs.270215	ESTs	1.00	1.00
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	1.00	1.00
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	1.00	1.00
75	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	1.00	1.00
	444963	A1916973	Hs.213603	ESTs	1.00	1.00
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.00	1.00
	442849	R10099	Hs.269805	ESTs	1.00	1.00
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	1.00	1.00
80	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	1.00	1.00
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	1.00	1.00
	459045	N69101	Hs.40730	ESTs	1.00	1.00
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	1.00	1.00
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	1.00	1.00

5	429932	AI095005	Hs.21586	ESTs	1.00	1.00
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	1.00
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	1.00	1.00
	431374	BE258532	Hs.251871	CTP synthase	1.00	1.00
	443162	T49951	Hs.9029	DKFZP434G032 protein	1.00	1.00
	432128	AA127221	Hs.296502	ESTs	0.99	2.33
	451838	AW005866	Hs.193969	ESTs	0.98	3.26
	438414	AA806794	Hs.131511	ESTs	0.97	3.61
10	435872	AA701357	Hs.192759	ESTs	0.97	0.96
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.97	1.08
	424001	W67883	Hs.137476	paternally expressed 10	0.96	2.25
	418869	AW516565		gbxq01d05.x1 Soares_NHCEC_cervical_tumo	0.96	2.07
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	0.94	2.18
15	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	0.94	1.31
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	0.94	2.12
	432093	H26383		gb:yf52c03.r1 Soares breast 3NbHBst Homo	0.94	2.19
	452239	AW379378		protein tyrosine phosphatase, receptor I	0.94	0.79
	403167			Target Exon	0.94	2.06
20	402209			Target Exon	0.92	2.04
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.92	0.74
	424090	X99599	Hs.139262	XIAP associated factor-1	0.91	2.11
	432816	N38913	Hs.221575	ESTs	0.91	2.15
	451779	AW968616	Hs.296234	ESTs, Weakly similar to T31613 hypotheti	0.91	2.14
25	406851	AA609784		major histocompatibility complex, class	0.89	1.04
	427698	AW972594	Hs.335499	ESTs	0.89	0.90
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	0.88	2.42
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.87	1.14
	426024	Z43405	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	0.87	2.04
30	400986			NM_024085: Homo sapiens hypothetical pro	0.87	2.10
	430353	AW952337		citrate synthase	0.86	2.28
	404975			uncharacterized hypothalamus protein HT0	0.86	2.50
	406673	M34996	Hs.198253	major histocompatibility complex, class	0.86	1.94
	431323	AW970623		gb:EST382705 MAGE resequences, MAGK Homo	0.80	2.08
35	404926			Target Exon	0.79	2.01
	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	0.77	0.86
	437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	2.10
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	0.76	2.66
	406646	M33600	Hs.308026	major histocompatibility complex, class	0.76	1.09
40	442195	NM_001430		endothelial PAS domain protein 1	0.76	2.00
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.76	0.78
	413916	N49813	Hs.75615	apolipoprotein C-II	0.73	2.06
	453716	AA037675	Hs.152675	ESTs	0.73	2.10
	437802	AI475995	Hs.122910	ESTs	0.70	2.08
45	422282	AF019225	Hs.114309	apolipoprotein L	0.68	2.95
	410361	BE391804	Hs.62661	guanylate binding protein 1, Interferon-	0.54	2.11
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	0.53	0.53

TABLE 34B:

50	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
55	Pkey	CAT Number	Accession
	442006	1239046_1	AW975183 AA973583 AI365103 AI699495 AI301787
	420195	28714_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676 AA455877 N65571 AA999864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669636 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645
60	437620	9575_20	AW976930 AW292808 AW451796 BF514112 AI806378 AI658903 AI769457 AW593455 AI625525 AI538551 AI660509 AA761825 AA973287 AA861483 W73065 AI735361 W60499 W76653 BG959557 AW044647 AI670953 AI656180 AA484715 AI659205 BF923472
65	430712	301999_1	BE088101 T05990 AW872477
	411880	1139083_1	AF231512 AW300273 BG779015 AW510935 AI989816 AA137069 AI748876 AW150861 AI862628 AI805872 AI675382 BE855437 AW044703 AI677769 AA886718 AI753144 AA626885 AI018092 AI263010 AW026173 BE221138 AA256268 AW571932 AW276137 AI634216 AW296259 AA977716 AI302589 AA348340 AI720838 AI311733 AA015867 N73713 AL047586 AW840354 AA256196 AW840357 AW840504 T35664 Z36755 AW954421 AA247424 AI056930 T31380 BI910428 H88489 BG675223 AA443427 BE879501 AA478530 R72977 AA298568 BF792417 AA356982 BF922499 BE764808 BE565636 BF903986 BF331881 N42207 BG623760 BG611090 BF735387 BE697757 BE697755 BE718853 N78560 AI984095 AA137140 AA053711 N59865 AI078134 AA643796 T57803 AA018642 N68799 AI004600 BG896323 BF895104 N73684 N73806 N73811 AW900287 AA018641
70	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	417563	2243443_1	AA203701 R86895
75	431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826
	455797	1511159_1	BE091833 BE091874 BE091871
	413059	1488711_1	BE063078 BE151503 BE151498
	417430	40161_2	AW872732 AW827432 AA199662 AA610519 R54983
	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
80	458208	45807_4	AI990640 AI380016 BM273298 BM273060
	457741	120741_1	BI017968 BE044740 BI017768 AW827360 BF380597 BI017970 BF746974 BF380582 BF380592 BF908552 BF907924 BF380784 BF380651 BF380634 BE166581 BE161439 BF908606 BI017961 BE044718 AW827623 BF907758 BI017967 AW827621 AA653908 BI017765 BI017955 BI017960 BI017798

	411010	1066474_1	AW813381 AW816094 AW813357 AW814469 AW813293 AW816099 AW813295 AW813425 AW813331 AW813325 AW813351 AW813427
	449780	31099_2	AW813339
5			BG721806 BG623574 AA367501 BG436403 BG619828 BG570704 BF086115 BF085118 R78932 BG620860 BG571920 BF997723 AA368244
			BG620631 BG621967 BG435818 BG620442 BG621518 H12650 BG573175 H61600 R67494 H01715 D78811 BG435953 BF107266 D79043 R67255
			H01310 BG570941 BG570693 R21776 AA327133 R32578 R30775 BG570963 T86946 H61601 W85279 BF991104 R21732 BF990905 BG622861
			BE928694 A1090290 BE929277 BE929284 AA367783 AA082581 D78839 H78318 N91085 BE929344 D63217 BE929334 H53536 R80360 H54070
			C17064 AW962470 R00900 BG619598 BG623946 H94918 BE929345 AA004267 BF957177 BG620685 BF086421 T87029 C17044 H60972
			BG573514 AA131924 D78838 BG003560 C18615 W86323 R09737 R02529 AA367502
10	406641	0_0	AJ235667 AJ235668 AJ235669 AJ235670
	454565	1061836_1	BE141160 BE141231 BE141793 BE141791 BE141167 BE141807 BE141806 BE141805 AW807591 AW807590 AW807585 AW807583 BE141803
			AW845918 BE141207 BE141168
	455657	1490185_1	BE065209 BE065364 BE065110 BE065111
	459189	MH1945_5	AV683451 AK057494 BG718853 BM152866 BG390826 BE709644 A1864727 B1045181 B1459837 A1909102 A1909090 BG722507 B1023834
15	454824	1073655_1	AW833783 AW833646 AW833525 AW833351 AW833526 AW833825
	444386	704733_1	AW268472 A1204197 AW592537
	413524	1518893_1	BE145894 BE145837 BM263472
	422259	140437_1	BF821471 AW795791 BF844843 BF821371 AA307584 AW795790 BF833724 BE154067 BE084709
	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
20	426603	1299162_1	AA994657 AA382291
	456235	1979764_1	AA203637 AA832266 H67452
	433930	19851_15	AW873618 AA620338
	413464	415532_1	AL527514 A1732432 AA133309 A1225224 AV700997 BF589361 AW291763 AL121500 AA129708
	411188	1072487_1	AW821260 BE162466 BE161168
25	410295	2817_1	BG402852 BG545066 AA150252 AL038760 AA452480 A1033256 W68776 W93372 N31248 A1052219 A1367635 W69374 N88610 R58194 B1524854
			B1497111 BF940043 A129268 A1359758 A1056480 AA121421 A1042150 AW449003 A1418180 A1419420 A1356058 BF832243 A1349330 A1359448
			W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268
			A1366371 A1989381 A131425 A1147483 A1311537 AW338638 A141649 A1709414 A1817177 AA780884 A1333805 AA045312 A1623918 A1349421
			W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 A1869152 N93462 N71889 A1537432 R71628
			AA303089 A1498550 T60941 AV705417 AW067848 A150677 AW338118 A1336313 AA826258 A1139518 AA662948 AA902723 A1970175 W68682
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			A1862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547
			N21313 BF674610 H02874 AW975323 R18904 AA328030 AA054671 R79546 BF832310 A1249109
	400279	2140_1	Y08200 NM_004581 BC003093 BE733834 B1753321 BG773890 BF091906 B1917541 A1023762 AA587230 BF435086 A1264282 A1687392 A1810536
35			AW589886 A1244419 AA749261 AA535435 AW205689 A1765770 A1765431 C02465 AW305347 A1818456 AA322111 AW381845 AW381829
			AV749407 AA811636 AU159893 AA603065 AA652542 A1468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051
			AA831504 AA134052 A1871759 AW089048 B1913532 AA367709 BG828155 BF093014
	445511	9560_8	BM471219 BE093160 BG177161 B1254009 A1050474 AA453162 AA829759 A1086559 AA776022 A1377446 BF589018 AA452822 AW614566
			AA443880 AA476733 AW970674 A1393291 AA988283 A1905528 AW384956 D78656
40	458091	452694_1	AF150286 AV739062 AA835857
	414221	685588_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	410253	132134_1	AA774785 AA584875 AA577705 AA683178 AA083204 AW362057 T92332 T51823 T02858 AA083375 T92381
	407102	7177_2	AW945170 BF930905 F33652 BG057818 A1368018 A1421485 A1300352 A1378525 A1264177 A1276261 A1245302 A1281050 A1190035 AW451438
			AW242903 AA910870 F22289 F19547 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17769 H42812 R09701 AA349096
			R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21380 H45809 AA007629 R47897 R83734 H45844 AW983553 H43970
45			H42536 H24495 R48875 H42961 H22079 R86018
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	409368	110612_1	AA071059 AA085201 AA085020
	433430	2181751_1	AA961588 A1863735 AA588325
	423790	888344_1	BE152393 AA330984 BE073904 BF176271
50	444083	10908_12	B1836699 A123195
	419618	252691_1	BG168298 AA247945 AA528295 AW971284
	408404	658475_1	BF308698 BE298629 BE298765 AW192518 BE299614 BE300025 BF307463
	459557	859794_1	BG623239 N58315 A1524952
55	455885	1524563_1	BE153524 BE153576 BE153583
	451385	85022_1	AA019761 AA017656 AA017374
	439781	2592493_1	AA845538 AA890229
	451331	28714_1	AK002039 AL117624 AV714494 AW954901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 A1886676
60			AA455877 N66571 AA999864 AU157344 A1817146 R54821 BE223107 AA455880 A1355752 BF589210 N63487 A1924033 A1923020 A1306145
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			AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 B1084973 BG257295 BG818471
			BE348449 A1420623 AW271213 BE048764 W44682 A1887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 B1045198 AW880645
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65			AA982057 AW516069 A1582546 BF221924 BF222543 A1801808 AW468599 AW000736 A1866625 AW235356 BM021837 AA911956 A1680606
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	430385	MH497_8	NM_032013 AB044943 AF308609 B1769254 A1819282 AA845639 A1289073 BE670187 AA207127 T33098 AA633492 BE328324 A1083620 A1204945
70			AA903471 A1372602 A1049836 A1049737 BF000101 A1686167 BF436896 A1659189 T32971 AA311302 AW7733149 A1435981 T03438 AA879206
			A1972177 T33083 AA613910 A1871019 A027140 AA853739 A1620528 A1637519 A1972307 BF054861 AK027665 BF082751 A1598127 T33663
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			AA405202 BF843940 A1743855 AA113356 BG990683 BE086729 BE535539
	443144	16112_3	AB058726 A1551414 BE245990 BE245765 BF439734 AA548422 AA040639 A1340155 AA255928 AA278365 BE766296 AA280771 AL555562
			A1474638 A1863068 B1260946 AK027039 BG615852 A1698039 AA252016 AA258886 BE905205 AW501167 BF514117 B1857400 AW297001
75			A1624923 AA125900 AW272165 AA190967 AA280729 AA035532 AW129692 AA125899 BG528645 BE614599 BE464693 A1560128 AA551511
			A1351149 AL555561
	432810	101919_1	BG292389 C06094 A1668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 A1810530 BF092924 AA334151 AA334725
			D31302 R20723 AA263003 B1824635 A1276287 A1684428 A1524234 A1335035 AW014704 A1911443 AA972102 A1367512 A1126670 AW016017
			A1266003 A1147163 AA626033 A1539156 AA565542 A1084253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA853400
			H17550 A1991439 R46187 BE929954 AA333976 D63102 BF744491
80	438874	52147_1	AF075017 R68779 R22463 H02780
	400221	9287_3	NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710
	437751	643238_1	AW978796 AA767373 AW173343 AA836163 N27563 AA905328 R97032

410899	1063474_1	BF374577 AW809840 AW809996 AW809798 AW809695 AW809646 AW809738 BF374582 AW809716 AW809826 AW809802 AW809747 AW810152
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG820022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 B057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
446526	11131_17	AK023419 BE464935 BE221668 AI148885 BI859909 AI374780 AA766892 AI347967 AI582917 AA477117 AA229236 AA652637 AA636109 AU134580 F21298 BF802607 BE769124 AV658891 H89616 AV659853
455577	1475566_1	BE006307 BE006341 BE006311
430858	73704_1	AF007190 AW820705 BE168488 AF007192 BF753303 BG978971 BG978568
400161	2656_2	U44839 NM_004651 BC000350 BI458316 AU117940 BG759024 BG749694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038 AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE206603 AI369814 AI984369 AW157545 BE221486 H99016 AU159025 AI074496 AI494516 BE245950 AA704385 AA280862 AI479595 AI369776 BE671398 T05538 AA682249 BI877303 BE645335 AI359434 H92868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W68696 AI497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 BI044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764 D62367 W22034 BG818979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267 W21941 AA328817
409959	2781_3	AW513804 BE179199 BE179195 BE179198 BE179204 BE162686
421341	1407_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 A7796676 AI749838 AA918144 AI814590 AI923531 BF513992 AJ270725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW652148 AW769047 AA565985 AW612888 AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311 AF116622 AI114507 AA640834 BF111602 AA377999
434051	73505_1	C16024 C15974 AW811056 AW811052 AW811020
410933	1064824_1	AI569131
406731	0_0	AK074473 BC017997 BI831060 BF971101 AI886394 AI082824 AV708785 W86073 W07772 AV660737 AI816793 R52250 BG183529 AA633473
446868	15525_1	AI91256 R44763 R19947 BF571346 W86257
400231	MH494_5	BC013310 AF261085 BC004109 AY007133 BC009081 BC001601 NM_002046 M33197 BC020308 J02642 M36164 BE794233 AV721080 BE255459 BG926429 BG389312 BG477333 AI031799 BI763443 BI260432 AA989106 AV728576 BI091380 AA402499 AI200513 AI284734 AI223995 AI269749 BG283291 BM013814 AW438544 AA650203 F35435 F33262 BE890952 AA401181 BG939668 F35525 BI088162 F34674 F33506 BM471326 F34677 AW276712 AA187508 F34866 AA114245 AA522581 N23935 AI076923 AI018505 BE879774 BM465637 AI753078 BG222159 AA595947 BF970917 BI094125 AA179841 BE893087 BG775178 BE793983 BE797071 BF339134 BE408272 BE266456 BE796770 BE745957 BG755835 BE265758 BE259342 BM450181 BG748174 BE299322 BM423587 BM467637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640 BM478743 BM459094 BM455308 BM472001 BM478247 BM478771 BM480379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176 BF569359 BM462924 BM455329 BM471815 BI862301 BG331736 H04903 AA374894 BE902964
432745	112643_1	AA658826 AI821926 AI791191 AA635129 AA564492
412477	8669_2	AI220117 AI857837 AI218371 BM091400 AI304964 AI198508 AI400738 AW571549 AW950042 AI089943 AA437280 AU150878 BF197070 AI267984 BF594181 BF196688 AI433152 AI338921 AI620364 AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121 AI281153 N51899 AI087072 AA954788 AW069054 AI346309 BG529629 AI340135 BF083036 AI167365 AW819657 AA935468 AI467868 AW148701 AI383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AJ553922 AI560688 AW950043 AI961682 AV706508 R01853 AA126514 N62757 AI536893 AI926052 AI418720 N99964 AI568933 AI915737 AI080691 AI185358 H48995 N58575 BE82824 H60037 AI247247 T95664 BF593863 AI749637 AW088541 AA991294 AA887452 AI073726 AA633132 AA629674 AA629649 AA629656 AA578595 AI168758 AA804572 AI085786 AA994396 AA991209 AA948563 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 AI382839 AA194837 AA406284 AI250750 R37035 AI525586 W01244
456076	8455_1	BG210376 BG217800 BE925778 W39114 BG682395 N70644 BE709097 AW275615 BC001469 AI564888 AI088126 AW003852 BF792438 AA161295 AW970131 AI127310 AW029307 AW192534 AA843144 AW606235 BE221641 AW008111 AA224203 AA604507 AW794761 AA134005 AA126850 N99165 AW769391 AW818302 AI269871 BE503027 AW401627 AA486231 AA486417 AA191542 AA028128 AA159991 AI498090 AI241024 BM145449 AA774661 AI626021 C18251 BE185811 AA291517 N38896 N59222 AI245611 AA169207 AI298572 AA169585 AI131139 AA157960 AI439983 AI208276 AA936061 W67305 AW337587 AI357055 W04739 AI214517 AA617789 AW241277 AI880213 AI582789 AI143996 BE814848 N49964 AI936222 AI817819 F08976 AA039349 AW805002 T35117 N94388 AI689530 AW384573 AW384555 AW384539 AW384473 AA129709 AW384466 BG194342 BG204579 BG027536 AL576075 AA399553 AW794949 T88866 AW511211 R26588 R36111 BG170598 BE937009 BG678833 AA862899 H96612 H02273 AA768487 BF211173 N32570 AA088287 R68451 AA297563 H16847 R06665 AA421891 W68402 R28379 R64119 R70109 R77661 R67963 BG701844 H68670 AA169664 AA114111 BE715243 R69317 BE715252 BE713804 BG336586 NM_001679 BC011835 U51478 BM463117 AU119746 BI462090 BI227086 BG706303 BF059073 BG706532 BI544716 AI568735 BE858747 AU122881 AU126210 AI186547 AU134705 BE281323 AI147220 BE263820 AW973937 BG281863 BE858367 BE278941 AI262814 AI001194 AI391616 AI200862 N32564 AI161064 AI089818 BF514359 AI370916 AI341797 BE263168 AI218416 AI131098 AI285310 AI928440 AI066642 AI376442 AW028327 AI217792 AI161020 AI342854 AI221544 AI304700 AI343005 BM148839 AA831536 AW074258 BF940569 AI149876 AI914574 AA298442 AI241343 AA668985 AW272172 AI160537 BG209220 AA028152 AA025989
430202	1233214_1	AW968345 AA468998 T85775
424017	888651_1	AW956107 AA334317 AA333789
437272	176_2	AB075828 BG107783 AW021313 BI492345 AW385707 AW580860 AW296117 BE072066 AW580775 BF679498 AW580828 BE003666 BE003872 AW580851 AW580908 BI037146 AW580894 AW580864 H17858 N50343 N54223 F05579 F07386 F05578 AA773248 AA354359 AA330257 C20685 BE548300 AW968728 AW968554 AA777644 AA706898 AA682517 AA832267 BG165087 N51097 N51567 R95837 BI256603 W89042 R55836 R97364 AW975957 AA747943 AA811289
453542	885_22	BF568186 BF899745 AW836724 BE243668
437585	696988_1	AW976857 AI809001 AA769369 AW102732 AA761235
430763	1400_7	AL578301 AI337389 AI871302 AA978185 BF591738 AI765912
409031	9531_1	BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AL270187 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI471258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39978 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA183411 AW444709 AW952455 AI887612 BF431948 AI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA881685 AA251595 AA625761 AA872090 AI826780 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69949 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302
430108	1233254_1	AA928810 AW968393 AA465294 AA811301
410276	641443_1	AA083514 AI545445 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
400247	2764_1	BC022339 BC009610 BC010537 X79805 NM_006713 U12979 BM467814 BM450743 AU132951 AU137129 BG493425 AV758819 BG708412 BG705885 BG702217 AV716638 BG777009 BI545689 BI552153 BM476712 BG770858 BG527656 BG528277 BG391388 AV716661 BI602926

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BG290073 BI667399 BM451469 BI667173 BI602139 BG532171 BI669216 BI544727 BG721852 AV716503 AV701327 BM090738 BI492000
 AI308858 BI544904 AI599813 AV715829 AV716505 AV714587 AV717902 BF668072 AV716385 BI461927 BM090954 AV717826 BG503676
 AV647719 BG501392 BG428433 BE895629 BM313117 AW021050 BG435032 BM152910 AA313503 AA872377 BG574714 AV712054 AV732696
 AA252476 AV712759 AL599643 BE790872 BG654930 W73337 AW675377 AV760376 AV725139 AV716379 AA887165 BE830003 AW023796
 AL599291 AI902948 BG944042 F00781 AA352483 BG217897 N33688 AW581924 BG654730 D31410 AA353088 D31288 AA295029 H95170
 BE935104 AU139980 BG772963 BG776470 BG532512 BG105449 BI545421 AV715456 AW386083 BG699714 AL535832 AL514940 BG190861
 BG210593 AW999254 H95138 AA353663 BE764809 N50375 BE091363 BG701255 BI860846 BI832485 BI668150 BG028647 BE546301
 BG900321 BI909737 BG702363 BG614141 BG611137 BG700121 BF031492 N58802 AV715940 N51590 BG993478 BE172016 AW893622
 AK056692 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145
 BF060834 BI019048 AW862002 AK056737 AA429538 AW063311 AW440655 AW231970 AA428584 AA995028 AW854593 AA984131 AA552874
 AA564758 AA528743 BG927275 BE045117 AW975234 AA664937 BF749390 BG928948 AA984546 BE009153 AV732487 BE078167 AW872716
 AW063245 AA578441 AI820704 AI732283 R55428 BF999154 BF880485
 AL134685 AW972760 AA525319 AA526644 AA525342 AA526632 AA525296 AV739423 AW972755
 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526
 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
 AW852530 AW852526 AW852527 AI597959
 AW811114 AW811095 AW811094 AW811124 AW811157 AW811054 AW811087
 AW810001 BF374633 AW809694 AW809672 BF374748 BF374562 AW810209 AW810092 AW809786 AW810428 AW810429 AW809884 BF374650
 BF374641 BF374764 BF374744 AW810552 BF374678 BF374653 BF374579 AW810168 AW810170 BF374611 BF374676 BF374667 AW810353
 BF374682 AW810154 BF374688 BF374555 BF374757 BF374637 BF374743 BF374719 AW809664 BF374643 BF374680 BF374714 BF374708
 BF374716 AW810432 BF374691 BF358066 AW810006 AW810345 AW809960
 AW963582 BE064192 BE064169 BE152580 AW963587
 AV704306 BF368780 AW867826 AW859896
 AA229752 AA230035
 AW972670 AA525808 H28359 H28383
 BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600738 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133
 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332
 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743
 AA609784 R97304
 BC010106 AL560552 AU133296 AU133086 BE268567 BE268523 BI544879 BE398161 BG473088 BI544445 BE258021 BE296339 BE255040
 BE263020 BG706790 AL598627 AW952337 BG758113 AW512753 BE267666 BE253415 BI225718 BE268350 BE258245 BI224965 AW772605
 BG723903 BE397282 BI196341 BG702880 AI878949 AL600437 AA416759 BE259917 AI031582 BF512142 AI088248 BE560328 AI802623
 AI288613 AL597585 AW768553 AI816352 BF732831 BI225687 AA833686 AA722593 AA807750 AW068064 AA405187 AI923238 N51593 AL527710
 BG282576 AL525927 AL525971 BI869547 AI064725 R91856 H46814 H20112 W01682 AW848870 AW848585 AW376662 AW848985 AW848937
 AW848862 AW848581 AW848512 AW848176 AW752623 AW752618 AW376822 AW376821 AW376684 AW376623 AW376622 BE706047
 AW752602 AW752691 AW752674 AW752652 AA379167 AW752610 AW752684 AW752613 AW752660 AW848709 AW848576 AW849155
 AW848981 AW848980 AW848979 AW848978 AW848973 AW848916 AW848713 AW848708 AW848642 AW848641 AW848639 AW848573
 AW848493 AW848492 AW848489 AW848488 AW848487 AW848353 AW848352 AW848220 AW752698 AW752697 AW752682 AW752681
 AW752680 AW752679 AW752664 AW752651 AW752638 AW752637 AW752636 AW752628 AW752626 AW752624 AW752619 AW752596
 AW752608 AL582019 BE875587 AL529175 AW965868 BG686208 AA259073 BE696973 AA459543 AA358314 W40564 BF926427 AW849000
 AW848718 AW848515 AW848507 AW848444 AW848440 AW848232 AW848222 AW752657 AW376786 AW376781 AW376615 AW376614
 BF752581 AA534520 AI748906 AA047799 AI014753 AL514460 AL581982 BG743146 W24171 H20102 H11227 AW752607 AW006596 AW130378
 BE716519 AW752661 AW848289 BF349557 AW752612 AW752632 AW848910 NM_004077 AF047042 AL560606 BI765896 BI196831 BI855656
 BE906674 BG749937 BE535486 BE019810 AA313713 AA992542 AA332541 AA682985 AA356125 BE140478 BG750945 BI457548 BG025661
 BF326302 AA325019 BG980676 AA337465 AA321974 BG949285 BG427585 R23979 BG611485 BE560678 W16977 N50379 BG824101 BG471750
 BI463171 W04691 AU099360 BG471590 BM011999 BE262945 BE559801 BF756438 BE881957 BE314546 BG911831 BG150811 BG112017
 AA157518 T92368 AW752620
 AW970623 AA502839 AA502819
 UB1984 NM_001340 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189
 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AI544018 BE002870 BE929314 BE090199 AL046650
 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403

TABLE 34C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
405443	7408143	Plus	90716-90887,101420-101577
401645	7657839	Minus	34986-35133
401673	7689903	Minus	122587-122705,122765-123047
405120	8099940	Plus	140176-140340
401785	7249190	Minus	165776-165996,166189-166314,166408-166556
402333	8844110	Minus	165693-165856
404942	7382153	Plus	92095-92252
403362	8571772	Plus	64099-64260
402641	9958129	Minus	122596-125136
405600	5923840	Plus	26662-27225
405061	7656744	Minus	132492-132932
402327	7656695	Minus	108675-108770,109801-109910
404342	9838093	Plus	115854-116033
404429	7407979	Plus	31352-31498
403344	8569726	Plus	70823-70990
401593	7230957	Plus	10368-10572,11293-12356
406461	9756020	Minus	158842-159136
400609	9887671	Minus	92037-92247
402674	8077108	Minus	39290-39502
401677	9965537	Minus	62856-63086,63603-63884
405579	6456174	Plus	100996-101542
405797	1934909	Minus	5599-5681,5821-6104

5	405159	9966252	Plus	79659-79804
	403520	7684483	Minus	97621-98084
	402538	9801137	Minus	96314-96539
	404151	7534014	Minus	69038-69399
	400496	9743564	Plus	41515-41695
	403010	3132346	Plus	78385-79052
	406387	9256180	Plus	116229-116371,117512-117651
	402865	9926751	Plus	71919-72049
10	404501	7229859	Minus	37270-37526
	402487	9797538	Plus	75677-75843
	404455	7677926	Minus	26927-27611
	401067	5764724	Minus	153366-153509
	402324	7630361	Plus	26052-26803
	402013	7407997	Plus	174540-174634,175449-175568
15	401116	9966559	Plus	123579-124447
	402998	2996643	Minus	17175-17373
	405550	1552494	Plus	91720-92115
	402917	7406502	Minus	1034-1177,3143-3266
20	402504	9797871	Plus	12366-12614
	405491	5801645	Plus	81857-82045
	400818	8569994	Plus	172644-172765,173085-173200
	406475	9797684	Plus	125417-125563,128052-128180
	401025	8117518	Minus	179287-179483,181044-181166,181844-18203
25	402308	7340295	Minus	92080-93638
	405213	6692345	Minus	50267-51151
	400740	7329267	Minus	79920-80510,80576-80746
	402825	6165330	Minus	78572-78807
	405973	8247789	Plus	103859-104254
30	405818	4071056	Plus	29055-29196
	402621	9930950	Plus	130806-131036
	401311	9212516	Minus	180124-180754
	401899	7230209	Minus	155620-155815
	403579	8101179	Minus	36167-36365
35	404600	8705107	Plus	118354-118444,118649-118792
	405531	9665194	Plus	35602-35803
	405542	9857564	Plus	71331-72183
	405131	8516051	Minus	138764-137594
	403026	7670575	Plus	56521-56840
40	405369	2078469	Minus	34183-34357,35686-35751
	405932	7767812	Minus	123525-123713
	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	402174	8575912	Plus	253499-253674
	405536	9795661	Plus	164091-164162,164397-164516,166720-16679
45	405109	9127147	Minus	58328-58485
	403162	9838085	Plus	82652-83613
	401404	7710968	Plus	136474-136646
	403167	9838127	Plus	162599-162935
	402209	8576119	Minus	53315-53472
50	400986	8085497	Minus	63140-63319
	404975	3419864	Minus	86096-86605
	404926	7341919	Minus	150411-151484

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TABLE 35A: About 323 genes upregulated in hypersensitivity pneumonitis relative to idiopathic pulmonary fibrosis or non-specific interstitial pneumonitis

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Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of HP AIs divided by 90th percentile of IPF AIs, where 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

R2: 90th percentile of HP AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.

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Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
402550			Target Exon	4.03	4.70
421563	NM_006433	Hs.105806	granulysin	3.37	2.70
424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, dacycin	3.31	2.42
417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	3.09	1.51
411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	2.99	1.28
416350	AF188625	Hs.189507	phospholipase A2, group IID	2.71	1.43
406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	2.70	1.53
459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	2.70	1.14
412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.69	2.99
452194	AI694413		olfactory receptor, family 2, subfamily	2.63	2.67
447709	U97145	Hs.19317	GDNF family receptor alpha 2	2.63	1.52
410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.59	1.00
454671	AW812929	Hs.336908	ESTs	2.50	2.34
441859	AW194364	Hs.94814	Interleukin-4 induced gene-1 protein (FI	2.45	1.90
422398	AI476149	Hs.334489	hypothetical protein FLJ21992	2.45	1.36
403244			C2002870:miR2698td[LU00985 hydroxypr	2.40	1.53

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	415462	R52692	Hs.12698	ESTs	2.40	1.00
	447028	AJ973128	Hs.167257	brain link protein-1	2.33	1.64
	412394	AW984150		gb:PM2-HN0008-170300-001-h09 HN0008 Homo	2.32	1.00
5	450165	AA007235	Hs.63931	ESTs	2.32	1.32
	431093	AB031038	Hs.301704	eomesodemin (Xenopus laevis) homolog	2.30	1.81
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	2.28	1.69
	413682	BE156991		gb:RC3-HT0371-290100-013-e02 HT0371 Homo	2.27	1.59
	441320	AJ768724		fibulin 1	2.27	1.87
10	456766	R87310	Hs.7740	oxysterol binding protein-like 1	2.27	1.36
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide (TTT3 com	2.26	1.98
	459721	AJ299050	Hs.143835	gb:qm14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.25	1.82
	405452			Target Exon	2.25	1.29
	458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.25	5.80
	401447			Target Exon	2.25	1.55
15	423066	Y18264	Hs.123094	sal (Drosophila)-like 1	2.24	1.51
	441704	AJ458766	Hs.192125	ESTs	2.24	1.00
	405097			ENSP00000175238*-A disintegrin and metal	2.24	1.00
	408544	AW293825		ESTs	2.22	1.95
20	413454	BE141162		gb:MR0-HT0076-021299-001-d03 HT0076 Homo	2.20	2.26
	444404	M31525		major histocompatibility complex, class	2.20	1.37
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.19	2.88
	436063	AK000028		ribosomal protein S24	2.19	1.42
	429212	NM_001504	Hs.198252	G protein-coupled receptor 9	2.18	1.22
	400712			Target Exon	2.18	1.00
25	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.17	1.79
	403478			NM_022342:Homo sapiens kinase protein 9	2.17	1.80
	418747	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 n	2.17	1.76
	429712	AW245825	Hs.211914	ENSP00000233627*-NADH-ubiquinone oxidore	2.16	1.44
30	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.16	2.12
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	2.15	2.88
	456057	AA947457	Hs.135560	ESTs, Weakly similar to T43458 hypotheri	2.15	2.50
	444346	AJ142274		ESTs	2.15	2.38
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.14	1.93
35	451318	AA028888	Hs.95071	ESTs	2.14	1.16
	458935	Y16521	Hs.24812	CDP-diacylglycerol synthase (phospholida	2.13	1.52
	417105	X60992	Hs.81226	CD6 antigen	2.13	2.61
	408219	BE061111	Hs.254211	gb:QV0-BT0041-011199-039-f02 BT0041 Homo	2.13	1.94
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TTT3 co	2.11	2.66
40	443711	N67861	Hs.49390	ESTs	2.10	1.00
	423234	AA323534	Hs.296162	AD037 protein	2.10	1.52
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.09	3.74
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	2.08	1.84
	405827			Target Exon	2.08	1.00
45	406909	L20777	Hs.73885	gb:Human MHC class I HLA-G gene (HLA-A33	2.08	2.29
	437295	AW779318	Hs.88417	ESTs	2.07	1.72
	424281	AA766243		gb:aa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	2.07	1.00
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.07	2.16
	423901	AA333006		gb:EST37064 Embryo, 8 week I Homo sapien	2.07	1.50
50	405075			Target Exon	2.07	1.15
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.07	2.67
	406267			Target Exon	2.07	1.30
	423365	AA324992	Hs.257168	ESTs	2.06	1.70
	449970	AJ678058	Hs.201227	ESTs	2.06	2.48
55	430733	AW975920	Hs.121036	ESTs	2.06	1.00
	446323	AJ288274	Hs.345792	ESTs	2.06	1.00
	402240			Target Exon	2.05	1.94
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheri	2.05	1.44
	424463	AW195353	Hs.119903	ESTs	2.04	1.32
60	400107			Eos Control	2.04	2.42
	404811			NM_021096:Homo sapiens calcium channel,	2.03	2.18
	403589			Target Exon	2.03	1.57
	404088			Target Exon	2.03	1.00
	414991	C17898		gb:C17898 Human placenta cDNA (TFufuwa	2.03	2.04
65	429073	AA446167	Hs.47385	ESTs	2.03	3.10
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	2.02	1.92
	401897			C17001987:gi7303380[gb]AAF58438.1[AE0	2.02	1.55
	431094	AW972276	Hs.116195	ESTs	2.02	1.00
	424899	AL119387	Hs.119062	ESTs	2.01	2.41
70	419711	C02621	Hs.159282	ESTs	2.01	1.92
	459019	AA017156	Hs.40719	hypothetical protein KIAA1164	2.01	1.76
	405453			NM_005748*:Homo sapiens YY1-associated f	2.01	1.24
	402516			Target Exon	2.01	1.00
	457365	AA577297	Hs.303249	EST	2.01	2.36
75	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfam	2.01	2.62
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	2.00	1.64
	406266			Target Exon	2.00	2.46
	419409	AW297831	Hs.143792	hypothetical protein MGC2656	2.00	1.60
	435028	AW193035	Hs.187370	ESTs	2.00	1.55
80	404696			NM_013443:Homo sapiens CMP-NeuAC(beta)-	2.00	1.21
	403533			Target Exon	2.00	1.17
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.00	1.00
	424148	BE242274	Hs.1741	Integrin, beta 7	1.99	3.66
	419833	AA251131	Hs.220697	ESTs	1.99	1.69

5	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	1.99	1.84
	426416	AW612744	Hs.169824	killer cell lectin-like receptor subfam	1.98	2.56
	449317	AW293413	Hs.132906	19A24 protein	1.98	2.44
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	1.97	2.51
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.97	3.32
10	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.96	1.86
	406303			C16000922:gil7499103 pir T20903 hypothe	1.96	2.16
	438676	AA813745	Hs.123446	ESTs	1.95	3.62
	404240			NM_018950:Homo sapiens major histocompat	1.95	2.06
	404056			Target Exon	1.94	2.60
15	425508	AA991551	Hs.97013	Homo sapiens, Similar to RIKEN cDNA 2310	1.93	3.24
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	1.93	2.35
	416941	BE000150	Hs.48778	niban protein	1.92	2.24
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.92	5.44
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	1.92	6.08
20	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	1.90	5.52
	446608	N75217	Hs.257846	ESTs	1.90	4.63
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.89	1.50
	414812	X72755	Hs.77367	monokine induced by gamma interferon	1.89	4.93
	422994	AW891802	Hs.296276	ESTs	1.88	3.30
25	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.88	2.17
	433671	AW138797	Hs.132906	19A24 protein	1.88	1.83
	412116	AW402166	Hs.784	Epslein-Barr virus induced gene 2 (lymph	1.86	3.12
	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	1.86	1.88
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TIT3	1.84	1.65
30	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	1.83	2.46
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	1.82	2.07
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.82	2.63
	436485	X59135	Hs.156110	immunoglobulin kappa constant	1.82	2.75
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.81	4.56
35	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.80	5.10
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.79	1.89
	429670	L01087	Hs.211593	protein kinase C, theta	1.78	3.34
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.78	3.55
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.78	1.97
40	406672	M26041	Hs.198253	major histocompatibility complex, class	1.76	2.12
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.75	1.55
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.73	2.04
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazarus	1.73	1.56
	414512	AL044336	Hs.6831	golgi phosphoprotein 1	1.73	2.00
45	426752	X69490	Hs.172004	titin	1.73	2.62
	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	1.72	2.30
	452334	D60471	Hs.13390	gb:HUM111D09B Clontech human fetal brain	1.72	2.12
	446227	AI281459	Hs.270114	ESTs	1.72	2.48
	407830	NM_001086	Hs.587	arylamide deacetylase (esterase)	1.72	2.72
50	423799	AW026300	Hs.132906	19A24 protein	1.71	2.40
	458332	AI000341		ESTs	1.70	3.71
	408380	AF123050	Hs.44532	diubiquitin	1.70	2.71
	437644	AA748575	Hs.136748	lectin-like NK cell receptor	1.70	2.58
	402736			NM_024852:Homo sapiens hypothetical prot	1.69	2.10
55	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.69	1.39
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.68	2.02
	426202	BE266484	Hs.82916	chaperonin containing TCP1, subunit 6A (1.68	2.14
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	1.68	3.30
	420440	NM_002407	Hs.97644	mammaglobin 2	1.67	2.42
60	416967	BE616731	Hs.80645	interferon regulatory factor 1	1.67	1.49
	415823	R81864	Hs.205103	ESTs	1.65	2.16
	421924	BE514514	Hs.109506	coronin, actin-binding protein, 1A	1.65	1.58
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	1.63	1.94
	444929	AI685841	Hs.161354	ESTs	1.63	2.16
65	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.63	1.74
	418196	AI745649	Hs.26549	KIAA1708 protein	1.62	2.76
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.62	4.42
	438568	R98865	Hs.11135	major histocompatibility complex, class	1.62	1.74
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.62	1.85
70	433934	AW273261	Hs.216292	ESTs	1.62	2.00
	443559	AI076765	Hs.269699	ESTs, Moderately similar to ALU8_HUMAN A	1.61	2.00
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	1.61	1.46
	415349	AI766697	Hs.13231	ESTs	1.60	2.00
	406656	M16714	Hs.89643	major histocompatibility complex, class	1.60	1.47
75	456974	M12529	Hs.169401	apolipoprotein E	1.60	1.63
	416401	N80139	Hs.268916	ESTs	1.59	1.68
	439372	AF088033	Hs.159225	ESTs	1.59	2.04
	434666	AF151103	Hs.112259	T cell receptor gamma locus	1.59	4.08
	417696	BE241624	Hs.82401	CD69 antigen (p50, early T-cell activati	1.58	3.06
80	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	1.58	2.37
	431903	AB029488	Hs.272100	SMS3 protein	1.57	2.14
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1.57	2.28
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	1.56	1.46
	412472	AW975398	Hs.293836	ESTs	1.56	2.26
	451406	AI694320	Hs.8295	ESTs, Weakly similar to T17248 hypotheti	1.56	2.38
	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.55	1.67
	449835	AW979300	Hs.293813	ESTs	1.55	2.16

	405545		Target Exon	1.55	2.64
	435299	AJ745458	ESTs, Weakly similar to T20593 hypothel	1.55	3.81
	422060	R20893	ESTs, Moderately similar to ALU5_HUMAN A	1.54	2.14
5	424243	AJ949359	ESTs, Highly similar to cis Golgi-locali	1.53	2.62
	457500	NM_002759	protein kinase, Interferon-Inducible dou	1.53	2.04
	424541	AW392551	ESTs, Weakly similar to A56194 thromboxa	1.53	2.00
	439039	AJ656707	ESTs	1.53	2.38
	449523	NM_000579	chemokine (C-C motif) receptor 5	1.52	2.65
10	457718	F18572	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.52	2.06
	415198	AW009480	natural killer cell transcript 4	1.52	1.40
	431594	AI823999	ESTs	1.52	2.12
	432656	NM_000246	MHC class II transactivator	1.52	2.20
	422426	W79117	ESTs	1.52	2.22
15	414372	AA143554	gb:z065a02r1 Stratagene pancreas (93720	1.51	2.80
	427247	AW504221	Integrin, alpha L (antigen CD11A (p180),	1.50	1.67
	433043	W57554	lymphoid nuclear protein (LAF-4) mRNA	1.49	3.12
	406621	X57809	Immunoglobulin lambda locus	1.49	1.78
	419166	AA234638	ESTs	1.49	2.10
20	418323	NM_002118	major histocompatibility complex, class	1.49	1.47
	435304	H10709	ESTs	1.48	2.96
	452834	AI638627	KIAA1688 protein	1.48	2.14
	446616	R65964	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.48	1.38
	429272	W25140	ESTs	1.48	3.19
25	428379	X06026	CD3G antigen, gamma polypeptide (TIT3 co	1.48	1.66
	433231	AB040926	KIAA1493 protein	1.47	2.16
	408847	AW290997	ESTs	1.46	2.08
	405441		Target Exon	1.46	2.99
30	443378	AW392550	proteasome (prosome, macropain) subunit,	1.45	1.56
	459644	AW197203	gb:xm38b01.x1 NCL_CGAP_GC6 Homo sapiens	1.45	2.44
	431433	X65018	surfactant, pulmonary-associated protein	1.45	1.70
	422934	BE244189	hypothetical protein	1.44	1.27
	409799	D11928	phosphoserine phosphatase-like	1.44	3.46
	406698	X03068	major histocompatibility complex, class	1.44	1.71
35	421407	T82331	ESTs, Weakly similar to CGHUSC collagen	1.43	1.56
	413420	AW410235	proteasome (prosome, macropain) activato	1.43	1.25
	400269		Eos Control	1.43	2.02
	420973	AA743415	ESTs	1.42	2.06
40	442104	L20971	phosphodiesterase 4B, cAMP-specific (dm	1.42	2.20
	430015	AW768399	ESTs	1.41	2.08
	427648	AI376722	proteasome (prosome, macropain) subunit,	1.41	1.31
	418870	AF147204	chemokine (C-X-C motif), receptor 4 (fus	1.40	1.72
	437479	R61866	ESTs	1.40	2.52
	425345	AL077297	protein tyrosine phosphatase, non-recept	1.40	2.17
45	416030	H15261	ESTs	1.40	2.62
	419886	AA251562	ESTs, Weakly similar to AF118023 1 SH3 d	1.40	1.68
	443951	F13272	ferritin, light polypeptide	1.40	1.64
	414875	H42679	major histocompatibility complex, class	1.40	1.42
	412471	M63193	endothelial cell growth factor 1 (platelet	1.40	1.34
50	428782	X12830	interleukin 6 receptor	1.40	2.30
	400680		NM_014207:Homo sapiens CD5 antigen (p56-	1.39	1.93
	428289	M26301	complement component 2	1.39	1.39
	441410	AA932689	ESTs, Weakly similar to I38022 hypothel	1.39	1.42
55	406645	M57466	major histocompatibility complex, class	1.39	1.45
	441379	AW175787	selenium binding protein 1	1.38	1.32
	416636	N32536	solute carrier family 16 (monocarboxylic	1.38	2.04
	418707	U97502	butyrophilin, subfamily 3, member A2	1.38	1.35
	423526	AB011086	KIAA0514 gene product	1.37	1.41
	424168	L29277	signal transducer and activator of trans	1.37	1.33
60	431723	AW068350	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.37	1.74
	426437	BE076537	ubiquitin-conjugating enzyme E2L 6	1.35	1.38
	446566	H95741	membrane-spanning 4-domains, subfamily A	1.35	1.64
	452353	C18825	epithelial membrane protein 2	1.34	1.47
	448406	AW772298	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.31	1.77
65	435106	AA100847	ESTs, Highly similar to AF174600 1 F-box	1.31	1.53
	444633	AF111713	junctional adhesion molecule 1	1.30	1.37
	430998	AF128847	Indolethylamine N-methyltransferase	1.29	1.49
	419092	J05581	mucin 1, transmembrane	1.28	1.36
	451864	N20370	ESTs	1.28	1.42
70	421140	AA298741	signal sequence receptor, delta (translo	1.28	1.31
	412790	NM_014767	KIAA0275 gene product	1.28	1.63
	446272	BE268912	hematopoietic cell-specific Lyn substrat	1.28	1.38
	422530	AW972300	bone marrow stromal cell antigen 2	1.28	1.36
	435822	T95594	ESTs	1.27	1.82
75	455863	AA907305	ESTs	1.27	1.36
	404277		NM_019111*:Homo sapiens major histocompa	1.27	1.52
	413497	BE177661	gb:RC1-HT0598-020300-011-h02 HT0598 Homo	1.27	1.54
	441835	AB036432	advanced glycosylation end product-speci	1.27	1.53
	418371	M13560	CD74 antigen (invariant polypeptide of m	1.26	1.27
80	434747	AA837085	ESTs	1.26	1.60
	425320	U29344	fatty acid synthase	1.25	1.35
	452363	AJ582743	Homo sapiens, Similar to complement comp	1.25	1.41
	434644	H98071	chromosome 21 open reading frame 50	1.25	1.30
	404854		Target Exon	1.25	1.57

5	406973	M34996	Hs.198253	major histocompatibility complex, class	1.25	1.57
	421071	AJ311238	Hs.104476	ESTs, Weakly similar to CGH1E collagen	1.24	1.26
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.24	1.39
	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	1.23	2.08
	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.23	1.20
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.22	1.24
	415661	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.22	1.16
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.22	1.17
10	420679	X57152	Hs.99853	fibrillarin	1.22	1.30
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	1.22	1.58
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfamily	1.21	1.33
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	1.21	1.60
	406825	AJ982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.20	1.20
15	436906	H95990	Hs.181244	major histocompatibility complex, class	1.19	1.27
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.19	1.62
	408279	AF216965	Hs.44095	Homo sapiens, clone MGC:12617, mRNA, com	1.18	1.25
	411372	AI147881	Hs.213289	low density lipoprotein receptor (family	1.17	1.33
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.16	1.49
20	406906	Z25424		gb.H.sapiens protein-serine/threonine ki	1.16	1.15
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	1.16	1.38
	432805	X94630	Hs.3107	CD97 antigen	1.16	1.22
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	1.16	1.41
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.16	1.36
25	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	1.15	1.27
	429832	AW293301	Hs.288472	ESTs, Weakly similar to UBPF_HUMAN UBIQU	1.15	1.72
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	1.15	1.21
	432680	T47364	Hs.278613	Interferon, alpha-inducible protein 27	1.14	1.21
	406782	AA430373		gb:zw2011.1.s1 Soares ovary tumor NbHOT H	1.14	1.41
30	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.12	1.25
	452547	AA335295	Hs.74120	adipose specific 2	1.11	1.39
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.11	1.22
	430280	AA361258	Hs.237868	interleukin 7 receptor	1.10	1.73
	441384	AA447849	Hs.288660	retinoic acid induced 3	1.09	1.22
35	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibitor	1.09	1.14
	419200	AW966405		EST	1.08	1.64
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	1.08	1.18
	409428	M33680	Hs.54457	CD81 antigen (target of antiproliferativ	1.07	1.12
	447023	AA356764	Hs.17109	Integral membrane protein 2A	1.07	1.71
40	421481	AW391972	Hs.104696	KIAA1324 protein	1.07	1.58
	408868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.07	1.23
	412819	T25829	Hs.24048	FK506 binding protein precursor	1.06	1.45
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.06	1.24
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.05	1.17
45	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.04	1.21
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.04	9.14
	418156	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	1.03	6.65
	438089	W05391		nuclear receptor subfamily 1, group I, m	1.03	8.00
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	1.01	1.25
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.18
	438091	AW373062		nuclear receptor subfamily 1, group I, m	0.99	12.84
	407018	U49669		NM_018955:Homo sapiens ubiquitin B (UBB)	0.99	1.07
	412896	AW804157	Hs.308026	major histocompatibility complex, class	0.98	1.57
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	0.97	1.40
55	426530	U24578	Hs.278626	complement component 4A	0.96	1.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	0.95	1.29
	407241	M34516		gb:Human omega light chain protein 14.1	0.94	1.11
	425371	D49441	Hs.155981	mesothelin	0.92	1.45
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (0.91	1.28

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TABLE 35B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

65

Pkey CAT Number Accession

70

411089 5597_6 BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291
 AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AI082382 AI955808 AI679895 AI679386 BF435555 AA586359
 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389
 AW897808 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680

452194 90339_1 AI694413 AW994700 AI912945 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043
 AI709339

75

410910 1063929_1 AW810196 AW810555 AW810507 AW810204 AW810619 AW810534
 412394 1174616_1 AW947794 AW947793 AW947802 AW947798 AW947792 AW984150 AW984166 AW984167 AW984168 AW984179 AW984134 AW984160
 AW984180 AW984194 AW984202 AW984190

413682 1527038_1 BE156943 BE157375 BE156965 BE156949 BE156956
 441320 58978_5 AI346734 AI377971 BG193341 BG548376 AA928353 AI768724 BG215700 AA449370 BI462157 BI060283 BG677508 AA318802 BG719160
 408544 683260_1 AW293825 AW235391

80

413454 1515217_1 BE141291 BE141306 BE141288 BE141283 BE141162 BE141168 BE141290 BE141161 BE141165
 444404 18138_1 BC013183 AW408658 NM_002119 M31525 M26039 BM456399 BF732381 BM152457 AW407685 BM193161 AW407778 BI819141 AA702254
 BF855074 BI761232

5	436063	5483_1	AK000028 AA494483 AJ298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512690 BG435593 AI147991 AI142274 AI198553 AA338252 AA338213 AW962691 AA333006 AA332289 D78831 C17899 D78863 BF330730 BF350539 BE153665 BE065062 BE064650 BE064863 BF330763 BE153820 BE064737 BE155079 BE064651 AW856751 AW856622 BE064691 BE153674 BE153698 BE064730 BE153536 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL545423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AJ361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AI556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AI000341 AI766341 AW873274 AI823999 AA970060 AA508176 AW972585 AI873427 AW972389 BI093452 AW970865 BG118265 AA569075 AA492132 AW753140 AA213770 AA143654 W03900 AW197203 AW753300 X55018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI821373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG868740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF198861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490918 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903557 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903510 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE982912 BM454584 AL134894 BF104082 H80591 AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N40935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520 BE177661 H06215 BE144709 BE144829 AW976537 AI033582 AA837085 AA745261 AA648395 AA430373 AA968771 BF036043 AW190448 BG194731 AW662036 AI445021 BE937550 AW818972 AW939132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994445 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358597 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA053287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI959467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75961 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797878 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898816 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
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TABLE 35C:

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Pkey:
Ref:

Strand:
NL_position:

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

80

Pkey	Ref	Strand	NL_position
402550	7652009	Minus	80413-80673
403244	7637828	Plus	175792-176144
405452	7656638	Minus	93876-94275

5	401447	8574299	Minus	65053-65283
	405097	8072599	Plus	171191-171360
	400712	8118874	Plus	36087-36268
	403478	9958258	Plus	116458-116564
	405827	7109593	Plus	10279-10972
	405075	7770506	Minus	124680-125321
	406267	7528342	Minus	2570-2731
	402240	7690131	Plus	104382-104527,106136-106372
10	404811	3702428	Plus	26424-26596,28854-28987
	403589	8101229	Plus	5-330
	404088	9958257	Plus	184131-184295
	401897	8569218	Plus	604-767
	405453	7656675	Minus	83710-83980
15	402516	9798099	Minus	195342-195511
	406266	7528342	Minus	2365-2518
	404696	9800109	Minus	60037-60144,62675-63081
	403533	8076874	Plus	162922-163658
	406303	8575868	Plus	173622-173786
20	404240	5002624	Minus	116132-116407,116653-116922
	404056	3548785	Plus	75843-76980,77146-78263
	402736	9212044	Minus	66876-67010
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405441	7408124	Plus	100952-101283
25	400680	8118752	Plus	118343-118684,120720-121013
	404277	1834458	Minus	91665-91946
	404854	7143420	Plus	14260-14537

30 TABLE 36A: About 52 genes upregulated in non-specific interstitial pneumonitis relative to hypersensitivity pneumonitis or idiopathic pulmonary fibrosis

35	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1:	90th percentile of NSIP AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50.				
	R2:	90th percentile of NSIP AIs divided by 90th percentile of IPF AIs, where the minimum value for the numerator and denominator was set to 50.				
40	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
	435140	AA668123	Hs.134170	ESTs	2.76	2.76
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
	435375	A1733610		ESTs	2.55	2.55
45	420813	X51501	Hs.99949	prolactin-induced protein	2.55	1.35
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.52	0.73
	421296	NM_002666	Hs.103253	perilipin	2.50	2.45
	419290	A128114	Hs.112885	spinal cord-derived growth factor-B	2.43	1.79
50	408882	H12084	Hs.31110	ESTs, Weakly similar to MAGE-B4 [Hsap]	2.42	1.77
	437318	AW362939	Hs.120721	ESTs	2.36	1.61
	421823	N40850	Hs.28625	ESTs	2.29	0.56
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.28	0.89
55	430536	A1809163	Hs.9908	nitrogen fixation cluster-like	2.25	2.80
	414009	R67516		ESTs	2.19	1.86
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.19	0.33
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	2.18	1.24
60	413722	BE247354	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.14	1.95
	433874	AW204429	Hs.155033	ESTs	2.13	1.72
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.12	0.91
	414290	A1568801	Hs.71721	ESTs	2.11	0.81
65	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.11	1.01
	406785	AA588061		gb:nk10d03.s1 NCI_CGAP_Co2 Homo sapiens	2.10	1.61
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.08	0.85
	444179	W35132	Hs.267442	ESTs	2.08	1.13
70	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.05	0.80
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.04	0.79
	439134	AA830599		ESTs	2.04	1.89
	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.02	2.02
75	457311	A497811	Hs.172753	Homo sapiens chromosome 19, BAC 41195 (C	2.00	1.45
	402274			C19000498:g14567179 gb AAD23607.1 AC00	1.88	2.24
	453222	AA033929	Hs.19156	ESTs	1.77	2.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.73	2.02
80	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	1.69	1.69
	406714	A1219304	Hs.266959	hemoglobin, gamma G	1.62	2.47
	418333	W92113		gbzh48e01.r1 Soares_fetal_liver_spleen_	1.59	2.04
	404090			Target Exon	1.48	2.03
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fls, clone K	1.39	2.06
	414386	X00442	Hs.75990	haploglobin	1.09	1.44
	439372	AF088033	Hs.159225	ESTs	1.05	2.13
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.01	2.08
	412472	AW975398	Hs.293836	ESTs	1.00	2.26
	432894	AW167668	Hs.279772	brain specific protein	0.97	1.19
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.96	2.06
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	0.95	1.08

5	424310	AA338648	Hs.50334	testes development-related NYD-SP22	0.93	1.47
	422109	S73265	Hs.1473	gastrin-releasing peptide	0.92	3.05
	420440	NM_002407	Hs.97644	mammaglobin 2	0.91	2.11
	418196	A1745649	Hs.26549	KIAA1708 protein	0.90	2.25
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	0.89	1.11
	419231	AL046294	Hs.135245	ESTs, Weakly similar to T17227 hypothet	0.85	1.74
	446608	N75217	Hs.257846	ESTs	0.82	2.10
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	0.73	1.32
10	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	0.70	1.76

TABLE 36B:

15	Pkey:	Unique Eos probeset Identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
	Pkey	CAT	Number	Accession
20	435375	130020_1	A1733610	A1049989 AA678769
	414009	438978_1	BE221268	R67515 AV730582 R67516
	406785	0_0	AA588061	
	439134	2581476_1	AA830599	AA970659 AA883802
	418512	12225_6	BMD46773	AA224297 T33786 T08951 T09274 T08592 T30936 AA350905
25	418333	73080_1	AF264624	AW668618 AV731448 R93353 AA584550 AV732728 BF602614 BF434359 AA077092 BI027317 AA199812 AW629027 AA831618 AI124782 AA765804 AA055698 AA677404 AA055366 AA889402 AA765530 BE503126 BE467367 AW139964 WB1697 AI887846 WB1696 AA447817 AA447667 F13631 BF055573 AW268271 AW088477 BF677839 AL601859 AW502118 AW502624 AA574189 BI020104

TABLE 36C:

35

Pkey:

Ref:

Strand:

NL_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) [Nature](#) 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

40

Pkey	Ref	Strand	NL_position
402274	2935596	Plus	5604-6527
404090	9967460	Minus	100815-100966

TABLE 37A: About 206 genes downregulated in lung fibrosis relative to normal lung

50	Pkey:	Unique Eos probeset Identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of normal lung AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.			
55	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	454229	AW957744	Hs.278469	lacrimal proline rich protein	11.67
	432128	AA127221	Hs.296502	ESTs	9.86
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	7.69
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.32
60	420958	AA309431	Hs.66	Interleukin 1 receptor-like 1	7.13
	402608			Homo sapiens defensin, alpha 1, myeloid-	6.67
	406714	A1219304	Hs.266959	hemoglobin, gamma G	5.40
	406673	M34998	Hs.198253	major histocompatibility complex, class	5.22
	416539	Y07909	Hs.79368	epithelial membrane protein 1	5.04
65	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.77
	409385	AA071267		gb:zm61g01.r1 Stratagene fibroblast (937	4.74
	450847	NM_003155	Hs.25590	stanniocalcin 1	4.46
	404518			CD83 antigen (activated B lymphocytes, I	4.38
	413951	AW061200	Hs.75640	neuropeptide precursor A	4.32
70	407570	Z19002	Hs.37096	zinc finger protein 145 (Krueppel-like, e	4.25
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23
	429509	AW614420	Hs.204354	ras homolog gene family, member B	4.14
	445769	A1741471	Hs.23666	ESTs	4.10
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.06
75	425571	AJ007292	Hs.158306	ephrin-A2	3.92
	423168	R34385	Hs.124940	GTP-binding protein	3.80
	401234			mitogen-activated protein kinase 8 Inter	3.78
	402181			Target Exon	3.77
	403479			NM_007064:Homo sapiens serine/threonine	3.68
80	435424	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL	3.68
	402911			NM_021158:Homo sapiens protein kinase d	3.66
	442195	NM_001430		endothelial PAS domain protein 1	3.65
	400089			Eos Control	3.60

	413948	C05145	Hs.75636	myosin light chain 2a	3.56
	438564	AA381553	Hs.198253	major histocompatibility complex, class	3.54
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.54
5	413119	AA873350	Hs.302232	ESTs	3.52
	434292	AF124358	Hs.306551	Homo sapiens IMAGE Consortium ID 839832,	3.48
	401540			NM_002675:Homo sapiens promyelocytic leu	3.46
	426477	AA379464	Hs.154073	gb:EST92386 Skin tumor 1 Homo sapiens cD	3.43
	402328			Target Exon	3.42
10	401590			Target Exon	3.42
	403645			NM_024513:Homo sapiens FYVE and coiled-	3.37
	403376			Target Exon	3.36
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.35
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.28
15	413719	BE439580	Hs.75498	small Inducible cytokine subfamily A (Cy	3.27
	401126			NM_006856:Homo sapiens activating trans	3.27
	408243	Y00787	Hs.624	Interleukin 8	3.23
	412429	AV650262	Hs.75765	GRO2 oncogene	3.22
	426420	BE383808	Hs.322430	NDRG family, member 4	3.21
20	449338	H73444	Hs.394	adenomedullin	3.19
	401904			Target Exon	3.16
	401919			NM_012448:Homo sapiens signal transduca	3.14
	406443			ENSP00000236574:Hypothetical 21.8 kDa p	3.14
	458232	BE217872	Hs.279537	ESTs	3.12
25	406016			Target Exon	3.12
	450912	AW939251	Hs.25647	v-fos FBI murine osteosarcoma viral onco	3.11
	451831	NM_001674	Hs.460	activating transcription factor 3	3.08
	450562	AW136468	Hs.202199	ESTs	3.07
	405938			Target Exon	3.04
30	451029	AA852097	Hs.25829	ras-related protein	3.02
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	2.98
	439839	AA889354		ESTs	2.98
	439891	AL389940	Hs.109968	ESTs	2.96
	418935	T28499	Hs.89485	carbonic anhydrase IV	2.95
35	418853	NM_005236	Hs.89296	excision repair cross-complementing rode	2.95
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.94
	410326	AI368909	Hs.47650	ESTs	2.88
	407244	M10014		fibrinogen, gamma polypeptide	2.85
40	459721	AI299050	Hs.143835	gb:q14d12.x1 NCL_CGAP_Lu5 Homo sapiens	2.84
	416212	R40290	Hs.124685	ESTs	2.84
	428686	AA431801	Hs.98764	ESTs, Weakly similar to A29861 actin gam	2.83
	437508	AI204354	Hs.121347	ESTs	2.82
	437990	AI686579	Hs.121784	ESTs	2.82
	443709	AI082692	Hs.134662	ESTs	2.81
45	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	2.80
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral onco	2.79
	404231			Target Exon	2.78
	434305	AI018280	Hs.130189	ESTs	2.77
	445493	AI915771		metallothionein 1E (functional)	2.76
50	418056	AA524886		gb:rh34f02.s1 NCL_CGAP_Pr3 Homo sapiens	2.76
	404102			Target Exon	2.75
	440206	AI762232	Hs.46794	ESTs	2.75
	403031			cathepsin D (lysosomal aspartyl protease	2.75
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	2.74
55	459330	C16931		gb:C16931 Clontech human aorta polyA mRN	2.74
	456967	AW004056	Hs.168357	T-box 2	2.74
	427602	AI375258	Hs.98005	ESTs	2.74
	431367	Z20964	Hs.323817	DKFZP547E1010 protein	2.72
	406059			Target Exon	2.71
60	420575	BE263301	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.71
	457275	AA463422	Hs.209431	ESTs	2.71
	432559	AW452948	Hs.257631	ESTs	2.71
	402483			NM_020389:Homo sapiens putative capacita	2.70
	416069	R37101	Hs.20982	ESTs	2.70
65	445445	AF238870	Hs.275706	Homo sapiens clone GLSH-3 similar to gll	2.69
	436232	AA707006	Hs.187863	ESTs	2.68
	418773	T39748	Hs.325474	Target CAT	2.67
	434038	AA622104		ESTs	2.67
	405448			Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.66
70	404439			ENSP00000067222:Mitochondrial 28S ribos	2.65
	435724	N39308	Hs.117898	ESTs	2.65
	404026			Target Exon	2.65
	400881			NM_025080:Homo sapiens hypothetical prot	2.64
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	2.62
75	405429			Target Exon	2.62
	402642			C1002296:gll6677617refl[NP_033126.1] rep	2.61
	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	2.61
	449293	AA001088	Hs.29739	ESTs, Weakly similar to C34323 GTP-bind	2.61
	418157	NM_003243	Hs.342874	transforming growth factor, beta recepto	2.60
80	446122	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.59
	433291	AF007191		gb:Homo sapiens SIB 276 Intestinal mucin	2.59
	426795	AI810474	Hs.196945	ESTs	2.58
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.58
	430768	AB030207	Hs.247888	guanine nucleotide binding protein 13, g	2.58

	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.57
	442681	AI809182	Hs.130907	ESTs	2.57
	408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	2.56
5	402217			C19001662*gi 5753872 ref NP_034345.1	2.56
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.56
	455674	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	2.56
	457831	AA706937	Hs.120802	ESTs, Moderately similar to A25641 Na7ex	2.56
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.55
10	458648	AW444551	Hs.35380	x 001 protein	2.55
	456663	BE251104	Hs.113052	RNA cyclase homolog	2.54
	440178	AW502463	Hs.195521	ESTs	2.53
	457139	AI557280	Hs.184270	capping protein (actin filament) muscle	2.52
	405857			Target Exon	2.51
15	410204	AJ243425	Hs.326035	early growth response 1	2.50
	412851	AI826502	Hs.97269	ESTs	2.49
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	2.49
	409209	AA460160	Hs.73217	ESTs	2.49
	447173	AW449385	Hs.157294	ESTs	2.48
20	440034	AI908639	Hs.246781	ESTs	2.44
	418168	R85350	Hs.101368	ESTs	2.43
	417295	AW993524	Hs.43148	epithelial membrane protein 1	2.43
	406305			transcriptional adaptor 3 (ADA3, yeast h	2.42
	427886	AA417083	Hs.104789	ESTs	2.42
25	436409	AJ238982	Hs.183656	VNN3 protein	2.42
	413861	BE175424		gb:RC4-HT0578-170300-012-d01 HT0578 Homo	2.40
	403605			C3000142*gi 4503015 ref NP_003900.1 co	2.37
	402594			C1002603*gi 9887091 gb AA01738.1 AF248	2.37
	402803			NM_001397:Homo sapiens endothelin conver	2.37
30	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.36
	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypothet	2.36
	442630	AW572938	Hs.130580	ESTs	2.35
	409368	AA071059		gb:zm66a10.r1 Stralagene neuroepithelium	2.33
	405156			NM_003213*:Homo sapiens TEA domain fami	2.31
35	448162	AL039531	Hs.323363	hypothetical protein FLJ22169	2.31
	403591			Target Exon	2.31
	406193			Target Exon	2.30
	420813	X51501	Hs.99949	prolactin-induced protein	2.30
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	2.28
40	400703			C11001794*gi 10946612 ref NP_067286.1	2.27
	415026	AA159356	Hs.72308	ESTs	2.25
	400334	Y13187		Homo sapiens drmd gene, intron 11	2.18
	445878	AI262974	Hs.145587	ESTs	2.18
	404975			uncharacterized hypothalamus protein HT0	2.18
45	436370	R01220	Hs.185679	ESTs	2.17
	400513			Target Exon	2.16
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.15
	415405	R59141		gb:yg96d11.r1 Soares Infant brain 1N1B H	2.15
	407612	U26403	Hs.37142	ephrin-A5	2.12
50	409837	AW501504		gb:UI-HF-BP0p-ajd-h-04-0-UI.r1 NIH_MGC_5	2.08
	458637	AV657446		gb:AV657446 GLC Homo sapiens cDNA clone	2.07
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	2.00
	418922	AW856580	Hs.42699	ESTs	1.98
	402404			NM_024967*:Homo sapiens hypothetical pro	1.98
55	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	1.98
	413731	BE243845	Hs.75511	connective tissue growth factor	1.96
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.96
	428193	NM_004235		Kruppel-like factor 4 (gut)	1.93
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.92
60	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	1.92
	433883	AI925688	Hs.222312	ESTs	1.91
	406564			msh (Drosophila) homeo box homolog 2	1.91
	403581			Target Exon	1.90
	403716			Target Exon	1.90
	404758			Target Exon	1.90
65	439500	W73158	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	1.89
	448793	AI864581		ESTs	1.84
	435857	AF253468	Hs.3736	della-like 4 homolog (Drosophila)	1.83
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.82
70	402051			Target Exon	1.81
	409859	AW501926		gb:UI-HF-BR0p-ajp-l-08-0-UI.r1 NIH_MGC_5	1.78
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.78
	405063			Target Exon	1.78
	405163			C5000561*gi 7513700 pf T14151 Inv pro	1.75
75	402388			Target Exon	1.73
	406755	N80129	Hs.199263	metallothionein 1L	1.73
	405811	AW500896		gb:UI-HF-BR0p-ajp-l-03-0-UI.r1 NIH_MGC_5	1.70
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.70
	400489			Target Exon	1.70
80	428704	AA432007	Hs.192090	ESTs	1.69
	429307	AU076592	Hs.198951	jun B proto-oncogene	1.67
	400116			Eos Control	1.65
	404795			Target Exon	1.65
	408053	AW139474	Hs.246862	ESTs	1.65

414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	1.63
428800	M57627	Hs.193717	Interleukin 10	1.63
451676	R84770	Hs.33538	ESTs, Weakly similar to oxygen-regulated	1.62
402394			Target Exon	1.61
404818			Target Exon	1.60
436364	X06096		gb:Human macrophage alpha1-antitrypsin c	1.55
420369	U96769	Hs.97220	chondroadherin	1.54
405590			CX001497:gi4557543[refNP_001384.1] ex	1.54
402448			Target Exon	1.53
433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.51
409020	AA062549	Hs.21162	retbindin	1.51
405443			Target Exon	1.12

TABLE 37B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409385	110758_1	T65940 T64515 AA071267 AA071334
442195	15007_1	U81984 NM_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650 BI053717 BE929315 BI054967 BF960055 BF925432 R05421 BF922073 T70331 BI004403
439839	2594580_1	AK023587 AA889354 AA846791
445493	423456_1	AV711317 AI809938 AI808768 AI240593 AI915771
418056	286199_1	AW971347 AA524886 AA211537 BF903005 BF357120
413164	1492512_1	BE068758 BE068745 BE068689 BE068778 BE068529 BE068883 BE068445 BE068392 BE068719 BE068473 BE068521 BE068628 BE068422 BE068618 BE068354 BE068390 BE068414 BE068433 BE068369 BE068384 BE068661 BE068324 BE068301 BE068436 BE068754 BE068329 BE068672 BE068494 BE068596 BE068332 BE068347 BE068588 BE068328 BE068493 BE068740 BE068685 BE068759 BE068307 BE068429 BE068303 BE068693 BE068374 BE068295 BE068625 BE068302 BE068653 BE068675 BE068579 BE068311 BE068674 BE068547 BE068602 BE068605 BE068352 BE068306 BE068401 BE068537 BE068552 BE068450 BE068723 BE068393 BE068671 BE068748 BE068317 BE068447 BE068568 BE068632 BE068357 BE068330 BE068498 BE068831 BE068540 BE068410 BE068626 BE068591 BE068522 BE068676 BE068499 BE068361 BE068598 BE068350 BE068299 BE068580 BE068567 BE068692 BE068321 BE068327 BE068739 BE068526 BE068538 BE068765 BE068340 BE068733 BE068293 BE068565 BE068480 BE068476 BE068761 BE068712 BE068705 BE068549 BE068419 BE068383 BE068434 BE068418 BE068525 BE068543 BE068752 BE068550 BE068623 BE068470
459330	105725_1	BG563152 BF846777 BF849354 BF849359 BF846636 BF849201 BF849356 C16931 AA056717 AW864542 AW882724 AA056567
434038	630986_1	AI910738 AW139227 AA932891 AA622104
433291	73706_1	AF007191 AW820706 BG978594 BF872238
423387	2612_2	L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW848084 AA903896 AA18962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
455674	1490762_1	BE065941 BE065997 BE066003 BE066070 BE066098
413861	1561647_1	BF352282 BE175424 BE175418 BE175383
409368	110612_1	AA071059 AA085021 AA085020
415405	1872126_1	W18191 R59141 R54142 R12130 F11362 Z47294 F08242 F07925 H21084 R54090 R59142
409837	915621_1	AW501504 AW501656 AW503048 AW502449 AW502098
458637	395206_1	AV657752 AV657446
428193	430_1	AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI266211 AW074303 AA620711 BF197792 AW008768 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF614079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI355073 AI024576 AA298805 H04001 H45668 BG682145 AL552388 BI462361 BG547513 BG895863 BI256661
448793	3006936_1	AI936948 AI864581 AI570541
409859	916430_1	AW501926 AW502566 AW501927
409811	58948_2	AK057581 AW500982 AW500896 AW501105
400116	5269_1	D42041 NM_014610 AJ000332 BI758702 BG720650 AU141129 AU130711 AU141380 AU132402 BM048556 AU127520 BE259984 AU128952 BE814151 AL601516 BM146777 AU128103 BM194094 BE937951 BE696396 AK026597 AK026567 BF959293 BE798100 BI086881 BG166248 BE877845 BG385414 AW886747 BF093789 AW390159 BF820311 AA421676 AW880845 AW404827 BF726465 BE161190 BE254102 AW406002 BE161223 AI912055 BF930228 AW374357 AW794531 BE720524 BE933982 BE933658 BE933694 BE933978 BE933654 BE933583 BE166557 BE933874 BE933641 BE933859 BE933628 BE933866 BE933633 BE933864 BE933631 BE933887 BE933634 BE933857 BE933624 BE933863 BE933650 BE720491 AA420426 BE720410 BE720458 BE720444 BE720411 AW368748 BF874616 BE933498 BE835979 BF926667 AW849921 AW850026 AW850022 AW849977 AW849900 BG250251 W87689 AI92825 AI692824 AA426263 AI090315 AI309537 AA877437 AA478438 AI538868 AW276162 AI279916 AA600318 AI188836 AW682284 AI262619 AA293457 BF347442 AA421677 AA658063 AA565510 AA937060 AI142684 AA788940 AA827426 AU152614 AI342784 AU148738 AA219664 AA047835 H99450 AA018563 AI073634 BM475120 BG875251 BG248778 U46372 AA383858 AU140356 BG821891 BF935049 BI760656 BI054103 BF982309 BE872215 BI257291 AU158469 AU160599 AU152469 AU152375 AU152059 AU148575 N32267 AU149554 AI627459 AI719840 AW779017 AI291493 AW304181 AW470055 AI086491 AI311387 AI634232 AI151241 AI288848 AW505088 AW589580 AI241353 AI880219 AA039309 AA026517 AA016238 AA013444 H86822 R87530 AA058462 N27082 Z39679 BE544309 W52619 AA018076 AI813668 AW189907 AI418104 AU159878 AU150087 R21754 AA015932 H87274 AU153097 AI961344 AA018208 W32429 R45344 R77453 BM470129 AU130415 BI227374 BE298179 AW844963 AW844983 AI904066 AA379005 BF850571 AA355641 BG747156 AL547262 AW367941 BE560004 BI116061 BG899031 BE560318 BF174177 BI051456 BE001967 BE388446 BF969326 BF808765 BF684480 BG421617 AI940607 AW875483 BE789632 BF808711 BI192691 AW904249 BI911430 BE265407 BE730343 BE397808 BI226516
414580	623093_1	BG333973 BE385437 BE408833 BE387650
436364	1414_37	X05826 X06096 BG468890 AW951851 W23562 T28392 H56742 H58030 T69205

TABLE 37C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
5	402608	9910096	Plus	37495-37669
	404518	8151988	Plus	84494-84603
	401234	9929642	Plus	120173-120337
	402181	8575912	Plus	449746-450040
10	403479	7329292	Minus	148369-148533,150678-150809
	402911	7263904	Plus	142689-142979
	401540	8072433	Plus	106838-107310
	402328	4464283	Minus	13758-13922,14558-14752
	401590	9966320	Minus	33547-33649
15	403645	8699714	Minus	4433-4582
	403376	9369545	Minus	108698-108830
	401126	8699701	Minus	68290-68487
	401904	8671966	Plus	60959-61603,62670-62890,63778-63838
	401919	9502466	Plus	67536-67666
20	406443	9280765	Plus	85951-87327
	406016	8272661	Plus	41341-41940
	405938	6758795	Minus	166671-167411
	404231	8218035	Minus	61077-61322
	404102	7229900	Plus	97685-98018
25	403031	7768597	Minus	1308-1416
	406059	9103984	Minus	13856-14004
	402483	7574980	Minus	65578-66119
	405448	7582529	Plus	136347-136532
	404439	7139680	Plus	55316-55585
30	404026	7582549	Minus	79574-79968
	400881	2842777	Minus	91446-91603,92123-92265
	405429	7321905	Minus	51577-51723
	402642	9958129	Minus	125599-125756
	402217	9795981	Minus	21521-21757
35	405857	6758728	Plus	26564-26819
	406305	8575869	Plus	108239-108386,112216-112378,115388-11557
	403605	6862654	Plus	91614-91718
	402594	7705170	Plus	103082-103414
	402803	3287156	Minus	55923-56033
40	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	403591	8101229	Plus	4201-4833
	406193	7289992	Plus	30183-30662
	400703	8118859	Plus	63657-63857,64802-64905
	404975	3419864	Minus	86098-86605
45	400513	9796593	Plus	74613-74823
	402404	3970932	Plus	53154-53280
	406564	7711604	Minus	52788-53013
	403581	8101182	Plus	6794-7396
	403716	7239669	Plus	86899-87122
50	404758	7706327	Minus	130204-130806
	402051	8082020	Minus	19346-19480,20041-20119
	405063	7658414	Minus	111047-111666
	405163	9966267	Minus	161171-161299
	402386	9799769	Plus	22069-22303
55	400489	8954013	Plus	131475-131652
	404795	4826439	Plus	147501-147780
	402394	9929690	Plus	33308-33482
	404818	2769655	Plus	33671-33839
	405590	6960456	Plus	90492-90818
60	402448	9796640	Plus	112942-113069,114303-114521
	405443	7408143	Plus	90716-90887,101420-101577

65 TABLE 38A: About 207 genes upregulated in lung fibrosis relative to normal tissues

70	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of lung fibrosis AIs divided by 70th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.			
75	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.28
	407891	AA486620	Hs.41135	endomucin-2	4.14
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.07
	410219	T98226	Hs.171952	occludin	3.96
80	434666	AF151103	Hs.112259	T cell receptor gamma locus	3.88
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	3.87
	406617			Target Exon	3.76
	420568	F09247	Hs.247735	protocadherin alpha 10	3.70
	425873	NM_013390	Hs.160417	transmembrane protein 2	3.69

	438797	C16161	Hs.283040	hypothetical protein PRO2543	3.68
	410315	AI638871	Hs.152519	Homo sapiens cDNA: FLJ22524 fis, clone H	3.65
	446714	W73818	Hs.110028	ESTs	3.64
5	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.61
	430259	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog	3.58
	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.56
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	3.56
	412654	AI093480		hypothetical protein FLJ11896	3.56
10	414386	X00442	Hs.75990	haploglobin	3.54
	451035	AU076785	Hs.430	plastin 1 (I isoform)	3.52
	436473	AI193122	Hs.132275	ESTs	3.51
	406714	AI219304	Hs.266959	hemoglobin, gamma G	3.46
	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	3.45
15	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.45
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	3.39
	452813	U54727	Hs.191445	ESTs	3.36
	442831	AI798959	Hs.131686	ESTs	3.35
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and Z3905 mRNA	3.34
20	445330	R52656	Hs.21691	ESTs	3.31
	436001	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.31
	431681	AK000378	Hs.267566	hypothetical protein FLJ20371	3.29
	432314	AA533447	Hs.312989	ESTs	3.28
	435129	AI381659	Hs.267088	ESTs	3.28
25	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.24
	422607	Z45471	Hs.118684	stromal cell-derived factor 2	3.21
	421205	AL137540	Hs.102541	netrin 4	3.20
	428582	BE336699	Hs.185055	BENE protein	3.20
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.19
30	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	3.17
	421233	AA209534	Hs.284243	tetraspan NET-6 protein	3.17
	429350	AI754634	Hs.131987	ESTs	3.16
	428727	AF078847	Hs.191356	general transcription factor IIH, polype	3.16
	434850	Z43161	Hs.283714	30 kDa protein	3.13
35	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.12
	446506	AI123118	Hs.15159	chemokine-like factor, alternatively spl	3.11
	416114	AI695549	Hs.183868	glucuronidase, beta	3.10
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	3.09
	444212	AW503976	Hs.10649	basement membrane-induced gene	3.08
40	422442	AA324998	Hs.147086	signal transducer and activator of trans	3.08
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	3.08
	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	3.07
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.07
	445107	AI208121	Hs.147313	ESTs, Weakly similar to I38022 hypotheti	3.06
45	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	3.04
	428106	BE620016	Hs.182470	PTD010 protein	3.04
	428403	AI393048	Hs.326159	leucine rich repeat (in FLI) interactin	3.04
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.03
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.02
50	423067	AA321355	Hs.285401	colony stimulating factor 2 receptor, be	3.01
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	2.96
	415000	AW025529	Hs.239812	Homo sapiens serologically defined breas	2.96
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	2.96
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	2.96
55	419660	BE280337	Hs.194693	solute carrier family 7 (cationic amino	2.96
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.95
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	2.94
	416883	AW140128	Hs.184902	ESTs	2.92
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	2.92
60	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	2.92
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.92
	429640	U83508	Hs.2463	angiotensin 1	2.91
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	2.91
	401958			Target Exon	2.90
65	416926	H03109	Hs.263395	HT018 protein	2.90
	433691	AA605012		ESTs	2.88
	441892	AB028981	Hs.8021	KIAA1058 protein	2.87
	439453	BE264974	Hs.5566	thyroid hormone receptor interactor 13	2.87
70	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.87
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	2.87
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	2.87
	435913	W85006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	2.86
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	2.85
	451356	AA748418	Hs.164577	ESTs	2.85
75	442085	AA975688	Hs.153955	ESTs	2.84
	427704	AW971063	Hs.292882	ESTs	2.83
	427247	AW504221	Hs.174103	Integrin, alpha L (antigen CD11A (p180),	2.83
	441965	AA972712	Hs.269737	ESTs	2.82
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	2.82
80	450056	BE047394	Hs.8208	ESTs, Weakly similar to S71512 hypotheti	2.80
	407245	X90568	Hs.172004	itin	2.80
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.80
	446601	AI312783	Hs.155772	Homo sapiens thymic stromal co-transport	2.80
	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.80

	449088	AI654048	Hs.196556	ESTs	2.80
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.80
	406648	AA583730	Hs.277477	major histocompatibility complex, class	2.79
5	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	2.78
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	2.78
	440255	AI932285	Hs.160569	ESTs	2.78
	410057	R65634	Hs.268107	multimerin	2.77
	417497	AW402482	Hs.82212	CD53 antigen	2.77
10	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.76
	431884	AA521246	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.75
	409869	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	2.75
	436729	BE621807		transmembrane 4 superfamily member 1	2.75
	431451	AA761378	Hs.192013	ESTs	2.74
15	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.74
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	2.74
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	2.74
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.74
	443194	AI954968		matrix Gla protein	2.71
20	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.71
	452870	AW502761	Hs.30909	KIAA0430 gene product	2.70
	430334	AI824719	Hs.143251	ESTs	2.70
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	2.70
	432279	N95104	Hs.274260	ATP-binding cassette, sub-family C (CFTR	2.70
25	413950	AA249096	Hs.32793	ESTs	2.70
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.70
	431710	AI735482		ESTs	2.70
	448749	AW858679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	2.69
	451154	AA015879	Hs.33536	ESTs	2.69
30	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	2.69
	446899	NM_005397	Hs.16426	podocalyxin-like	2.68
	418031	AA648744	Hs.269493	ESTs	2.68
	453902	BE502341	Hs.3402	ESTs	2.68
	405121			mitogen-activated protein kinase 8 inter	2.68
35	410163	AF151977	Hs.59260	NTT5 protein	2.67
	429632	AW195336	Hs.148910	ESTs	2.67
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	2.67
	455004	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo	2.67
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	2.67
40	401113			solute carrier family 22 (organic cation	2.66
	419462	AF071076	Hs.112255	nucleoporin 98kD	2.66
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-fin	2.66
	419175	AW270037		KIAA0779 protein	2.66
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.66
45	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.66
	430592	AJ224864	Hs.9688	leukocyte membrane antigen (IRC1)	2.65
	446830	BE179030		Human DNA sequence from clone RP5-1174N9	2.64
	433327	AI674779	Hs.126744	ESTs	2.64
	424868	AJ568170	Hs.96886	ESTs	2.64
50	429854	R55508	Hs.99472	ESTs	2.63
	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.63
	456711	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	2.63
	419777	D60134	Hs.270975	ESTs	2.63
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	2.62
55	427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.62
	452445	AB002438	Hs.29596	Homo sapiens mRNA from chromosome 5q21-2	2.62
	447482	AB033059	Hs.18705	KIAA1233 protein	2.62
	419110	AA234171	Hs.187626	ESTs	2.62
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	2.62
60	419828	T81422	Hs.14922	ESTs	2.62
	427202	BE272922	Hs.173936	Interleukin 10 receptor, beta	2.62
	412491	W31589	Hs.73957	RAB5A, member RAS oncogene family	2.61
	436496	AA281959	Hs.5210	glia maturation factor, gamma	2.61
	435053	AW629386		ESTs	2.61
65	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.61
	425978	C75094	Hs.334514	NG22 protein	2.60
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	2.60
	430539	AK001489		ADP-ribosylation factor-like 1	2.60
	419825	AJ754011	Hs.7326	ESTs	2.59
70	412577	Z22968	Hs.74076	CD163 antigen	2.58
	425894	AW954011	Hs.180711	ESTs	2.58
	410883	D43767	Hs.66742	CCL17 chemokine (TARC) (SCYA17)	2.58
	441028	AJ333660	Hs.17558	Homo sapiens cDNA FLJ14446 fis, clone HE	2.58
	413949	AA316077	Hs.75639	Human TB1 gene mRNA, 3' end	2.58
75	434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	2.58
	443805	H06865	Hs.134131	ESTs	2.57
	425017	AL119305	Hs.26409	ESTs	2.57
	440334	BE276112	Hs.7165	zinc finger protein 259	2.56
80	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.56
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.56
	407174	T79938	Hs.77062	leukocyte immunoglobulin-like receptor,	2.56
	443834	AI741510	Hs.173548	ESTs	2.55
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.55
	420539	AA282735	Hs.44004	AD031 protein	2.55

421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	2.54
437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.54
422994	AW891802	Hs.296276	ESTs	2.54
411992	AW816214	Hs.143055	ESTs	2.54
451180	H61899	Hs.171937	steroid dehydrogenase-like	2.54
415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.53
429752	H52348	Hs.36636	ESTs	2.53
414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.53
453329	T97205	Hs.193400	ESTs, Weakly similar to 2109260A B cell	2.53
436503	AJ277750	Hs.183924	ubiquitin associated and SH3 domain cont	2.52
445911	AJ985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.52
433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.52
435943	R60194	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.52
452253	AA928891	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H	2.52
442506	BE566411	Hs.41726	ESTs	2.52
419972	AL041465	Hs.182982	golgin-67	2.52
431074	BE072772	Hs.8997	ESTs, Moderately similar to A46010 X-fin	2.52
449129	AI631602	Hs.258949	ESTs	2.52
440524	R71264	Hs.16798	ESTs	2.51
419203	AA488719	Hs.190151	ESTs	2.51
404370			Target Exon	2.51
432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.61
439219	N33883	Hs.41322	ESTs	2.51
428044	AA093322	Hs.301404	RNA binding motif protein 3	2.50
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.50
437644	AA748575	Hs.136748	lectin-like NK cell receptor	2.50
442566	R37337	Hs.12111	ESTs	2.50
409317	U20165	Hs.53250	bone morphogenetic protein receptor, typ	2.50
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	2.50
447484	AA464839	Hs.292566	hypothetical protein FLJ14697	2.50
415165	AW887604	Hs.78065	complement component 7	2.50
435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	2.50

TABLE 38B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412654	1350_1	BG743181 AI830050 BE695688 AA126591 AI903503 R26045 N62894 N63950 AA131619 AI681480 N79626 AA461603 R78979 AW608865 N66622 BF448838 AA779000 AA460314 AI092721 AI870182 AI436284 AI494151 AI127704 AI127702 BE349350 AI093480 AA115264 AA131567 R26840 R78885
433691	2203511_1	AI223854 AI129852 AA605012
436729	6624_1	X75684 AL573167 AJ445461 AJ453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI798814 AA129575 AI671727 AI470033 BE546195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C05123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI885583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035578 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AI574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW606193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773499 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF767734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI587995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE158360 T65026 AW242958 AW197954 BE905184 AA722208 AI344943 AI348877 AI334850 BE821857 BE156280 AA454099 AA037722 BF843897 AW086183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG07601 BI818593 BF691383 BG721129 BG541578 BE906668 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429895 BE392488 AW961686 BG721056 BE908365 BE546556 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142165 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308838 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA93445 AI916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AI598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568964 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF688788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI433352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI793882 BF824747 AI741800 BG982862 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058268 AI362370 AI143352 AA508721 AI928079 D67214 BE045265 AA541785

5			BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 FZ7562 AA614749 D56645 F20774 F30660 F25646 AW023542 AA827300 AA582214 AI701289 AA228293 AI906950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518 AV704158 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215 AI422419 AA514370 AI741578 AI735482 AI735081 AI371436 AW850587 AW850589 AW850318 AW850303 AB018322 BC012480 BI524873 AW655554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA659046 AA961064 AI018062 H80618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA255551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314 BC020595 BI488430 BG168023 BE179030 AW294203 BF849776 AA459064 AI917452 AW403072 W27419 BF914568 BF798468 AW370558 T35055 AW370623 AA399232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060706 AA194237 T25074 C01285 BI489433 AI332638 AA663215 AW629386 AK001489 AU129447 BF959274 BG565452 AI245327 AU116848 BF358559 BF358554 BF358570 BG678119 AL515852 AU154607 AI357567 AW874359 AI122554 AA406478 AI091013 AI866679 AI686163 AA662158 AA911580 D31095 AI302576 BF588761 AU151560 AU143828 AI291610 AW169600 D31161 AA905362 C21179 BE327258 D31474 AW439053 D31309 BF756901 BI838626 BF979839 AU149562 BM142116 AU156455 AA452028 AW473972 AW468490 AA410271 AI475944 BF821859 AA658188 AI360390 AA226320 F37355 F27660 F36093 AA152126 BF930021 BF375775 AW821784 AW975085 W16475 D31031 BG696392 AW860676 AW752864 BI013705 BF965715 BF326604 AW821786
10	431710	1611592_1	
	455004	1089114_1	
	419175	35068_1	
15	446830	41421_1	
20	435053	124009_1	
	430539	31268_1	

TABLE 38C:

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
406617	8439858	Plus	36430-36552
401958	3258613	Plus	108411-108629
405121	8102330	Minus	35816-36004,36587-36684
401113	9966541	Minus	19419-19959
404370	7631003	Plus	127858-128244

TABLE 40A: 656 genes upregulated in fibrosis relative to normal body tissues

Table 40A lists about 656 genes upregulated in fibrosis relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar accession number, GenBank accession number
UniGeneID:	UniGene number
Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title:	UniGene gene title
R1	95th percentile of fibrosis AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

442275;	AW449467;	Hs.54795;	Homo sapiens secretoglobulin, family 3A, m; Uteroglobulin;TM=M;SS=Y; 39.47
428434;	AW363590;	Hs.65551;	Homo sapiens, Similar to DNA segment, Ch; LBP_BPL_CETP_C;TM=M;SS=Y; 32.35
439335;	AA742697;	Hs.62492;	NM_052863;Homo sapiens secretoglobulin, fa; none; 28.49
406964;	M21305;	;	FGENES predicted novel secreted protein; none,none; 27.90
425211;	M18667;	Hs.1867;	progastricsin (pepsinogen C); asp;TM=M;SS=M; 27.90
441835;	AB036432;	Hs.184;	advanced glycosylation end product-spec; homeobox,Acyltransferase,notch,EGF,ank,Acyltransferase; 27.23
446921;	AB012113;	Hs.16530;	small inducible cytokine subfamily A (C); IL8; 24.97
428330;	L22524;	Hs.2256;	matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 24.38
431723;	AW058350;	Hs.278966;	Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22_Claudin,none; 23.35
409153;	W03754;	Hs.50813;	hypothetical protein FLJ20022; fibrinogen_C; 23.29
431089;	BE041395;	Hs.374629;	ESTs, Weakly similar to unknown protein ; none,none; 18.23
425371;	D49441;	Hs.155981;	mesothelin; none;TM=M;SS=M; 18.17
448133;	AA723157;	Hs.73769;	folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 17.64
421502;	AF111856;	Hs.105039;	solute carrier family 34 (sodium phosphat; Ribosomal_L20,Na_PL_cotrans;TM=Y;SS=N; 17.33
421798;	N74880;	Hs.355462;	N-acylsphingosine amidohydrolase (acid c; SAPA,Surfactant_B,none; 16.81
419556;	U29615;	Hs.91093;	chitinase 1 (chilotriosidase); Glyco_hydro_18,CBM_14;TM=M;SS=Y; 16.24
419092;	J05581;	Hs.89603;	mucin 1, transmembrane; SEA;TM=Y;SS=M; 16.06
426174;	AA547959;	Hs.115838;	Homo sapiens similar to Echinoidin (LOC1; none,none; 15.84
406672;	M26041;	Hs.198253;	major histocompatibility complex, class ; ig,MHC_II_alpha;TM=M;SS=M; 15.42
421110;	AJ250717;	Hs.1355;	cathepsin E; asp; 15.08
444342;	NM_014398;	Hs.10887;	similar to lysosome-associated membrane ; Lamp;TM=Y;SS=M; 14.94

- 405621; X57809; Hs.181125; Immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M;SS=N; 14.36
 443709; A1082692; Hs.134662; ESTs; SNF,fn3,none; 14.05
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 13.88
 457200; U33749; Hs.197764; thyroid transcription factor 1; homeobox;TM=M;SS=N; 13.86
 432519; A1221311; Hs.130704; ESTs, Weakly similar to BCHUA S-100 pro; none,none; 13.82
 422355; AW403724; Hs.300697; coagulation factor VII (serum prothrombin; none,Ig; 13.62
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 13.47
 415457; AW081710; Hs.7369; Homo sapiens testis specific A2 homolog ; MORN,sugar_tr;TM=Y;SS=M; 13.35
 431164; AA493650; Hs.94367; thyroid transcription factor 1; none,homeobox; 13.32
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 12.83
 400269; Hs.253495; Eos Control; lectin_c,Collagen,Xlink; 12.30
 424310; AA338648; Hs.50334; testes development-related NYD-SP22; none;TM=M;SS=N; 11.81
 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1; ABC_tran,SRP54;TM=Y;SS=M; 11.79
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine ; none,none; 11.68
 445537; A1245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM; 11.56
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 11.41
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 11.31
 430832; A1073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none,none; 11.25
 407910; AA650274; Hs.41296; fibronectin leucine rich transmembrane p; fn3,LRR,LRRCT,LRRNT;TM=Y;SS=M; 11.15
 451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF,WIF; 11.07
 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 11.07
 411020; NM_006770; Hs.67726; macrophage receptor with collagenous str; SRCR,Collagen;TM=Y;SS=M; 11.05
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin; ; Osteopontin; 11.01
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.97
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,fn3,lectin,Xlink;TM=Y;SS=M; 10.93
 432231; AA339977; Hs.274127; CLST 11240 protein; none;TM=M;SS=M; 10.81
 416402; NM_000715; Hs.1012; complement component 4-binding protein; ; sushi;TM=M;SS=M; 10.77
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.63
 436553; AW407157; Hs.181125; Immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M;SS=N; 10.58
 421071; A1311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen ; none;TM=Y;SS=M; 10.57
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (Interstitial; hemopexin,Peptidase_M10,Aslactin,PG_binding_1; 10.33
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fn3,wrap; 10.30
 407766; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 10.28
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 10.26
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPase;TM=M;SS=N; 10.22
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 10.09
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alphi; vwa,Cacha;TM=M;SS=N; 10.03
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 10.02
 408562; A1436323; Hs.31141; roundabout (axon guidance receptor, Dros; Ig,fn3;TM=M;SS=N; 10.02
 448782; AL050295; Hs.362806; KIAA0758 protein; 7tm_2,Ig,GPS,SEA;TM=Y;SS=N; 9.88
 419235; AW470411; Hs.288433; neurotrophin; none,none; 9.79
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; none;TM=Y;SS=M; 9.74
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 9.70
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.69
 442652; A1005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 9.68
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 9.64
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin;TM=M;SS=N; 9.54
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.52
 449494; AW237014; Hs.315369; aquaporin 4; MIP,none; 9.51
 456062; A1866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none,none; 9.42
 446428; AW082270; Hs.12498; ESTs, Weakly similar to ALU4_HUMAN ALU S; none,none; 9.41
 421852; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); none,none; 9.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal_S14,ank,pkinase,death,none; 9.16
 456034; AW450979; ; gb:U1-H-B13-ata-e-12-0-ULs1 NCI_CGAP_Sur; none,none; 9.15
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ethand,S_100,S_100,ethand; 9.15
 416965; N26223; Hs.160438; MDAC1; none,NA,NA; 9.03
 443324; R44013; Hs.164225; ESTs; none,none; 9.03
 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid; Ig;TM=Y;SS=M; 9.00
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fis, clone L; none,none; 8.99
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374 gene NF2 ; Zn_carbOpept,none; 8.80
 409203; AA796873; Hs.687; cytochrome P450, subfamily IVB, polypept; p450;TM=M;SS=Y; 8.76
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 8.74
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 8.73
 425387; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 8.68
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; Ig;TM=Y;SS=M; 8.56
 421563; NM_006433; Hs.105806; granulysin; none; 8.55
 450726; AW204600; Hs.355462; HUMPSPBA Human pulmonary surfactant-asso; SAPA,Surfactant_LB,none; 8.51
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 8.51
 424450; AL137526; Hs.374425; dynein intermediate chain 2; WD40; 8.42
 402474; ; NM_004079;Homo sapiens calhepsin S (CTSS; Peptidase_C1; 8.41
 458079; A1796870; Hs.54277; Homo sapiens similar to RIKEN cDNA 28100; none;TM=M;SS=N; 8.40
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 8.36
 453310; X07697; Hs.553; solute carrier family 6 (neurotransmitter; SNF,5HT_transporter;TM=Y;SS=N; 8.34
 448140; AF146761; Hs.20450; BCM-like membrane protein precursor; Ig;TM=Y;SS=N; 8.33
 404240; ; NM_018950;Homo sapiens major histocompat; Ig,MHC_I;TM=Y;SS=M; 8.28
 459702; A1204995; ; gb:am03c03.x1 Stratagene schizo brain S1; none,none; 8.17
 445523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.17
 442994; A1028718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.12
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFp564B2062 (f; PMP22_Claudin,none; 8.07
 420137; AA305478; Hs.95327; CD3D antigen, delta polypeptide (TIT3 co; ITAM;TM=Y;SS=M; 8.01
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; Ig;TM=M;SS=M; 7.99
 432441; AW292425; Hs.163484; Intron of hepatocyte nuclear factor-3 at; Fork_head,none; 7.99
 409208; Y00093; Hs.172631; Integrin, alpha X (antigen CD11C (p150); ; vwa,FG-GAP,Integrin_A_vwa,Integrin_A-FG-GAP; 7.94

- 432605; NM_002104; Hs.3066; granzyme K (serine protease, granzyme 3; trypsin; TM=Y; SS=M; 7.92
 442832; AW206560; Hs.253569; ESTs; none, none; 7.90
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN cDNA 2210; none; TM=M; SS=N; 7.89
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig; TM=Y; SS=M; 7.86
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin; none; 7.84
 418299; AA279530; Hs.83966; Integrin, beta 2 (antigen CD18 (p95), ly; integrin_B, EGF_PSI; TM=Y; SS=M; 7.79
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (lazarus; none; TM=Y; SS=N; 7.78
 423961; D13666; Hs.136348; periosin (OSF-2os); Fasciclin; TM=M; SS=M; 7.73
 424917; A1636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M; SS=N; 7.72
 438564; AA381553; Hs.198253; major histocompatibility complex, class I; Ig_MHC_JL_alpha; none; 7.65
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, com; none, PK, PK_C, myosin_head, RhoGAP; 7.64
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR_c6; 7.63
 436954; AA740151; Hs.130425; ESTs; none, none; 7.58
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain; SH2; 7.56
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 7.55
 417105; X00992; Hs.81226; CD6 antigen; SRCR; TM=Y; SS=M; 7.51
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig; TM=Y; SS=M; 7.48
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 7.40
 432222; A1204995; ; gb:an03c03.x1 Stratagene schizo brain S1; none, none; 7.38
 422667; H25642; Hs.132821; ESTs; FMO-like, FMO-like; 7.37
 444527; NM_005408; Hs.11383; small inducible cytokine subfamily A (Cyr; IL8; 7.36
 457411; AW085961; Hs.130093; Iroquois-class homeobox protein IRX2; none, none; 7.32
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP; none; 7.32
 419231; A1046294; Hs.136245; ESTs, Weakly similar to T17227 hypothet; none, none; 7.30
 438873; A1302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fis, clone L; none, none; 7.27
 424027; AW337575; Hs.201591; ESTs; 7tm_2_HRM; none; 7.26
 428927; AA441837; Hs.90250; Homo sapiens hypothetical protein FLJ231; none, none; 7.24
 432435; BE218886; Hs.282070; ESTs; none, none; 7.22
 428467; AK002121; Hs.184465; hypothetical protein FLJ11259; none; TM=Y; SS=M; 7.21
 416030; H15261; Hs.21948; ESTs; none, none; 7.20
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; none; TM=M; SS=N; 7.18
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosome; pkinase, Activin_rec, pkinase, Activin_rec; 7.16
 420658; AA279098; Hs.187636; ESTs; none, none; 7.14
 427698; AW972594; Hs.335499; ESTs; none, none; 7.11
 432268; BE311856; Hs.274230; 3-phosphoadenosine 5-phosphosulfate sy; APS_kinase, ATP-sulfurylase; TM=M; SS=N; 7.06
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kina; SAM_PNT; none; 7.04
 430413; AW842182; Hs.241392; small inducible cytokine A5 (RANTES); IL8; TM=M; SS=Y; 7.04
 452363; A1582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen; 7.03
 421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 7.01
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.97
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide, TGF-beta; none; 6.96
 458124; AW005548; Hs.124590; ESTs; none, none; 6.94
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3, PX; TM=M; SS=N; 6.93
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; Inositol_P_Ig; TM=M; SS=N; 6.92
 428820; AA436187; Hs.172631; Integrin, alpha M (complement component; vwa, Integrin_A, FG-GAP; TM=Y; SS=M; 6.90
 423575; C18863; Hs.163443; intron of periosin (OSF-2os); Fasciclin; none; 6.89
 419490; NM_005144; Hs.90708; granzyme A (granzyme 1, cytotoxic T-lymp; trypsin; TM=M; SS=M; 6.89
 450954; A1904740; Hs.25691; receptor (calcitonin) activity modifying; none; TM=Y; SS=M; 6.87
 426976; C75094; Hs.334514; NG22 protein; voltage_CLC; TM=Y; SS=M; 6.84
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fis, clone L; LRR; TM=M; SS=N; 6.81
 414991; C17898; ; Homo sapiens up-regulated by BCG-CWS (LO; Zip; none; 6.80
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 6.80
 422163; AF027208; Hs.112360; promitin (mouse)-like 1; none; TM=Y; SS=M; 6.79
 445885; A1734009; Hs.127699; KIAA1603 protein; none, none; 6.77
 436576; A458213; Hs.77542; ESTs; 7tm_1_Dna; 6.77
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 6.76
 424711; NM_005795; Hs.152176; calcitonin receptor-like; 7tm_2_HRM; TM=Y; SS=M; 6.75
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 6.73
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54); Ig1, CAM_N; TM=M; SS=M; 6.71
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; Ig, abhydrolase; 6.70
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none, lectin_c; 6.70
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cyr; IL8; TM=M; SS=Y; 6.68
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans_K_tetraasp; 6.65
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, integrin_B, Ricin_B, lectin; 6.62
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 6.60
 453142; AA033648; Hs.7473; Homo sapiens gap junction protein, alpha; connexin; TM=Y; SS=M; 6.60
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none, none; 6.56
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 6.54
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; SS=N; 6.51
 446932; AA961459; Hs.125644; ESTs; none, LRR, LRRNT; 6.50
 427247; AW504221; Hs.174103; Integrin, alpha L (antigen CD11A (p180); vwa, Integrin_A, FG-GAP; TM=Y; SS=M; 6.48
 425998; A1076629; Hs.165950; fibroblast growth factor receptor 4; Ig, pkinase; TM=M; SS=M; 6.47
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none; TM=M; SS=M; 6.46
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadherin repeat; none, none; 6.43
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; WHEP-TRS, tRNA-syn1b; 6.41
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3_Y_phosphatase; TM=M; SS=N; 6.40
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lung and nas; none; 6.39
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BclA, RUN; TM=M; SS=N; 6.37
 413385; M34455; Hs.840; indoleamine-pyrole 2,3 dioxygenase; IDO; TM=M; SS=N; 6.36
 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 6.34
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/-pep; PTR2; TM=Y; SS=N; 6.32
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, Ig, FAD_Synth, Idh, Kdh_C, pkinase; 6.32

- 444090; S69115; Hs.10306; natural killer cell group 7 sequence; PMP22_Claudin; TM=Y; SS=M; 6.31
 416819; U77735; Hs.80205; pim-2 oncogene; kinase; 6.30
 421659; NM_014459; Hs.106511; protocadherin 17; cadherin; TM=M; SS=M; 6.27
 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; SS=N; 6.26
 424273; W40460; Hs.144442; phospholipase A2, group X; phospholipase; TM=M; SS=Y; 6.24
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; SS=N; 6.23
 452194; A1694413; Hs.373599; olfactory receptor, family 2, subfamily; none; none; 6.22
 424144; AA454033; Hs.11644; AKAP-associated sperm protein; Rila; 6.21
 414142; AW358397; Hs.334485; hemiscentin (fibulin 6); EGF; Ig; isp_1; hormone4; squash; TIL; Adeno_E3_CRI; TM=M; SS=M; 6.21
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482 hypothet; none; none; 6.20
 420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin (vascular; cadherin; Cadherin_C_term; TM=Y; SS=M; 6.19
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 6.17
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_HUMAN CALCY; none; NA; NA; 6.17
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 6.16
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor tyrosine phosphatase; none; 6.15
 410381; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP; GBP_C; TM=Y; SS=M; 6.13
 415765; NM_005424; Hs.78824; tyrosine kinase with immunoglobulin and ; EGF; fn3; Ig; kinase; laminin_EGF; TM=M; SS=Y; 6.12
 430478; NM_014349; Hs.241535; apolipoprotein L 3; Mo1A_ExtB; TM=Y; SS=M; 6.12
 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; none; TM=Y; SS=M; 6.09
 446608; N75217; Hs.175622; ESTs; Armadillo_seg; HEAT_PBS; TM=M; SS=M; 6.08
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily; IL2; 6.08
 426116; AA868729; Hs.144694; ESTs; none; none; 6.06
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 6.05
 426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012 hypothet; zf-C2H2; TM=M; SS=N; 6.05
 429228; A1553633; Hs.356828; ESTs; none; none; 6.05
 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase; 6.04
 437669; A1358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none; kinase; kinase_C; 6.03
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran; ABC_membrane; TM=Y; SS=M; 6.02
 428667; A1375550; Hs.346868; nucleolar protein p40; homolog of yeast; none; none; 6.01
 432731; R31178; Hs.287820; fibronectin 1; fn1, fn2, fn3; none; 5.95
 445566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.95
 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2; 5.94
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide (p32); Ig; TM=Y; SS=M; 5.94
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.94
 408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemin; TM=M; SS=N; 5.94
 438670; A1275803; Hs.123428; ESTs; none; NA; NA; 5.91
 424238; AA337401; Hs.137635; ESTs; none; TM=M; SS=M; 5.90
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2; none; 5.89
 423690; AA329548; Hs.23804; ESTs, Weakly similar to PNO099 son3 prot; ion_trans; IQ; none; 5.88
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 5.81
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor; ; Ig; TM=Y; SS=M; 5.81
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y; SS=M; 5.80
 420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 com; ITAM; TM=M; SS=M; 5.79
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr; TM=Y; SS=N; 5.79
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; SS=N; 5.79
 443257; A1334040; Hs.11614; HSPC065 protein; trypsin; TM=M; SS=N; 5.76
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; Ig; TM=Y; SS=N; 5.70
 435299; A1745458; Hs.343026; ESTs, Weakly similar to T20593 hypothet; none; NA; NA; 5.69
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2; PI-PLC-Y; PI-PLC-X; TM=M; SS=N; 5.67
 436772; AW975688; Hs.348918; metallothionein 1E (functional); 7tm_2; HRM; none; 5.67
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none; none; 5.66
 419833; AA251131; Hs.220597; Homo sapiens tryptophanyl-tRNA synthetase; WHEP-TRS; tRNA-synL1b; none; 5.66
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank; PH; ArfGAP; 5.64
 407756; AA116021; Hs.38260; ubiquitin specific protease 18; UCH-1; UCH-2; 5.63
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 5.63
 423533; NM_014339; Hs.129751; Interleukin 17 receptor; none; TM=Y; SS=M; 5.63
 419577; L36531; Hs.91296; Integrin, alpha 8; Integrin_A; FG-GAP; TM=Y; SS=N; 5.61
 452561; A1692181; Hs.49169; KIAA1634 protein; TPR; PDZ; WW; Guanylate_kin; TM=M; SS=N; 5.61
 428677; A1657119; Hs.351582; tropoin I, cardiac; none; TM=M; SS=N; 5.60
 425509; AF079363; Hs.158213; sperm associated antigen 6; Armadillo_seg; HEAT_PBS; TM=M; SS=N; 5.58
 453852; AW961818; Hs.211592; MUM2 protein; kinase; DAG_PE-bind; C2; kinase_C; none; 5.57
 421924; BE514514; Hs.109606; coronin, actin-binding protein, 1A; WD40; kln; C; TM=M; SS=N; 5.57
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 5.55
 431630; NM_002204; Hs.265829; Integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP; Rhabd_glycop; Integrin_A; TM=Y; SS=M; 5.53
 410257; BE244044; Hs.61469; hypothetical protein; none; none; 5.53
 441665; AA972712; Hs.269737; ESTs; kinase; Activin_rec; TSPN; Collagen; 5.52
 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; Integrin_B; Glyco_hydro_56; 5.52
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MA; SH2; STAT; STAT_bind; STAT_prot; none; 5.50
 447357; A1375922; Hs.132821; ESTs; FMO-like; FMO-like; 5.46
 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin; Defensin_propep; TM=M; SS=M; 5.46
 447033; A1357412; Hs.157601; Predicted gene: Eos cloned; secreted w/v; none; none; 5.45
 417412; X16896; Hs.82112; Interleukin 1 receptor, type I; Ig; TIR; TM=M; SS=M; 5.45
 436057; AJ004832; Hs.5038; neuropathy target esterase; cNMP_binding; ion_trans; Palatin; TM=Y; SS=M; 5.41
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4; TM=Y; SS=M; 5.41
 439285; A1133916; Hs.47850; hypothetical protein FLJ20093; Ig; kinase; LRR; LRRNT; LRRCT; none; 5.40
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1; TM=Y; SS=M; 5.40
 443623; AA345519; Hs.9641; complement component 1, q subcomponent; ; C1q; Collagen; 5.40
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3; HS1_rep; TM=M; SS=N; 5.38
 437275; AW976035; Hs.292396; ESTs, Weakly similar to A47582 B-cell gr; none; Frizzled; Fz; 5.37
 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino ; aa_permeases; TM=Y; SS=M; 5.37
 449653; AF068823; Hs.24040; potassium channel, subfamily K, member 3; ion_trans; TM=Y; SS=M; 5.36
 442434; AA995787; Hs.129583; ESTs; IRK; none; 5.36
 428065; A1634046; Hs.157313; ESTs; ICE_p20; DED; ICE_p10; ICE_p20; DED; 5.36

- 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,art,TK; 5.33
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium specific prote; none; TM=M;SS=N; 5.32
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase; TM=M;SS=N; 5.32
 452416; AA026115; Hs.114777; ESTs; none; Porphobil_deam; 5.29
 425205; NM_005854; Hs.155106; receptor (calcitonin) activity modifying; none; TM=Y;SS=N; 5.29
 440475; AJ807671; Hs.24040; potassium channel, subfamily K, member 3; ion_trans; none; 5.28
 417355; D13168; Hs.82002; endothelin receptor type B; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rvs,zf-B_box; TM=Y;SS=M; 5.28
 436120; AI248193; Hs.119860; ESTs; heme_1; none; 5.27
 418307; U70867; Hs.83974; solute carrier family 21 (prostaglandin); OATP_N,OATP_C; TM=Y;SS=M; 5.27
 409745; AA077391; gb:7814E12 Chromosome 7 Fetal Brain cDNA; 7tm_1,zf-C3HC4,fn3,SPRY,KRAB,zf-C2H2,rvs,zf-B_box; TM=Y;SS=M; 5.26
 421554; AW137676; Hs.97775; ESTs; none; none; 5.23
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none; none; 5.22
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR; TM=M;SS=M; 5.21
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2 ; 7tm_1; TM=Y;SS=M; 5.19
 400261; Hs.1802; Eos Control; Ig,MHC_II_beta; TM=Y;SS=M; 5.19
 436856; AI469355; Hs.127310; ESTs; pkinase,rm; TM=M;SS=N; 5.18
 408761; AA057264; Hs.238936; ESTs; Weakly similar to (define not av); 7tm_1; none; 5.17
 425023; AW956889; Hs.154210; EDG-1 (endothelial differentiation, sph; 7tm_1; TM=Y;SS=M; 5.16
 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub: ABC,tran,ABC,membrana,SRP54,Thymidylate_kin; TM=Y;SS=M; 5.16
 451220; AF124251; Hs.26054; novel SH2-containing protein 3; SH2; TM=M;SS=N; 5.15
 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazar); none; none; 5.14
 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation ant; PAAD_DAPIN,HIN; 5.14
 451059; R52795; Hs.25954; Interleukin 13 receptor, alpha 2; fn3; TM=Y;SS=M; 5.13
 427509; M62505; Hs.2181; complement component 5 receptor 1 (C5a r; 7tm_1; TM=Y;SS=M; 5.12
 423186; AK001866; Hs.125139; hypothetical protein FLJ11004; none; TM=M;SS=N; 5.12
 433671; AW138797; Hs.132906; 19A24 protein; Ig; TM=M;SS=M; 5.11
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-blind,RhoGAP,SH2; TM=M;SS=N; 5.06
 431890; X17033; Hs.271966; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin_A,FG-GAP; TM=Y;SS=M; 5.05
 418185; AW958272; Hs.347326; Interleukin adhesion molecule 2 (ICAM; none; TM=Y;SS=M; 5.05
 437352; AL353957; Hs.284181; hypothetical protein DKFZp434P0531; DUF221; TM=Y;SS=M; 5.03
 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc; TM=M;SS=N; 5.02
 452924; AW580939; Hs.97199; complement component C1q receptor; EGF,lectin_c,Tissue_fac,Xlink,TIL; TM=Y;SS=M; 5.02
 426535; AU077012; Hs.288582; ESTs; Weakly similar to ubiquitous TPR m; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 4.99
 432805; X94630; Hs.3107; CD97 antigen; 7tm_2,EGF,GPS,FecCD; TM=Y;SS=M; 4.95
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP; 4.95
 414291; AI289619; Hs.13040; G protein-coupled receptor 86; 7tm_1; TM=Y;SS=M; 4.94
 428981; BE313077; Hs.93135; ESTs; Weakly similar to ALU2_HUMAN ALU S; none; rm; 4.92
 451154; AA015879; Hs.33536; ESTs; TIMP; none; 4.92
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid_DH_C; TM=M;SS=N; 4.90
 413011; AW068115; Hs.821; biglycan; LRR,LRRNT; 4.90
 422732; AA577455; Hs.24937; transformer-2 alpha (tra-2 alpha); rm; lg; 4.89
 417075; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox; TM=Y;SS=M; 4.88
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc; TM=M;SS=N; 4.88
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1,LRR; TM=Y;SS=N; 4.87
 405102; C15001220; gl4469558[gb]AAD21311.1 [AF]; DAG_PE-blind,PH,RhoGEF,DC1; 4.86
 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1,kazal,A2M,A2M_N; TM=Y;SS=M; 4.84
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C; TM=M;SS=N; 4.83
 414936; C14774; gb:C14774 Clontech human aorta polyA mRNA; ank,pkinase,death; none; 4.82
 430152; AB001325; Hs.234642; aquaporin 3; MIP; TM=Y;SS=M; 4.82
 444838; AV651680; Hs.208558; ESTs; Integrin_A,FG-GAP; none; 4.81
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-recept; SH2,Y_phosphatase,DSPc; TM=M;SS=N; 4.81
 453107; NM_016113; Hs.279746; vanilloid receptor-like protein 1; ank,ion_trans; TM=Y;SS=N; 4.80
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.80
 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF,sugar_br; 4.78
 419542; AA366037; Hs.90911; solute carrier family 16 (monocarboxylic; none; none; 4.76
 438899; AF085833; Hs.135624; ESTs; none; PI3_P14_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 4.75
 427418; AA402587; Hs.356667; LAT1-3TM protein; none; none; 4.75
 431924; AK000850; Hs.272203; Homo sapiens cDNA FLJ20843 fis, clone AD; SH3; none; 4.73
 424218; AF031824; Hs.143212; cystatin F (leukocystatin); cystatin; 4.72
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17; none; 4.72
 416178; AI808527; Hs.192822; serologically defined breast cancer ent; none; TM=M;SS=N; 4.71
 430037; BE409649; Hs.227789; mitogen-activated protein kinase-activat; pkinase; TM=M;SS=N; 4.71
 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none; none; 4.71
 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP,Integrin_A,NIF; 4.71
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3; none; 4.70
 438543; AA810141; Hs.192182; ESTs; SH2,pkinase; none; 4.70
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN; TM=M;SS=N; 4.70
 438113; AI457908; Hs.8882; ESTs; 7tm_1; none; 4.70
 422164; NM_014312; Hs.112377; cortic al thymocyte receptor (X laevis ; lg,Gemini_mov; TM=Y;SS=M; 4.69
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y;SS=M; 4.69
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker; aldo_ket_red; none; 4.67
 432314; AA533447; Hs.285173; ESTs; Xlink; none; 4.66
 453518; AW503205; Hs.27268; gb:U1-HF-BNO-akt-g-03-0-U1r1 NIH_MGC_50; SH3,PH,RhoGEF; TM=M;SS=N; 4.66
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase,CNH; TM=M;SS=N; 4.66
 446063; AI720140; Hs.151079; ESTs; ISK_Channel; none; 4.65
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 4.65
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y;SS=N; 4.65
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis ; none,PDZ,LIM,pkinase; 4.65
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y;SS=N; 4.64
 427535; R29543; Hs.2164; pro-platelet basic protein (includes pla; IL8; TM=M;SS=M; 4.64
 437119; AJ379921; Hs.177043; XP_171387 similar to rhotekin; none; none; 4.63
 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK; 4.63
 429784; M89796; Hs.30; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=N; 4.62

- 415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phospho; 4.61
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delta; none, none; 4.61
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase; TM=M;SS=N; 4.59
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase; WW,HECT,RNA_pol_A,none; 4.59
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehfand,spectrin,GAS2,SH3,Plectin,RA,Xylose_Isom,FltD,bZIP,Tropomyosin,Myc-
 5 LZ,Mdh_C,CH,AlP3;TM=M;SS=N; 4.59
 431087; H12723; Hs.290791; ESTs; ion_trans,none; 4.58
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 4.58
 422427; AA310514; Hs.96692; ESTs; PH,Els,CH,spectrin,Ca_channel_B,none; 4.57
 10 441527; W19504; Hs.7884; solute carrier family 21 (organic anion); OATP_N,OATP_C;TM=Y;SS=N; 4.56
 416464; NM_000132; Hs.79345; coagulation factor VIII, procoagulant co; Cu-oxidase,F5_F8_type_C; 4.56
 421233; AA209534; Hs.284243; tetraspan NET-8 protein; transmembrane4;TM=Y;SS=M; 4.56
 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3;TM=M;SS=N; 4.55
 444895; AB74383; Hs.22891; solute carrier family 7 (cationic amino); ASC,death,TNFR_c6; 4.55
 15 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled); Nramp;TM=Y;SS=N; 4.55
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 4.54
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con,none; 4.54
 450086; AW016343; Hs.233301; ESTs; ank,death,ZU5,NMU,none; 4.54
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH,PAS,IL6;TM=M;SS=N; 4.54
 20 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase;TM=M;SS=N; 4.53
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M;SS=N; 4.53
 427557; NM_002559; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_int; 4.53
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 4.53
 434158; T66534; Hs.14372; ESTs; adenylatekinase,none; 4.52
 25 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain,none; 4.52
 447341; AF106941; Hs.18142; arrestin, beta 2; arrestin,arrestin_C,PX,PH,PLDc; 4.52
 447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of; SH3,PH;TM=M;SS=N; 4.51
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related; SH2,SH3,pkinase;TM=M;SS=N; 4.51
 422893; X98411; Hs.380077; myosin IF; SH3,myosin_head,IQ;TM=M;SS=N; 4.51
 30 407202; N58172; Hs.109370; ESTs; F5_F8_type_C,pkinase,Els,none; 4.51
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.s.a; zf-C2H2,zf-C3HC4,UIM;TM=M;SS=N; 4.51
 450747; AL064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 4.50
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; Ig,pkinase;TM=Y;SS=M; 4.50
 453856; AA804789; Hs.379109; PDZ-LIM protein myotique; LIM,PDZ;TM=M;SS=N; 4.49
 35 432744; AA988835; Hs.38664; ESTs; none,none; 4.49
 419032; W81330; Hs.99877; ESTs, Highly similar to JAK3B [H.sapiens; pkinase,SH2,Insulin,pkinase,SH2; 4.48
 444009; AJ380792; Hs.135104; ESTs; TNFR_c6,TIL,none; 4.48
 426416; AW612744; Hs.169824; killer cell lectin-like receptor subfamily; lectin_c;TM=Y;SS=M; 4.48
 412802; U41518; Hs.74602; aquaporin 1 (channel-forming integral pr; MiP;TM=Y;SS=M; 4.48
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 4.47
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed; ehfand,ion_trans,K_tetra,none; 4.47
 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M;SS=N; 4.46
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 4.45
 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 4.45
 45 434308; N51517; Hs.47282; ESTs; pkinase,pkinase_C,none; 4.45
 434448; W26667; Hs.184581; Homo sapiens cDNA FLJ14821 fis, clone OV; pkinase,pkinase_C; 4.45
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Niem,Integrin_B; 4.44
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 4.44
 430259; BE550182; Hs.375142; RafGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.44
 436001; AW903849; Hs.173840; HUEL (C4orf1)-interacting protein; Ig;TM=M;SS=M; 4.44
 50 452355; H54926; Hs.29202; G protein-coupled receptor 34; 7tm_1,OATP_C;TM=Y;SS=N; 4.43
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2,none; 4.43
 410068; AB633888; Hs.58435; FYN-binding protein (FYN-120/130); SH3;TM=M;SS=N; 4.43
 449961; AW265834; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain,none; 4.42
 55 451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate); IQ,7tm_1;TM=M;SS=N; 4.42
 410598; AB817130; Hs.9195; Homo sapiens cDNA FLJ13698 fis, clone PL; RasGEF,PRK; 4.42
 439411; AA044876; Hs.58043; ESTs, Weakly similar to CYA2_HUMAN ADENY; guanylate_cyc;TM=Y;SS=M; 4.42
 433179; AW362945; Hs.162459; ESTs; Armadillo_seg,none; 4.42
 414849; AW372721; Hs.291623; ESTs, Weakly similar to unnamed protein; pkinase,none; 4.42
 60 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD,helicase_C,CARD;TM=M;SS=N; 4.41
 445903; AJ347487; Hs.132781; class I cytokine receptor; fn3;TM=Y;SS=N; 4.41
 438507; AA809052; Hs.356627; ESTs; none,none; 4.41
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily; TNF;TM=Y;SS=M; 4.40
 65 453037; AA045175; Hs.17914; ESTs; none;TM=Y;SS=M; 4.40
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vt; sushi;TM=Y;SS=M; 4.40
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehfand,CH,Adaptin_N; 4.40
 415149; X12451; Hs.78058; cathepsin L; Peptidase_C1; 4.39
 408105; AW152207; Hs.270977; ESTs, Weakly similar to I38022 hypothetical; Y_phosphatase,carb_anhydrase,DSPC,none; 4.39
 70 423099; NM_002837; Hs.123641; protein tyrosine phosphatase, receptor t; fn3,Y_phosphatase,DSPC,COX6C;TM=M;SS=M; 4.39
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 4.39
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20; 4.39
 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.39
 426410; BE298446; Hs.305890; BCL2-like 1; Bcl-2,BH4,none; 4.38
 434511; R26982; Hs.18106; ESTs; pkinase,Glyco_hydro_39; 4.38
 75 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M;SS=N; 4.37
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3,Ig_Y_phosphatase,MAM;TM=Y;SS=M; 4.38
 432583; AW023824; Hs.162282; potassium channel TASK-4; potassium chan; ion_trans,X;TM=Y;SS=M; 4.36
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high aff; SDF;TM=Y;SS=M; 4.36
 426828; NM_000020; Hs.172670; activin A receptor type II-like 1; pkinase,Activin_rec;TM=M;SS=M; 4.36
 80 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 4.36
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3_cotransp;TM=Y;SS=N; 4.38
 429670; L01087; Hs.211593; protein kinase C, theta; DAG_PE-bind,pkinase,pkinase_C,DNA_pol_viral_N,PHD,DC1;TM=M;SS=N; 4.35
 421195; BE464560; Hs.133017; ESTs; none,none; 4.35

- 415758; BE270465; Hs.78793; protein kinase C, zeta; pkinase,DAG_PE-bind,pkinase_C,OPR; 4.35
- 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metallothio_5;TM=M;SS=N; 4.34
- 419150; T29618; Hs.89640; TEK tyrosine kinase, endothelial (venous); EGF,fn3,pkinase,lg,laminin_EGF,DSL;TM=Y;SS=M; 4.34
- 440675; AW005054; Hs.279788; ESTs; Weakly similar to KCC1_HUMAN CALCI; pkinase,none; 4.34
- 429657; D13626; Hs.2465; KIAA0001 gene product; putative G-protein; 7tm_1;TM=Y;SS=M; 4.34
- 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 4.34
- 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; SH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.34
- 452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.33
- 407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.33
- 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H; SH3,none; 4.33
- 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.32
- 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.32
- 437527; AI241019; Hs.145644; ESTs; PIP5K,none; 4.32
- 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG_PE-bind,RBD; 4.31
- 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated); lg,ITAM,Zn_cus;TM=Y;SS=M; 4.31
- 416269; AA177138; Hs.161671; ESTs; pkinase,DAG_PE-bind,RBD,none; 4.30
- 425458; H89317; Hs.182889; ESTs; ion_trans,none; 4.30
- 424206; NM_003734; Hs.198274; amine oxidase, copper containing 3 (vasc); Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 4.29
- 451876; T63141; ; gb:yb99a12.s1 Stratagene lung (937210) H; SH3,none; 4.29
- 417801; AA417383; Hs.82582; Integrin, beta-like 1 (with EGF-like rep; EGF; 4.29
- 435240; AI025435; Hs.117532; ESTs; GHMP_kinases,none; 4.27
- 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none,none; 4.26
- 423523; AW299828; Hs.193580; ESTs; none,none; 4.26
- 426274; D38122; Hs.2007; tumor necrosis factor (ligand) superfamily; TNF;TM=Y;SS=N; 4.26
- 425356; BE244879; Hs.155539; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;SS=N; 4.26
- 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 4.26
- 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 4.26
- 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; lg,pkinase;TM=Y;SS=M; 4.26
- 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,wwc,TSPN; 4.25
- 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.25
- 436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCOO_cotransp,Glyco_hydro_63,PH; 4.24
- 439658; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Fizzled,Fz,7tm_2,tuxin_2;TM=Y;SS=M; 4.24
- 418255; AW135405; Hs.37251; ESTs; pkinase,none; 4.24
- 400328; X87344; ; transporter 2, ATP-binding cassette, sub; none;TM=Y;SS=N; 4.24
- 405121; ; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,wwc,vwd,TIL,DUF139; 4.24
- 425795; AJ000479; Hs.159543; EDG-6 (endothelial differentiation, G-p; 7tm_1;TM=Y;SS=M; 4.23
- 405786; AW161678; Hs.111334; ferritin, light polypeptide; ferritin;TM=M;SS=N; 4.23
- 449843; R85337; Hs.24030; solute carrier family 31 (copper transp; none;TM=Y;SS=M; 4.23
- 445657; AW612141; Hs.279575; Homo sapiens G-protein coupled receptor; 7tm_1;TM=Y;SS=M; 4.23
- 413795; AL040178; Hs.142003; ESTs; none,pkinase,LRR,LRRCT; 4.22
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 4.22
- 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 4.22
- 417318; AW953937; Hs.240845; ESTs; SH3,PH,RhoGEF; 4.21
- 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 4.21
- 408278; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, com; none,none; 4.20
- 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 4.20
- 424618; L29472; Hs.1802; major histocompatibility complex, class ; lg,MHC_II_beta;TM=Y;SS=M; 4.19
- 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK,none; 4.19
- 432882; NM_013257; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase,PX,pkinase_C; 4.19
- 425481; AW978162; Hs.372811; ESTs; none,Oxysterol_BP; 4.19
- 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;SS=N; 4.18
- 401083; ; ; NM_016582; Homo sapiens peptide transp; PTR2;TM=Y;SS=M; 4.18
- 420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 4.18
- 424377; AF081675; Hs.146322; killer cell lectin-like receptor subfamily; lectin_c;TM=Y;SS=M; 4.17
- 424148; BE242274; Hs.1741; Integrin, beta 7; Integrin_B,EGF,metalithio,PSI;TM=Y;SS=M; 4.17
- 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; lg,none; 4.17
- 452100; AI668688; Hs.379032; inositol polyphosphate-5-phosphatase, 75; Exo_endo_phos,RhoGAP,none; 4.17
- 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidyl); SH2,SH3,C2,PH,PI-PLC-X,PDGF; 4.17
- 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,lg; 4.17
- 444034; AL161957; Hs.10177; pleckstrin homology domain interacting p; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,Ribosomal_S15,bromodomain,WD40;TM=M;SS=N; 4.16
- 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,lg,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.16
- 407245; X90568; Hs.172004; ligin; fn3,lg,SGXXSG,pkinase;TM=M;SS=N; 4.16
- 418962; AA714835; Hs.271863; ESTs; RhoGAP,SH2,pkinase,POLO_box,none; 4.15
- 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 4.15
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.15
- 446967; AI699629; Hs.156781; ESTs; none,none; 4.14
- 432176; AW090386; Hs.112278; arrestin, beta 1; arrestin,arrestin_C,none; 4.14
- 452571; W31518; Hs.34665; ESTs; none;TM=M;SS=N; 4.14
- 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.14
- 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 4.14
- 417871; AA521368; Hs.24252; ESTs; IBB,Armadillo_seg,none; 4.13
- 429819; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (tr; none,none; 4.12
- 424522; AL134847; Hs.149957; ribosomal protein S8 kinase, 90kD, polyp; pkinase,pkinase_C; 4.12
- 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase,RGS;TM=M;SS=N; 4.12
- 413019; BE281604; Hs.75140; low density lipoprotein-related protein-; none;TM=M;SS=Y; 4.12
- 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;SS=N; 4.11
- 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 4.11
- 449656; AA002008; Hs.188633; ESTs; PIP5K,none; 4.11
- 406403; ; ; NM_002162; Homo sapiens intercellular ad; lg;TM=Y;SS=M; 4.10
- 427732; NM_002980; Hs.2189; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 4.10
- 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,RIO1,none; 4.10
- 432885; AA595607; Hs.368129; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,pkinase_C,none; 4.10

- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1; TM=M; SS=N; 4.10
 418342; BE002723; Hs.334330; leptin receptor; ICE_p20, DED, ICE_p10, ICE_p20, DED; 4.10
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanesa; 4.10
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; SS=N; 4.10
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 4.10
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none; TM=Y; SS=M; 4.10
 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH, RhoGAP, SH3; TM=M; SS=N; 4.09
 435140; AA668123; Hs.134170; ESTs; none, none; 4.09
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.08
 428483; AJ908539; Hs.184592; KIAA0344 gene product; none, none; 4.08
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3; none; 4.07
 431674; AA098901; Hs.301642; G-protein coupled receptor; none, GCV_H; 4.07
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZP434L0827 (f; ABC_tran, ABC_membrane; TM=M; SS=M; 4.07
 441518; AW161697; Hs.294150; ESTs; Y_phosphatase, DSPc; none; 4.07
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 4.06
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extracellular mat; tsp_1, Reeler; 4.05
 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP, 7tm_1; 4.05
 439549; AW937885; Hs.137314; ESTs; SH2; none; 4.04
 419981; AA897581; Hs.128773; ESTs; pkinase, DAG_PE-bind, pkinase_C, OPR; none; 4.04
 418836; AI655499; Hs.161712; ESTs; pkinase, Activin_rec, PDZ_ZU5, death; 4.04
 408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3, PDZ, Guanylate_kin; none; 4.04
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin; none; 4.03
 426086; T94507; Hs.188572; ESTs; PH_Ets, CH_spectrin, Ca_channel_B; none; 4.03
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 4.03
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 4.03
 416350; AF188625; Hs.189507; phospholipase A2, group IID; phospho; TM=M; SS=Y; 4.02
 434457; AF141332; Hs.200333; apolipoprotein B48 receptor; none; TM=M; SS=N; 4.02
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain, PHD, PWWP, zf-MYND; TM=M; SS=N; 4.02
 425694; U51333; Hs.159237; hexokinase 3 (white cell); hexokinase, hexokinase2; TM=M; SS=N; 4.02
 449943; AF104266; Hs.24212; latrophilin; 7tm_2, GPS, Gal_Lectin, OLF, Latrophilin, HRM; TM=Y; SS=M; 4.01
 408938; AA059013; Hs.22607; ESTs; fn3_Y_phosphatase, carb_anhydase; none; 4.01
 426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affin; none; TM=M; SS=M; 4.00
 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExcB; TM=Y; SS=M; 4.00
 410726; AI623859; Hs.15936; ESTs; pkinase, pro_isomerase; none; 4.00
 428318; BE300110; Hs.183842; ubiquitin B; lipocafin, aldedh, ubiquitin, IRK; 4.00
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK; TM=M; SS=N; 3.99
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase, ubiquitin, Enterotoxin_A, PHO4, pkinase, ubiquitin; 3.99
 414700; H63202; Hs.38163; ESTs; 7tm_1; TM=Y; SS=M; 3.99
 432259; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 3.99
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 3.98
 427541; AI798983; Hs.375835; solute carrier family 35 (CMP-saltic act; none, none; 3.98
 440248; AA876138; Hs.369458; ESTs; SH2; none; 3.98
 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6, laminin_EGF; TM=Y; SS=N; 3.98
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 3.98
 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (letr; transmembrane4; TM=Y; SS=M; 3.98
 437151; AA745618; Hs.380121; BANP homolog, SMAR1 homolog; none, none; 3.98
 443574; U83993; Hs.321709; purinergic receptor P2X, ligand-gated lo; P2X_receptor; TM=Y; SS=M; 3.97
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49, EGF, Ig, Neuregulin; TM=M; SS=N; 3.97
 411574; BE242842; Hs.6780; protein tyrosine kinase 9-like (A6-relat; LRR, LRRCT, TIR, coflin_ADF; TM=M; SS=N; 3.97
 432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo; none, IRK; 3.97
 457675; AF119917; Hs.306574; Homo sapiens PRO3098 mRNA, complete cds; none; 3.97
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; SS=N; 3.96
 437157; BE048860; Hs.17287; ESTs; IRK; none; 3.96
 453641; AA444140; Hs.90960; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4; none; 3.96
 446714; W73818; Hs.110028; ESTs; 7tm_1, 7tm_1; 3.96
 427648; AI376722; Hs.180062; proteasome (prosome, macropain) subunit; proteasome; 3.96
 453686; AL110326; Hs.304679; ESTs, Moderately similar to Z195_HUMAN Z; none, lectin_c, fig_chan; 3.96
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase, pkinase; 3.95
 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4, LIM; TM=M; SS=N; 3.95
 435411; AW444618; Hs.138211; ESTs; none, pkinase; 3.94
 440209; H05049; Hs.247837; neurexin 3; laminin_G, EGF; none; 3.94
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none, none; 3.94
 432272; AA906415; Hs.110041; ESTs; none, pkinase; 3.93
 402550; ; Target Exon; none, none; 3.93
 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY, SAP, pkinase, fn3, Ig; 3.93
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), a; Slathmin, Vinculin; 3.92
 453548; AL079983; Hs.115774; Integrin, alpha 1; none, vwa, FG-GAP, Integrin_A; 3.92
 417226; AW505054; Hs.4283; ESTs; pkinase, RGS, PH, myosin_head, Myosin_tail; 3.92
 446755; AW451473; Hs.16134; serine/threonine kinase 10; pkinase, TYA; TM=M; SS=N; 3.92
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp, STAS; 3.92
 418516; NM_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, at; PI3_P14_kinase, PI3Ka, PI3K_C2, PI3K_rbd, PI3K_p85B; none; 3.91
 423069; M15613; Hs.1613; adenosine A2a receptor; 7tm_1; TM=Y; SS=M; 3.91
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ; Ig, pkinase; TM=Y; SS=N; 3.91
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase; none; 3.91
 429615; AF258627; Hs.211562; ATP-binding cassette, sub-family A (ABC1; ABC_tran; TM=Y; SS=M; 3.91
 414774; Q02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plasmin_thionins; 3.91
 442831; AI798959; Hs.131686; ESTs; ABC_tran, PRK, ABC_tran; 3.91
 441657; BE314693; Hs.7936; BAI1-associated protein 2; SH3; TM=M; SS=N; 3.91
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypothel; lipoxigenase, PLAT; none; 3.90
 447560; AF065214; Hs.18858; phospholipase A2, group IVC (cytosolic; ; PLA2_B; TM=M; SS=N; 3.90
 437897; AA770561; Hs.146170; hypothetical protein FLJ2969; zf-DHHC; none; 3.89
 429379; NM_014840; Hs.200596; KIAA0537 gene product; pkinase, RIO1; TM=M; SS=N; 3.89
 410179; W27723; Hs.59498; cell division cycle 2-like 5 (choinaster; pkinase; 3.89

- 428713; AA432067; Hs.268551; ESTs, Moderately similar to CYA4 RAT ADE; pkinase; 3.89
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 3.89
 425190; AW026302; Hs.155079; protein phosphatase 2, regulatory subunit; B56;TM=M;SS=N; 3.89
 426752; X69490; Hs.172004; titin; fn3,lg,pkinase,SGXXSG;TM=M;SS=N; 3.89
 417767; BE242241; Hs.82542; acyltoxyacyl hydrolase (neutrophil); Upase_GDSL;TM=M;SS=M; 3.88
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dep; Man-6-P_recep;TM=M;SS=M; 3.88
 416140; A1918035; Hs.301198; roundabout (axon guidance receptor, Dros; none,none; 3.88
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe co; fn3;TM=Y;SS=M; 3.89
 410011; AB020641; Hs.57856; PFTAIKE protein kinase 1; pkinase;TM=M;SS=N; 3.87
 405908; Z25437; ; gbr.Hsapiens protein-tyrosine kinase gen; none,none; 3.87
 425289; AW139342; Hs.155530; Interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN; 3.87
 441859; AW194364; Hs.9877; Interleukin-4 induced gene-1 protein (FI; Amino_oxidase,FAD_binding_3,TBC;TM=M;SS=N; 3.87
 439975; AW328081; Hs.6817; Inosine triphosphatase (nucleoside triph; Ham1p_like;TM=M;SS=N; 3.87
 415392; Z44067; Hs.10957; ESTs; PIP5K,none; 3.86
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 3.86
 414649; A1672727; Hs.76753; endoglin (CD105 antigen) (ENG); none;TM=Y;SS=M; 3.85
 425729; L22647; Hs.159360; prostaglandin E receptor 1 (subtype EP1); 7tm_1;TM=Y;SS=M; 3.85
 414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short,none; 3.84
 412204; A125507; Hs.24937; ESTs; Ig_rn,none; 3.84
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin; 3.84
 444981; AW855398; Hs.12210; hypothetical protein FLJ13732 similar to; SH2;TM=M;SS=N; 3.84
 412309; M23892; Hs.73809; arachidonate 15-lipoxygenase; lipoxygenase,PLAT; 3.84
 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.84
 407143; C14076; Hs.332329; EST; none;TM=Y;SS=M; 3.84
 420593; AA280358; Hs.187634; ESTs; B56,none; 3.84
 413420; AW410235; Hs.75348; proteasome (prosome, macropain) activator; PA28_alpha,PA28_beta,bioplerin_H; 3.83
 448253; H25899; Hs.201591; ESTs; 7tm_2,HRM,none; 3.83
 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHIT; ABC_tran,PRK,GBP;TM=Y;SS=N; 3.83
 430397; A1924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp;TM=Y;SS=N; 3.83
 423087; AA321355; Hs.285401; colony stimulating factor 2 receptor, beta; fn3;TM=Y;SS=M; 3.83
 458188; AW297226; Hs.137840; ESTs, Moderately similar to SIX4_HUMAN_H; pkinase,WD40; 3.82
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (f; pkinase,none; 3.82
 428791; AA435661; Hs.264750; ESTs; zf-C3HC4,none; 3.82
 438068; A1927209; Hs.306210; Homo sapiens cDNA: FLJ23133 fis, clone L; NusG; 3.82
 453370; A1470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=N; 3.82
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 3.82
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none,none; 3.82
 420679; X57152; Hs.165843; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M;SS=N; 3.82
 417916; NM_006416; Hs.82921; solute carrier family 35 (CMP-sulfate ec; DUF6;TM=Y;SS=M; 3.81
 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta; none,none; 3.81
 417365; D50683; Hs.82028; transforming growth factor, beta receptor; pkinase,WD40;TM=Y;SS=N; 3.64
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 3.52
 422398; A1476149; Hs.334489; hypothetical protein FLJ21992; SH2,SH3; 3.51
 418432; M14156; Hs.85112; insulin-like growth factor 1 (somatomedin; Insulin; 3.50
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androgen receptor; none,C2,WV,HECT; 3.48
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3,Jg_Y_phosphatase,MAM;TM=Y;SS=M; 3.38
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 3.37
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR; 3.24
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolog; EGF_cadherin,laminin_G;TM=Y;SS=M; 3.11
 419721; NM_001650; Hs.315369; aquaporin 4; MIP,none; 2.99
 433147; AF091434; Hs.43080; platelet derived growth factor C; PDGF,CUB; 2.91
 417976; BE565892; Hs.83077; Interleukin 18 (interferon-gamma-inducin; none;TM=M;SS=N; 2.89
 439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.69
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.23
 411089; AA458454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none,none; 2.07
 428800; M57627; Hs.193717; Interleukin 10; IL10; 1.10

TABLE 40B

60	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
65	Accession:	Genbank accession numbers		
	Pkey	CAT Number	Accession	
70	456034	585586_1	AA136553 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945	
	459702	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354	
75	432222	539529_1	BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354	
	414991	1785136_1	D78831 C17898 D78863	
80	409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA268833 AA150722 BI007625	
			BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377	
85			AA150780 BI033518 BI027816 BG015789 BI033807 AA341445	
	414936	1782849_1	C14774 C17911 D79033	
90	451876	2328579_1	T63141 AI821021 BF370092 BF370127 BF370060 T62998	
	432639	1237887_1	AW973785 H60163 AA557608	

TABLE 40C

80	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
85	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		

	Pkey	Ref	Strand	ML_position
5	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	404240	5002624	Minus	116132-116407,116653-116922
	405102	8076881	Minus	120922-121296
	405121	8102330	Minus	35816-36004,36587-36684
10	401083	3242744	Plus	33192-33360
	406403	9256305	Minus	151426-151680
	402550	7652009	Minus	80413-80673
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182

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TABLE 41A: 556 GENES UP-REGULATED IN PANCREATIC TUMORS OR PANCREATITIS RELATIVE TO NORMAL TISSUES

20 Table 41A lists about 556 genes up-regulated in pancreatic tumors or pancreatitis relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

25	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigenID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of pancreatic cancer/median of normal pancreas			
	Pkey	ExAccn	UnigenID	Unigene Title	R1
30	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	7.25
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.64
	444995	AJ272265	Hs.12230	secreted phosphoprotein 2, 24kD	3.58
	453863	X02544	Hs.572	orosomucoid 1	114.18
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	922.40
35	421344	AW631030	Hs.103665	villin-like	2.19
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	61.10
	438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group 1, m	607.40
	418888	AJ076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	228.20
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	4.97
40	443162	T49951	Hs.9029	DKFZP434G032 protein	38.01
	423096	AA732684	Hs.278428	progesterin induced protein	189.60
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	11.06
	448243	AW369771	Hs.52620	Integrin, beta 8	116.90
45	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	21.52
	407768	BE514982	Hs.38991	S100 calcium-binding protein A2	8.74
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	3.11
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	307.70
	457059	BE561665	Hs.177677	exosome component Rrp40	33.60
	451945	BE504055	Hs.211420	ESTs	7.31
50	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	133.70
	443247	BE614387	Hs.333893	c-Myc target JPO1	349.10
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	330.00
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	3.78
	413835	AJ272727	Hs.249163	fatty acid hydroxylase	3.53
55	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	73.90
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.39
	410639	BE269047	Hs.65234	hypothetical protein FLJ20695	1.72
	410541	AA065003	Hs.64179	syntenin-2 protein	10.29
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	6.79
60	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	4.62
	407604	AW191982	Hs.249239	collagen, type VIII, alpha 2	366.30
	431193	AW749505	Hs.296770	KIAA1719 protein	6.99
	442080	AW444761	Hs.44565	ESTs	118.00
	427670	BE812888	Hs.180224	myosin regulatory light chain	2.73
65	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	647.30
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	738.90
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	68.43
	407792	AJ077715	Hs.39384	putative secreted ligand homologous to f	3.03
	419216	AJ076718	Hs.164021	small inducible cytokine subfamily B (Cy	7.73
70	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	227.30
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	115.60
	452355	N54926	Hs.29202	G protein-coupled receptor 34	192.20
	419481	AJ879195	Hs.90606	15 kDa selenoprotein	119.90
	407230	AA157857	Hs.182265	keratin 19	12.11
75	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	6.63
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	592.10
	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	120.40
	445517	AF208855	Hs.12830	hypothetical protein	117.40
	446519	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.25
80	428385	AF112213	Hs.184062	putative Rab5-interacting protein	3.12
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	135.20
	408867	AA157857	Hs.182265	keratin 19	11.32
	417426	NM_002291	Hs.82124	laminin, beta 1	406.20

	406366	AF026692	Hs.105700	secreted frizzled-related protein 4	0.62
	401201	#(NOCAT)		Target Exon	0.75
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	0.63
5	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.75
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	0.67
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.83
	403207	#(NOCAT)		C2000960:gi131432:sp P23132 LTH_BOVIN	0.80
	427858	NM_001971	Hs.21	elastase 1, pancreatic	0.98
10	426004	AW500300	Hs.124123	ESTs, Moderately similar to SYN1 RAT SYN	0.88
	401541	NA		Target Exon	0.91
	429793	AI417638	Hs.114648	estrogen regulated gene 1	0.85
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.81
	433110	D56494	Hs.3191	rat regenerating islet-derived-like, hum	0.72
15	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	0.95
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	0.87
	412470	M93283	Hs.73923	pancreatic lipase-related protein 1	0.89
	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	0.97
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.95
20	412688	AW583062	Hs.74502	chymotrypsinogen B1	0.95
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.07
	420937	AW966719	Hs.1340	colipase, pancreatic	0.99
	418058	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	1.02
	410839	NM_006849	Hs.66581	protein disulfide isomerase	1.00
25	437986	AA774575	Hs.121776	testis expressed sequence 11	1.02
	415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	1.06
	427955	D00306	Hs.181289	elastase 3, pancreatic (protease E)	1.22
	406399	#(NOCAT)		NM_003122*Homo sapiens serine protease	1.08
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.11
30	414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	1.22
	421243	AW873803	Hs.102876	pancreatic lipase	1.13
	419263	AW583874	Hs.89832	insulin	1.12
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.13
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductanc	1.32
35	436217	T53925	Hs.107	fibrinogen-like 1	1.72
	435975	AL118990	Hs.41997	alpha-1-B glycoprotein	1.60
	431330	X69532	Hs.2777	Inter-alpha (globulin) inhibitor, H1 pol	2.02
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	1.82
	415003	M11437	Hs.77741	kininogen	3.83
40	422281	M36803	Hs.1504	hemopexin	2.14
	414910	X12662	Hs.289057	arginase, liver	97.90
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	236.70
	400836	#(NOCAT)		Target Exon	2.47
	452983	L32140	Hs.531	afamin	117.10
45	419768	T72104	Hs.93194	apolipoprotein A-I	4.87
	413841	M34276	Hs.75576	plasminogen	374.00
	400560	#(NOCAT)		NM_030878*Homo sapiens cytochrome P450,	144.50
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	266.50
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	77.80
50	426205	D63521	Hs.167877	leukocyte cell-derived chemotaxin 2	169.80
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	3.60
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	400.40
	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	4.72
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.26
55	425260	L47726	Hs.1870	phenylalanine hydroxylase	73.78
	443316	AJ478463	Hs.18443	aldehyde dehydrogenase 8 family, member	182.20
	413318	AU076607	Hs.75285	Inter-alpha (globulin) inhibitor, H2 pol	335.00
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	173.40
	421126	M74587	Hs.102122	Insulin-like growth factor binding prote	565.30
60	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	86.20
	413585	AJ133452	Hs.75431	fibrinogen, gamma polypeptide	477.20
	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	201.50
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	426.10
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibitor	1.10
65	421905	AJ660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	0.62
	406672	M26041	Hs.198253	major histocompatibility complex, class	4.02
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (5.34
	421712	AK000140	Hs.107139	hypothetical protein	5.62
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	8.85
70	442896	R37725	Hs.261108	ESTs	157.70
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	137.70
	428486	AW583497	Hs.184604	pancreatic polypeptide	2.59
	457489	AJ693815	Hs.127179	cryptic gene	3.23
	404866	NA		ENSP00000251112*:Sodium/potassium-transp	2.84
75	432874	W94322	Hs.279651	melanoma inhibitory activity	2.48
	445891	AW391342	Hs.199460	ESTs	70.38
	404682	NA		C9001188*:gi12738842:ref NP_073725.1 p	1.38
	429547	AW009166	Hs.99376	ESTs	6.85
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	5.21
80	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.74
	446868	AV660737	Hs.135100	ESTs	102.10
	404287	NA		C6001909:gi7704441:kb JBA18909.1 (D298	242.70
	443267	AW450630	Hs.133851	ESTs	98.90
	451635	AA018899	Hs.127179	cryptic gene	2.16

5	417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	131.70
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	128.70
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	92.90
	410309	BE043077	Hs.278153	ESTs	108.80
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	170.10
10	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	75.70
	449592	AI655494	Hs.195718	ESTs	4.58
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	188.50
	406685	M18728		gb:Human nonspecific crossreacting antig	1123.60
	411573	AB029000	Hs.70823	KIAA1077 protein	995.60
15	429201	X03178	Hs.198246	group-specific component (vitamin D bind	11.32
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	8.38
	428698	AA852773	Hs.334838	KIAA1866 protein	662.00
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	4.00
	432596	AJ224741	Hs.278461	matrilin 3	283.50
20	428824	W23624	Hs.173059	ESTs	4.55
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.01
	424971	AA479005	Hs.154038	tumor suppressing subtransferable candid	4.21
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	4.80
	448844	AI581519	Hs.177164	ESTs	362.80
25	420908	AL049974	Hs.100261	Homo sapiens mRNA: cDNA DKFZp564B222 (fr	133.90
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil doma	128.20
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	13.83
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	316.00
	452571	W31518	Hs.34665	ESTs	245.50
30	443646	AI085198	Hs.164226	ESTs	189.40
	436032	AA150797	Hs.109276	latexin protein	291.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	252.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	278.20
	430407	H23551	Hs.30974	ESTs	6.20
35	419235	AW470411	Hs.288433	neurotrimin	423.50
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.01
	444301	AK000136	Hs.10760	asporin (LRR class 1)	499.90
	427333	AF067797	Hs.176658	aquaporin 8	1.05
	417931	W95642	Hs.82951	trefoil factor 3 (intestinal)	4.33
40	407777	AA161071	Hs.71465	squalene epoxidase	3.64
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	1.47
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	3.98
	453935	AI633770	Hs.42572	ESTs	2.08
	431629	AU077025	Hs.265827	Interferon, alpha-inducible protein (clo	3.84
45	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	14.21
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	315.70
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.53
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.13
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	9.33
50	440484	BE328156	Hs.150356	ESTs	1.03
	447395	AW18412	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	1.09
	440099	AL080058	Hs.6909	DKFZP554G202 protein	14.74
	434665	AA642125		gb:nr60c01.s1 NC1_CGAP_Lym3 Homo sapiens	0.98
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	2.23
55	408915	NM_016651	Hs.48950	hepatocellular carcinoma novel gene-3 pro	329.40
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.71
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.69
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10198 fis, clone HE	1.70
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	3.19
60	429010	Y18198	Hs.194725	one cut domain, family member 2	1.96
	414420	AA043424	Hs.76095	Immediate early response 3	2.54
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	3.30
	414004	AA370333	Hs.7155	ESTs, Moderately similar to 2115357A TYK	312.80
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	177.80
65	406173	#(NOCAT)		ENSP00000250148*:Growth hormone variant	1.46
	403776	#(NOCAT)		ENSP00000226542*:Small Inducible cytokin	121.80
	403574	NA		Target Exon	16.12
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.94
	458449	H04482	Hs.29019	ESTs	71.60
70	409958	NM_001523	Hs.57697	hyaluronan synthase 1	1.77
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	3.13
	451181	AI796330	Hs.207461	ESTs	68.00
	440508	BE267911	Hs.196970	ESTs	38.00
	429636	AA455692	Hs.163232	ESTs	30.70
75	419570	W68738		gb:zd37p06.s1 Soares_fetal_heart_NbHH19W	1.02
	431779	AW971178	Hs.268571	apolipoprotein C-I	3.36
	431723	AW058350	Hs.16762	Homo sapiens mRNA: cDNA DKFZp564B2062 (f	10.20
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	3.94
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascidin	1171.10
80	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	809.50
	440482	AA86658	Hs.50873	ESTs	9.95
	414602	AW630088	Hs.76550	Homo sapiens mRNA: cDNA DKFZp564B1264 (f	30.70
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	82.90
	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	26.01
	433364	AI075407	Hs.296083	ESTs, Moderately similar to 154374 gene	5.38
	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	0.54
	420876	AA918425	Hs.177744	ESTs	0.89

	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	0.94
	401732	#(NOCAT)		NM_001176: Homo sapiens Rho GDP dissociation	1.13
	404142	NA		Target Exon	1.33
5	424165	AW582904	Hs.142255	islet amyloid polypeptide	2.95
	413880	AI660842	Hs.110915	interleukin 22 receptor	1.34
	407007	U22961		gb:Human mRNA clone with similarity to L	1.57
	426300	U15979	Hs.169228	della-like homolog (Drosophila)	1.48
	432855	AF017988	Hs.279565	secreted frizzled-related protein 5	1.28
10	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.31
	445730	AI624342	Hs.170042	ESTs	2.14
	406666	V00495	Hs.184411	albumin	2.95
	435849	BE305242	Hs.16098	claudin 2	1.96
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	2.49
	430272	X04898	Hs.237658	apolipoprotein A-II	3.29
15	412374	X01388	Hs.73849	apolipoprotein C-II	2.42
	419276	BE165909	Hs.306881	MSTP043 protein	63.40
	415448	T68645	Hs.952	solute carrier family 10 (sodium/bile ac	3.52
	423541	AA296922	Hs.129778	gastrointestinal peptide	3.16
20	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	6.24
	425551	AA359252	Hs.126485	hypothetical protein FLJ12604; KIAA1692	14.67
	455630	AV655701	Hs.75183	cytochrome P450, subfamily 11E (ethanol-	4.30
	428786	Y16577	Hs.2314	mannose-binding lectin (protein C) 2, so	92.10
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	203.30
25	451253	H48299	Hs.26126	claudin 10	1.37
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	3.38
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibitor	7.04
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.84
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.65
30	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	9.28
	422237	M13149	Hs.1498	histidine-rich glycoprotein	34.26
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	1.92
	414386	X00442	Hs.75990	haptoglobin	8.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	1.74
35	452689	F33868	Hs.284176	transferrin	6.51
	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	35.08
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	170.30
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis I	2.34
	405849	#(NOCAT)		Target Exon	103.10
40	405281	#(NOCAT)		NM_002864: Homo sapiens pregnancy-zone pr	31.20
	419078	M93119	Hs.89584	insulinoma-associated 1	6.28
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.89
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.80
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.82
45	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	13.15
	450400	AI694722	Hs.279744	ESTs	5.22
	413916	M49813	Hs.75615	apolipoprotein C-II	8.60
	444632	AI184027	Hs.146986	ESTs, Weakly similar to FATH_HUMAN CADHE	71.30
	415906	AI761357	Hs.288741	Homo sapiens cDNA: FLJ22255 fis, clone H	1.70
50	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.65
	417356	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	3.01
	436961	AW375974	Hs.156704	ESTs	164.60
	446319	AW207590	Hs.160711	ESTs	1.88
	427899	AA829286	Hs.332053	serum amyloid A1	6.98
55	419092	J05581	Hs.89603	mucin 1, transmembrane	2.12
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, I	132.20
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.23
	405319	NA		CX000780: gij5679197ref[NP_032800.1] pol	51.50
	404286	NA		C6001909: gij704441[jdbjBAA18909.1] (D298	1.75
60	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	52.80
	406293	NA		Target Exon	68.30
	431912	AI680552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	102.43
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	206.30
	425200	BE255203	Hs.155101	ATP synthase, H transporting, mitochondr	5.76
65	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	200.10
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	97.70
	434599	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.96
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	30.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.66
70	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	193.80
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma	3.05
	420001	J05064	Hs.1282	complement component 6	159.00
	449038	AL133084	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	39.10
	423184	NM_004428	Hs.1624	ephrin-A1	2.39
75	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	327.90
	444783	AK001458	Hs.62180	anillin (Drosophila Scraps homolog), act	90.50
	445593	AW203963	Hs.150896	ESTs	49.20
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.12
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.93
80	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferti	39.90
	417940	R28205	Hs.24230	ESTs	57.20
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	2.51
	439920	H05430	Hs.288433	neurotrophin	1.91
	432542	AW083920	Hs.16098	claudin 2	3.47

	410418	D31382	Hs.63325	transmembrane protease, serine 4	3.82
	415989	AJ267700	Hs.317584	ESTs	182.50
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.84
5	400024			AFFX control - HUMRGE/M10098_5	4.82
	418057	AI127958	Hs.83393	cystatin E/M	4.19
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B)	2.92
	405909	NA		Target Exon	71.80
	448811	AI590371	Hs.174759	ESTs	6.74
10	430044	AA464510	Hs.152812	ESTs	14.91
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	757.80
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	1.65
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapi	104.70
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	143.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	311.80
15	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ly	63.00
	422330	D30783	Hs.115263	epiregulin	141.70
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	2.59
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	181.90
	430691	C14187	Hs.103538	ESTs	95.80
20	401682	NA		Target Exon	6.17
	422440	NM_004812	Hs.115724	aldo-keto reductase family 1, member B10	318.60
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.51
	442560	AA365042	Hs.228598	ESTs, Weakly similar to 2004399A chromos	3.90
25	414812	X72755	Hs.77367	monokine induced by gamma interferon	434.60
	425211	M18667	Hs.1867	progastrin (pepsinogen C)	6.58
	421430	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	35.10
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	2.45
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kafini	8.56
30	448437	AW470125		gb:wx60c04.x1 NCL_CGAP_Pan1 Homo sapiens	79.80
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	147.30
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	30.07
	424586	NM_003401	Hs.150930	X-ray repair complementing defective rep	55.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	405.20
35	438746	AI885815	Hs.184727	ESTs	3.57
	456032	AW957446	Hs.301711	ESTs	136.80
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	36.10
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	9.93
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length Insert cDN	146.40
40	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	20.60
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithell	1.58
	437157	BE048860	Hs.120655	ESTs	91.80
	404285	NA		C6001909:gil704441 kbjBAA18909.1 (D298	123.80
	424036	AA770688	Hs.28777	H2A histone family, member L	5.26
45	422026	U80736	Hs.110826	trinucleotide repeat containing 9	130.40
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	48.80
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	3.15
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	253.20
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	80.00
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	3.05
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.66
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length Insert cDN	23.02
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	78.10
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	1.74
55	421298	AW172431	Hs.13012	ESTs	133.10
	422424	AI186431	Hs.296638	prostate differentiation factor	2.65
	421582	AI910275	Hs.1406	trefoil factor 1 (pS2)	5.17
	401480	NA		Target Exon	73.70
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	137.70
60	409757	NM_001898	Hs.123114	cystatin SN	9.36
	449722	BE280074	Hs.23960	cyclin B1	162.70
	452240	AI591147	Hs.61232	ESTs	151.90
	415165	AW887604	Hs.78065	complement component 7	2.85
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	290.30
65	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.89
	409041	AB033025	Hs.50081	KIAA1199 protein	334.10
	453331	AI240665	Hs.8895	ESTs	12.85
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	12.42
	453160	AI263307	Hs.239884	H2B histone family, member L	156.40
70	444015	AI472865	Hs.135534	ESTs	14.60
	421308	AA587322	Hs.192843	leucine zipper protein FKSG14	87.20
	448045	AJ297436	Hs.20166	prostate stem cell antigen	526.20
	422426	W79117	Hs.58559	ESTs	58.30
	450737	AW007152	Hs.203330	ESTs	281.00
75	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	31.25
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	78.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	212.10
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	3.40
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	3.48
80	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	281.50
	431753	X76029	Hs.2841	neuromedin U	60.50
	428651	AF196478	Hs.188401	annexin A10	508.30
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	85.80
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	55.30

	435039	AW043921	Hs.130526	ESTs	64.00
	447033	AJ357412	Hs.157601	ESTs	123.20
	433578	BE336886	Hs.3416	adipose differentiation-related protein	9.22
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	525.70
5	411274	NM_002776	Hs.69423	kallikrein 10 (KLK10) (PRSSL1) (nes1)	44.36
	452705	H49805	Hs.246005	ESTs	120.10
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	92.30
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	29.37
10	422562	AI962060	Hs.118397	AE-binding protein 1	3.84
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	27.80
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.09
	440868	R79707	Hs.263339	ESTs, Moderately similar to I38022 hypot	76.30
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.37
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	3.44
15	426320	W47595	Hs.169300	transforming growth factor, beta 2	138.10
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	3.45
	459309	AA040620	Hs.5672	hypothetical protein AF140225	127.80
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	361.20
	422553	AI697720	Hs.171455	ESTs, Weakly similar to T31613 hypothet	136.60
20	432375	BE536069	Hs.2962	S100 calcium-binding protein P	6.87
	400534	#(NOCAT)		C22000015.gij12741327[refXP_008833.2] z	89.00
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.78
	423739	AA398155	Hs.97600	ESTs	135.60
25	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	148.50
	423554	M80516	Hs.1674	glutamine-fructose-6-phosphate transamin	87.70
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	76.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	110.60
	419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (234.60
30	428471	X57348	Hs.184510	stratfin	3.72
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	437.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothet	219.20
	419842	AA765489	Hs.104350	ESTs	3.80
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; inters	606.60
35	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.62
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	258.70
	413763	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	304.80
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	8.78
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	10.95
40	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	199.70
	438199	AW016531	Hs.122147	ESTs	67.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	107.20
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.59
	417389	BE260964	Hs.82045	midkine (neuro growth-promoting factor	3.45
45	421937	AI878857	Hs.109706	hematological and neurological expressed	3.17
	427961	AW293165	Hs.143134	ESTs	109.30
	422043	AL133649	Hs.110953	retinoic acid induced 1	2.98
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	276.50
50	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	5.28
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	27.85
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	342.30
	424086	AJ351010	Hs.102267	lysyl oxidase	213.50
	432731	R31178	Hs.287820	fibronectin 1	185.10
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	106.10
55	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.27
	417308	H60720	Hs.81892	KIAA0101 gene product	405.30
	438146	Z36842	Hs.57548	ESTs	8.38
	424800	AL035588	Hs.153203	MyoD family inhibitor	172.10
	416143	AI956650	Hs.79033	glutamyl-peptide cyclotransferase (glu	45.70
60	408380	AF123050	Hs.44532	diubiquitin	11.18
	412140	AA219691	Hs.73825	RAB6 interacting, kinesin-like (rakbnes	149.10
	422963	M79141	Hs.13234	ESTs	33.60
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	6.73
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	8.86
65	424897	D63216	Hs.153684	fizzled-related protein	312.40
	421110	AJ250717	Hs.1355	cathepsin E	790.80
	411789	AF245505	Hs.72157	DKFZP564I1922 protein	3.17
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	8.52
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	558.00
70	406837	R70292	Hs.156110	immunoglobulin kappa constant	4.36
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.83
	421470	R27495	Hs.1378	annexin A3	242.90
	407242	M18728		gb:Human nonspecific crossreacting anti	36.91
	432101	AI918950	Hs.123642	EphA3	221.60
75	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	5.34
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	292.00
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	184.90
	435202	AI971313	Hs.170204	KIAA0551 protein	64.80
	407216	N91773	Hs.102267	lysyl oxidase	73.70
80	409231	AA446644	Hs.692	GAT33-2 antigen; epithelial glycoprotein	3.20
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	288.70
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	502.60
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	6.13
	441020	W79283	Hs.35962	ESTs	178.90

5	453857	AL080235	Hs.35861	DKFZP586E1621 protein	504.30
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	242.10
	413435	X51405	Hs.75360	carboxypeptidase E	7.30
	436476	AA326108	Hs.33829	bHLH protein DEC2	247.20
	406747	AJ925153	Hs.217493	annexin A2	110.00
10	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	112.10
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	583.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	6.56
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	460.90
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	204.40
15	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	7.75
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	14.61
	424560	AA158727	Hs.150555	protein predicted by clone 23733	99.80
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	242.20
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	17.88
20	410668	BE379794	Hs.65403	hypothetical protein	4.18
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	116.40
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	60.30
	442577	AA292998	Hs.163900	ESTs	4.18
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	334.20
25	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	8.16
	451277	AK001123	Hs.26176	hypothetical protein FLJ10251	375.30
	445133	AW157646	Hs.153506	ESTs	292.40
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	4.38
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamI	89.00
30	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	322.10
	410687	U24389	Hs.65436	lysyl oxidase-like 1	9.10
	417409	BE272506	Hs.82109	syndecan 1	4.05
	426471	M22440	Hs.170009	transforming growth factor, alpha	138.60
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	250.50
35	448625	AW970788	Hs.178470	hypothetical protein FLJ22662	4.89
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.76
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.79
	408491	AI088063	Hs.7882	ESTs	8.25
	437802	AI475995	Hs.122910	ESTs	4.54
40	408296	AL117452	Hs.44155	DKFZP586G1517 protein	175.10
	421155	H87879	Hs.102267	lysyl oxidase	170.10
	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-447F3	2.91
	439867	AA847510	Hs.161292	ESTs	261.60
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazaru	723.00
45	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	251.70
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	155.50
	457180	R26022	Hs.194662	calponin 3, acidic	68.00
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	17.19
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	5.32
50	425139	AW630488	Hs.325820	protease, serine, 23	371.90
	432978	AF126743	Hs.279884	DNAJ domain-containing	7.27
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	19.30
	421991	NM_014918	Hs.110488	KIAA0990 protein	190.50
	421814	L12350	Hs.108623	thrombospondin 2	15.02
55	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	28.57
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	519.20
	413048	M93221	Hs.75182	mannose receptor, C type 1	240.60
	404210	#(NOCAT)		NM_005936:Homo sapiens myeloid/lymphoid	404.60
	452862	AW378065	Hs.8687	ESTs	364.20
60	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	226.20
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	4.31
	427390	AI432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	10.41
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	22.46
	451295	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	23.74
65	446569	BE382657	Hs.21486	signal transducer and activator of trans	5.68
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	190.80
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	230.50
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	361.90
	422545	X02761	Hs.287820	fibronectin 1	8.81
70	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	7.30
	417412	X16896	Hs.82112	Interleukin 1 receptor, type I	267.20
	422110	AI378736	Hs.111779	secreted protein, acidic, cysteine-rich	5.07
	431512	BE270734	Hs.2795	lactate dehydrogenase A	270.10
	417433	BE270265	Hs.82128	ST4 oncofetal trophoblast glycoprotein	504.60
75	426369	AF134157	Hs.169487	Kreiser (mouse) mal-related leucine zip	10.62
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.80
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	14.01
	428797	AA495205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f	9.15
	434423	NM_006769	Hs.3844	LIM domain only 4	297.30
80	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	485.20
	422573	AW297885	Hs.295726	integrin, alpha V (vitronectin receptor	9.73
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	762.90
	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	7.81
	400133	NA		Eos Control	357.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1150.30
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.50
	446019	AI362520	Hs.279789	histone deacetylase 3	11.26

426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	459.50
422687	AW068823	Hs.119206	Insulin-like growth factor binding prote	2.68
432401	NM_013330	Hs.274479	NME7	4.99
437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	7.65

Table 41B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
419570	1860604_1	W68738 W68831
423733	231476_1	AA330281 OAA330232 AW962521
434665	390530_1	AA642125 AA654516
448437	763310_1	AW470125 AJ734872 AJ749559 AW856504 AI583942 AW779036 AW843429 AW844876 AI520713 AW847236

Table 41C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400534	6981826	Minus	278637-279292
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400836	8954179	Plus	677-1188
401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401541	8072607	Minus	50018-50158
401682	4755167	Plus	13022-13473
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,20067-20130,20215-20414
403207	7630829	Plus	89914-90033,90729-90855,91131-91198
403574	8101156	Plus	5542-6178
403776	7770611	Minus	1414-1513,1624-1756
404142	9856692	Minus	80316-80459
404210	5006246	Plus	169926-170121
404285	2326514	Plus	32282-32416
404286	2326514	Plus	51086-51301
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404866	9366919	Minus	11743-11929
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405849	7651817	Minus	17705-18287
405909	7705180	Minus	86985-87233
406173	7230224	Plus	12925-13213
406293	5686274	Minus	17646-17953
406319	9211730	Minus	82320-82581
406399	9256288	Minus	63448-63554

TABLE 42A: 574 genes upregulated in pancreatic cancer relative to normal body tissues

Table 42A lists about 574 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
 R2: 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Protdomains; R1; R2

426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin, toxin 4; SS=M; 107.29; 1.07
 415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phospholipase A2; SS=M; 83.67; 1.06
 421996; AW593807; Hs.1460; glucagon; hormone 2; SS=M; 59.35; 1.61
 406399; ; NM_003122; Homo sapiens serine protease; kazal; SS=M; 55.49; 1.08
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 53.65; 43.61

- 406685; M18728; ; gb:Human nonspecific crossreacting anti; Ig; TM=M; SS=M; 52.73; 22.83
- 428698; AA852773; Hs.334838; KIAA1866 protein; none; NA; NA; 32.44; 13.11
- 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO₃ cotransp; TM=Y; 29.80; 1.46
- 426874; W32133; Hs.194366; transthyretin (prealbumin, amyloidosis t; Transthyretin; SS=M; 29.42; 1.94
- 444754; T83911; Hs.374341; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 28.78; 3.13
- 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS protein d; none; TM=M; SS=M; 28.61; 0.98
- 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zt-C4; none; 25.38; 3.63
- 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; SS=M; 24.64; 7.21
- 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none; none; 23.77; 6.74
- 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c; TM=Y; SS=M; 22.96; 4.57
- 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 22.31; 5.42
- 425573; AB006423; Hs.158308; serine (or cysteine) proteinase inhibitor; serpin, GCV_H; TM=M; SS=M; 21.91; 1.03
- 433110; D56494; Hs.3191; rat regenerating Islat-derived-like, hum; lectin_c; TM=M; SS=M; 21.90; 0.60
- 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC, PAS; TM=M; 21.41; 19.89
- 453863; X02544; Hs.572; oncosmucoid 1; lipocalin, eldedh, ubilquin; IRK; SS=M; 20.80; 8.12
- 421126; M74587; Hs.102122; insulin-like growth factor binding prote; thyroglobulin_1, IGFBP; SS=Y; 20.60; 8.48
- 451035; AU076785; Hs.430; plectin 1 (I isoform); ehand, CH, Adaplin_N; SS=M; 19.25; 3.53
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kin; SAM_PNT; none; 18.38; 2.53
- 420332; NM_001756; Hs.1305; serine (or cysteine) proteinase inhibitor; serpin; TM=M; SS=M; 18.19; 2.29
- 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zt-C4; none; 17.67; 4.80
- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Ntern, Integrin_B; SS=M; 17.08; 6.37
- 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7m_1; TM=Y; SS=M; 16.89; 7.15
- 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C, G-alpha, arf; TM=M; SS=M; 16.59; 7.74
- 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 16.28; 9.22
- 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 15.96; 2.38
- 444784; D12485; Hs.11951; actonucleotide pyrophosphatase/phosphodi; Somatomedin_B, Endonuclease, Phosphodiect; TM=Y; SS=M; 15.65; 1.33
- 408243; Y00787; Hs.624; interleukin 8; HLH, PAS, IL8; TM=M; 15.53; 4.34
- 419355; AA428520; Hs.90061; progesterone binding protein; hema_1; TM=Y; SS=M; 15.45; 10.50
- 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 15.17; 0.58
- 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; SS=M; 14.84; 3.04
- 422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c; SS=M; 14.71; 2.89
- 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3; none; 14.28; 11.47
- 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran, ABC_membrane, PRK, Bac_export_3; TM=Y; 13.98; 1.18
- 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 13.81; 7.69
- 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPc, Y_phosphatase, Ribosomal_S3_N; TM=M; 13.59; 2.24
- 425988; BE045897; Hs.53985; ESTs, Weakly similar to I38022 hypotheti; none; none; 13.54; 0.95
- 409512; AW978187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; 13.48; 3.59
- 429556; AW139399; Hs.98988; ESTs; none; TM=M; 13.20; 1.18
- 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 12.83; 7.72
- 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway; SH3, TonB_box_C; TM=M; 12.72; 9.01
- 431912; A1660552; Hs.356183; ESTs, Weakly similar to A56154 Abl subst; none, Acyl-CoA_dh, Acyl-CoA_dh_M, Acyl-CoA_dh_N; 12.72; 6.72
- 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7m_1; TM=Y; SS=M; 12.71; 12.56
- 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolv, HATPase_c; SS=M; 12.52; 4.92
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromos; ABC_tran, M, SMC_N, SMC_C, DUF164; none; 12.38; 7.59
- 428157; A1738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2; none; 12.34; 11.53
- 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 12.32; 3.02
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; Ig; TM=Y; SS=M; 12.29; 2.21
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3, TPR; TM=M; 12.16; 4.14
- 427283; AL119796; Hs.174185; actonucleotide pyrophosphatase/phosphodi; Sulfatase, Somatomedin_B, Phosphodiect, Endonuclease; TM=M; SS=Y; 11.97; 5.93
- 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK; TM=Y; 11.76; 1.58
- 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7m_1; TM=Y; SS=M; 11.75; 3.56
- 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 11.67; 3.77
- 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin, Id_recept_a; none; 11.65; 4.52
- 439750; AL1359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, Integrin_B, Ricin_B, Lectin; 11.56; 5.46
- 431512; BE270734; Hs.2795; lactate dehydrogenase A; kdh, kdh_C, SH3, pkinase, UBA; TM=M; 11.55; 5.11
- 429538; A1916682; Hs.211577; kinectin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP, BPL, CETP, B56; TM=Y; SS=M; 11.47; 4.65
- 445133; AW157646; Hs.198689; ESTs; ehand, spectrin, GAS2, SH3, Plectin, RA_Xylose_isom, FIID, bZIP, Tropomyosin, Myc-LZ, M, kdh_C, CH, AIP3; TM=M; 11.41; 12.62
- 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activa; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 11.24; 9.95
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none; none; 11.19; 4.16
- 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS, AIRS_C; TM=M; 11.17; 5.98
- 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3, Y_phosphatase; TM=M; 11.14; 9.09
- 440594; AW445187; Hs.126036; ESTs; none; none; 11.05; 16.45
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD, DAPIN, HN; SS=M; 11.05; 10.38
- 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese, DSPc; TM=M; 11.05; 4.70
- 448811; A1590371; Hs.199460; ESTs; none; TM=Y; 10.85; 9.69
- 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; 10.72; 8.65
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 10.51; 12.97
- 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, Ig, FAD_Synth, kdh, kdh_C, pkinase; SS=M; 10.37; 6.35
- 436856; A1469355; Hs.127310; ESTs; pkinase, rrm; TM=M; 10.36; 2.74
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig; TM=Y; SS=M; 10.34; 3.14
- 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2, SH3, pkinase; TM=M; 10.34; 4.47
- 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; Integrin_B, EGF, PSI; TM=Y; SS=M; 10.21; 4.58
- 451820; AW058357; Hs.199248; ESTs; 7m_1; TM=Y; SS=M; 10.18; 2.67
- 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2, lectin_c, Ricin_B, Lectin, Xlink; TM=Y; SS=M; 10.17; 8.35
- 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 10.13; 12.35
- 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phor; MORN, sugar_in; TM=Y; SS=M; 10.08; 8.74
- 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 10.05; 6.06
- 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7m_1; TM=Y; SS=M; 9.98; 3.16
- 416389; AA180072; Hs.149846; Integrin, beta 5; Integrin_B; none; 9.85; 9.59
- 421044; AF061871; Hs.101302; Human DNA sequence from clone RP1-238D15; fn3, vwa, Collagen, TSPN; TM=M; SS=M; 9.78; 5.96
- 446620; AA128808; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 9.75; 2.64
- 405102; ; C15001220; [g]4469558[gb]AAD21311.1 [AF; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 9.74; 1.88
- 418693; A1750878; Hs.87409; thrombospondin 1; EGF, lsp_1, vwa, TSPN, lsp_3; SS=M; 9.72; 6.94

- 426535; AU077012; Hs.288582; ESTs. Weakly similar to ubiquitous TPR m; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 9.68; 10.58
- 448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl_recept_L, trypsin; TM=Y; SS=M; 9.67; 4.06
- 456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD; TM=Y; SS=M; 9.62; 2.35
- 410240; AL157424; Hs.61289; synaptotagmin 2; Exo_endo_phos,Syja_N,rm,Gram-ve_porins; TM=M; 9.62; 3.77
- 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec,zf-C4,Melathio_5; TM=M; 9.60; 8.05
- 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A; none; TM=Y; 9.57; 3.77
- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; 9.56; 10.50
- 437158; AW090198; Hs.348709; KIAA1150 protein; none; NA:NA; 9.55; 8.87
- 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M; 9.47; 5.67
- 403344; ; NM_000341; Homo sapiens solute carrier fa; alpha-amylase; TM=Y; 9.47; 1.42
- 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,ion_trans,none; 9.46; 3.12
- 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4; TM=M; 9.42; 4.01
- 444838; AV551680; Hs.208558; ESTs; Integrin_A,FG-GAP,none; 9.42; 1.87
- 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none,none; 9.41; 5.55
- 428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin; SS=M; 9.40; 3.46
- 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 9.38; 6.32
- 432810; AA863400; Hs.374489; ESTs; none; Skp1,AAA; 9.38; 4.36
- 427581; NM_014788; Hs.179703; KIAA0129 gene product; SPRY,zf-B_box; TM=M; 9.34; 8.26
- 413109; AW389845; Hs.110855; ESTs, similar to leukemia virus receptor; PHO4,none; 9.34; 4.67
- 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,phkase; TM=M; 9.31; 4.24
- 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 9.24; 7.12
- 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 9.23; 6.03
- 437672; AW748265; Hs.5741; flavohemoprotein b57; heme_1,NAD_binding,lipoxygenase,FAD_binding_6; TM=M; 9.22; 10.72
- 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans; TM=Y; SS=M; 9.20; 4.46
- 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB & TGF-beta,TGFb_propeptide,Tub; SS=M; 9.19; 16.46
- 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none; START; 9.15; 2.18
- 416838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodi; Phosphodiect; TM=Y; SS=M; 9.14; 3.03
- 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t Y_phosphatase,none; 9.14; 11.75
- 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF; SS=M; 9.11; 4.29
- 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; 9.06; 9.68
- 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; 9.05; 5.61
- 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr; TM=Y; 9.04; 5.79
- 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPc; TM=M; 9.02; 5.75
- 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestine; cadherin; TM=Y; SS=M; 8.94; 5.01
- 446406; AJ553681; Hs.348490; Arg/Abi-interacting protein ArgBP2; Sorb,none; 8.91; 1.77
- 428820; AA436187; Hs.172631; Integrin, alpha M (complement component 1; vwa,Integrin_A,FG-GAP; TM=Y; SS=M; 8.85; 4.74
- 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); pkinase,POLO_box; TM=M; 8.78; 4.54
- 453902; BE502341; Hs.3402; ESTs; none,none; 8.72; 3.71
- 433334; AJ927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
- 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase; SS=M; 8.70; 3.71
- 450247; AF123303; Hs.24713; hypothetical protein; ehfand,milo_carr; TM=Y; SS=M; 8.68; 3.40
- 432101; AW18950; Hs.123642; EphA3; fn3,pkinase,SAMEPH_bdt; TM=Y; SS=M; 8.62; 5.62
- 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 8.61; 13.53
- 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2; TM=Y; SS=M; 8.55; 4.82
- 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR; TM=M; 8.50; 3.18
- 419111; AA234172; Hs.137418; ESTs; none,IRK; 8.47; 7.51
- 430024; AJ808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP; TM=Y; SS=M; 8.45; 3.46
- 447574; AF162666; Hs.16895; tousel-like kinase 1; pkinase; TM=M; 8.45; 5.30
- 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C; TM=M; SS=M; 8.44; 6.30
- 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase; TM=M; 8.43; 4.87
- 405555; ; homeodomain-interacting protein kinase 3; trypsin; TM=M; 8.39; 0.68
- 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR; TM=M; SS=M; 8.35; 4.74
- 405556; ; homeodomain-interacting protein kinase 3; trypsin; TM=M; 8.31; 0.87
- 407687; AK002011; Hs.37558; hypothetical protein FLJ11149; lys,lg,FAD_Synth,ldh,ldh_C,pkinase; SS=M; 8.28; 3.12
- 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 8.27; 5.65
- 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1; TM=Y; SS=M; 8.26; 5.49
- 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 dom; SH2; SS=M; 8.24; 8.91
- 405204; ; NM_002086; Homo sapiens growth factor re; SH2,SH3; TM=M; 8.23; 6.43
- 426808; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073; SS=M; 8.20; 6.11
- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xa; pkinase; TM=M; 8.18; 8.37
- 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase dom; Repolysin,Pep_M12B_propep,disintegrin,Repolysin,Pep_M12B_propep,disintegrin; 8.17; 12.24
- 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20; TM=M; SS=M; 8.15; 4.61
- 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic; PKI; SS=M; 8.15; 11.12
- 428513; BE220808; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
- 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 8.13; 1.15
- 425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; per; none; TM=M; 8.12; 4.54
- 425836; AW955696; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 8.11; 7.47
- 406366; ; secreted frizzled-related protein 4; trypsin; SS=M; 8.05; 0.69
- 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; ; C2,PLA2_B; TM=M; 8.04; 5.20
- 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 8.02; 1.93
- 425280; U31519; Hs.1872; phosphoenolpyruvate carboxylkinase 1 (sol; PEPCK; TM=M; 7.97; 19.33
- 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none,none; 7.90; 11.44
- 449444; AW818438; Hs.351306; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 7.89; 7.00
- 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS; 7.83; 11.16
- 400408; S75765; ; Homo sapiens delta CCK-B gene, partial c; 7tm_1,none; 7.81; 0.78
- 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 siml; sugar_tr; TM=Y; SS=M; 7.78; 7.02
- 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substr; SH3; TM=M; 7.75; 2.63
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; 7.72; 2.68
- 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED; TM=M; 7.68; 2.40
- 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg; SS=M; 7.49; 6.57
- 434659; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2,none; 7.47; 2.53
- 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi; TM=M; SS=M; 7.38; 5.60
- 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 7.29; 5.78

- 428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3; TM=Y; SS=M; 7.26; 11.00
 426761; A015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing ma; none; TM=Y; SS=M; 7.25; 7.22
 413880; A1660842; Hs.110915; Interleukin 22 receptor; Tissue_fac; TM=Y; SS=M; 7.24; 0.98
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase; PLAT; TM=M; 7.22; 6.45
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3; TM=M; 7.20; 5.72
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 7.13; 3.97
 428474; A0203182; Hs.184523; KIAA0965 protein; pkinase; TM=M; 7.13; 5.43
 421582; A1910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil, Gastrin; SS=M; 7.08; 21.61
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpor; none; TM=Y; SS=M; 7.07; 6.18
 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PL; pkinase, Activin_recpt, none; 6.94; 4.82
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase, DAG_PE-bind, pkinase, C_OPR, none; 6.92; 15.34
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU S; Y_phosphatase, Adaplin_N_Y_phosphatase; 6.88; 1.94
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIC; 7tm_1, Idl_recept_L, LRR; SS=M; 6.86; 0.97
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; SS=M; 6.83; 7.24
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3, ig_Y_phosphatase, MAM; TM=Y; SS=M; 6.83; 11.43
 400539; ; Target Exon; none; TM=M; 6.70; 1.19
 431113; AK000673; Hs.274337; hypothetical protein FLJ20666; pkinase; TM=M; 6.65; 2.21
 445280; A015709; Hs.343220; v-crik avian sarcoma virus CT10 oncogene; SH2, SH3, none; 6.61; 10.66
 425834; NM_001639; Hs.1957; amyloid P component, serum; pentad; TM=M; SS=M; 6.57; 2.20
 435708; W31254; Hs.7045; GL004 protein; PDEase, GAF; none; 6.55; 11.44
 415908; A1751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone H; Ephrin, none; 6.45; 5.25
 408308; ALD33377; Hs.44197; hypothetical protein DKFZp564D0462; none, none; 6.42; 9.14
 432335; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm, pkinase; TM=M; 6.42; 4.12
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; 6.42; 2.26
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1; TM=Y; SS=M; 6.41; 4.54
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; Idl_recept_L, PKD, MHC, I; TM=M; SS=Y; 6.38; 3.55
 412970; A026436; Hs.177534; dual specificity phosphatase 10; Rhodanese, DSPc; SS=M; 6.35; 4.95
 422583; AA10506; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; 6.35; 3.56
 452355; NS4926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; 6.32; 11.02
 422282; AF019225; Hs.114309; apolipoprotein L; MoA_ ExbB; TM=Y; SS=M; 6.32; 5.15
 407235; D20569; Hs.169407; SAC2 (suppressor of actn mutations 2, y; none, Ribosomal_S13, Galactosyl_T_Zip, adh_shortzf-C3HC4; 6.30; 8.35
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.25; 3.51
 408847; AW290997; Hs.30348; ESTs; pkinase, ig, none; 6.28; 3.63
 428179; A127772; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase, PX, pkinase_C; SS=M; 6.28; 3.50
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none, none; 6.26; 7.48
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 6.25; 3.98
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 6.21; 4.10
 428180; A129787; Hs.182874; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; 6.18; 4.62
 409245; AA361037; Hs.356436; tRNA isopentenylpyrophosphate transferase; Armadillo_seg; TM=M; 6.17; 11.15
 417952; A1192838; Hs.372643; dual-specificity tyrosine-(Y)-phosphoryl; pkinase, none; 6.17; 3.05
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; 6.16; 11.90
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 6.10; 2.96
 426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_B, SH3; 6.03; 3.17
 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M; 5.99; 2.55
 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone H; 7tm_3, none; 5.97; 13.12
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none; NA; NA; 5.92; 6.47
 418506; AA084248; Hs.85339; Unknown protein for MGC:29643; none, none; 5.91; 1.94
 436345; AA873008; Hs.121572; ESTs; CARD, BIR, zf-C3HC4, CARD, BIR, zf-C3HC4; 5.90; 1.40
 414087; W19712; ; gbzb36d03.r1 Soares_parathyroid_tumor_N; pkinase, none; 5.85; 0.90
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank, death, ZUS, EGF, kringle, trypsin, Nebulin, LIM; SS=M; 5.77; 1.24
 413855; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none, none; 5.71; 4.00
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR, LY6, ET, PLA2_inh; SS=M; 5.71; 3.83
 414171; AA360328; Hs.865; RAP1A, member of RAS oncogene family; pkinase, DAG_PE-bind, RBD, ras, DC1, GFP; TM=M; 5.69; 3.07
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1, 7tm_2; TM=Y; SS=M; 5.68; 12.92
 425317; AW205118; Hs.210546; Interleukin 21 receptor; none; TM=Y; SS=M; 5.60; 5.45
 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 5.59; 4.19
 400151; ; Eos Control; AT_hook, DNA_mis_repair, HATPase_c, UQ_con; TM=M; 5.63; 8.13
 450139; AK001838; Hs.355608; serum/glucocorticoid regulated kinase; none, none; 5.52; 8.61
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 5.52; 10.04
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kin; pkinase, none; 5.51; 6.75
 424701; NM_005923; Hs.151988; mitogen-activated protein kinase kinase; pkinase; TM=M; 5.47; 4.58
 415875; AA894876; Hs.5687; protein phosphatase 1B (formerly 2C), ma; PP2C; TM=M; 5.43; 6.30
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not ava; 7tm_1, none; 5.42; 2.59
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4, LIM; TM=M; 5.37; 8.69
 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20; pkinase, RIO1, APH, KOW; TM=M; 5.36; 3.32
 410434; AF051152; Hs.63568; toll-like receptor 2; LRR, LRRCT, TIR; TM=M; SS=M; 5.38; 3.94
 429023; NM_000312; Hs.2351; protein C (inactivator of coagulation fa; EGF, trypsin, gla; SS=M; 5.31; 4.30
 421559; NM_014720; Hs.105751; Ste20-related serine/threonine kinase; pkinase, UVR; TM=M; 5.31; 3.26
 429922; Z97630; Hs.226117; H1 histone family, member O; linker_histone; TM=M; 5.27; 3.12
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin, bZIP; TM=M; 5.26; 4.82
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 5.25; 11.26
 428234; U93553; Hs.183123; nuclear receptor subfamily 5, group A, m; hormone_rec, zf-C4; SS=M; 5.20; 1.11
 408683; RS8665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos; TM=M; 5.19; 6.25
 408657; AA782601; Hs.173328; ESTs; B56, none; 5.18; 5.47
 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferin, Guanylate_kin, PDZ, SH3; 5.17; 4.02
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypotheli; lipoxygenase, PLAT, none; 5.16; 2.91
 442200; AW590572; Hs.235768; ESTs; none, none; 5.11; 4.22
 418738; AW388833; Hs.6682; solute carrier family 7, (cationic amino; none, none; 5.08; 2.71
 419088; A1538323; Hs.367688; Integrin, beta 8; Integrin_B, none; 5.07; 3.53
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets; phospho; TM=M; SS=Y; 5.05; 3.42
 408414; A114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell; fn3, ig; TM=Y; SS=M; 5.05; 3.41
 430407; H23551; Hs.30974; ESTs; pkinase, PBD, none; 5.03; 1.63
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 5.00; 5.14

- 452194; A1694413; Hs.373599; Ubiquitin-like protein FAT10777 - diubiq; none;none; 4.98; 2.65
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), α ; Stathmin,Vinculin;SS=M; 4.97; 10.60
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese;none; 4.96; 2.87
 432841; M33425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase;SS=M; 4.88; 21.69
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 4.79; 5.47
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehfand,kazal,arf,ras,7tm_1;TM=M; 4.75; 5.41
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M; 4.74; 9.76
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 4.73; 4.68
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 4.66; 5.61
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none;none; 4.63; 6.62
 427333; AF067797; Hs.176658; aquaporin 8; MIP;TM=Y;SS=M; 4.63; 0.80
 431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 4.58; 11.38
 428085; A1634046; Hs.157313; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 4.53; 4.51
 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 4.54; 8.76
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding; ehfand;SS=M; 4.54; 19.57
 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothet; ABC_tran,ABC_membrane,Ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.49; 10.47
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 4.41; 7.27
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.41; 10.25
 433208; AW002834; Hs.24095; ESTs; arf,Ca_channel_B,SH3; 4.39; 12.14
 403208; ; Target Exon; iactin_c;none; 4.37; 0.76
 440486; BE243513; Hs.7212; hypothetical protein PP1044; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 4.36; 10.34
 414278; AA330116; Hs.355877; Human glucose transporter pseudogene; none;none; 4.35; 7.95
 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS;SS=M; 4.34; 6.23
 422573; AW297985; Hs.295726; Integrin, alpha V (vitronectin receptor; FG-GAP,Integrin_A;none; 4.32; 5.85
 418721; NM_002731; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase,pkinase_C;SS=M; 4.31; 3.09
 412330; NM_005100; Hs.788; A kinase (PRKA) anchor protein (gravin) ; none;TM=M; 4.25; 12.74
 421939; BE169531; Hs.109727; TAK1-binding protein 2; KIAA0733 protein; zf-RanBP,CUE;TM=M; 4.25; 12.54
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,brypsin,plant_lionins;SS=M; 4.24; 6.91
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 4.22; 5.27
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y; 4.16; 7.22
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 4.16; 9.27
 445496; AB007860; Hs.12802; development and differentiation enhancer; SH3,ank,PH,ArfGAP;TM=M; 4.15; 23.43
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 4.14; 3.76
 414462; BE622743; Hs.301064; arfapin 1; none;none; 4.08; 13.43
 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-Hacid_DH_C;TM=M; 4.06; 9.12
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y; 4.04; 10.05
 429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase,RIO1;TM=M; 4.00; 6.35
 429617; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M; 3.98; 5.66
 405203; ; NM_002086; Homo sapiens growth factor re; SH2,SH3;TM=M; 3.95; 17.71
 409335; NM_001502; Hs.53985; glycoprotein 2 (zymogen granule membrane; zona_pellucida;TM=M;SS=M; 3.94; 0.58
 446008; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.89; 7.59
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanlylate_kin;TM=M; 3.84; 8.89
 438000; A1825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M; 3.83; 4.22
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 3.81; 6.45
 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 3.78; 8.49
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 3.77; 4.22
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 3.68; 4.92
 438113; A1467908; Hs.8882; ESTs; 7tm_1;none; 3.59; 12.12
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 3.58; 10.93
 429952; AF080158; Hs.226573; Inhibitor of kappa light polypeptide gene; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 3.57; 5.10
 415088; NM_007288; Hs.374374; serum/glucocorticoid regulated kinase; none;none; 3.56; 4.60
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 3.55; 4.52
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M; 3.54; 8.19
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 3.52; 9.70
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A,FG-GAP;TM=Y; 3.45; 6.44
 445350; AF052112; Hs.12540; lysophospholipase 1; abhydrolase_2;TM=M; 3.41; 6.03
 418255; AW135405; Hs.37251; ESTs; pkinase;none; 3.41; 13.97
 408822; AW500715; Hs.57079; Homo sapiens cDNA FLJ13267 fis, clone OV; PIP5K;none; 3.40; 8.97
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase;TM=M; 3.39; 11.24
 431629; AU077025; Hs.265827; Interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 3.39; 5.10
 414291; A1289619; Hs.13040; G protein-coupled receptor 86; 7tm_1;TM=Y;SS=M; 3.38; 10.25
 457329; A1634860; Hs.247043; type 1 tumor necrosis factor receptor sh; Peptidase_M1;SS=M; 3.38; 13.78
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 3.36; 4.17
 443710; A1928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha;none; 3.32; 20.33
 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M; 3.31; 6.94
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 3.29; 3.07
 426728; NM_007118; Hs.367689; triple functional domain (PTPRF Interact; SH3,Ig,pkinase,PH,spectrin,RhoGEF;TM=M; 3.27; 14.90
 427202; BE272922; Hs.173936; Interleukin 10 receptor, beta; Tissue_fac;TM=Y;SS=M; 3.24; 4.49
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M; 3.24; 12.27
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 3.23; 13.40
 417534; NM_004998; Hs.82251; myosin IE; SH3,myosin_head,IQ;TM=M; 3.21; 15.21
 458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 3.21; 7.34
 437928; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epimerase/N-ac; hexokinase,FGGY,ROK,Epimerase_2;SS=M; 3.20; 8.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 3.19; 5.09
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none;none; 3.18; 4.17
 453489; AA300067; Hs.102000; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Ets,F5_F8_type_C,pkinase,Ets; 3.17; 7.88
 414914; U49844; Hs.77613; ataxia telangiectasia end Rad3 related; FAT,FATC,PI3_P14_kinase;TM=M; 3.16; 4.71
 412767; AA233808; Hs.286241; protein kinase, cAMP-dependent, regulator SH3,7tm_2,cadherin,GPS,laminin_G,EGF,laminin_EGF,Sulfata_transp,STAS,cNMP_binding,RIIa; 3.16; 7.19
 415662; AW972481; Hs.170610; ESTs, Highly similar to G01887 MEK kinase; pkinase;none; 3.16; 7.21
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 3.15; 22.66

- 437175; AW968078; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase, pkinase_C, none; 3.14; 11.72
 409270; BE090051; Hs.23120; PIST; fn3, pkinase, PDZ, DUF139; TM=Y; SS=M; 3.09; 7.81
 419591; AF090900; Hs.91393; Homo sapiens cDNA: FLJ21887 fs, clone H; PDZ, LZ27; TM=M; 3.06; 5.46
 447225; R62676; Hs.17820; Rho-associated, coiled-coil containing p; PH, pkinase, HR1, none; 3.04; 13.05
 412692; AF044288; Hs.74515; aryl hydrocarbon receptor nuclear trans; HLH, PAS, PAC; TM=M; 2.95; 12.28
 409274; NM_003930; Hs.52644; SKAP55 homologues; SH3, PH; SS=M; 2.90; 14.62
 417707; AL035786; Hs.82425; actin related protein 2/3 complex, subunit; none; TM=M; 2.90; 11.00
 427045; H86504; Hs.173328; protein phosphatase 2, regulatory subunit; B56; TM=M; 2.89; 6.12
 431177; NM_003304; Hs.250587; transient receptor potential channel 1; ion_trans, ank; TM=Y; 2.89; 6.53
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; 2.87; 9.18
 418546; AA224827; ; gbnc32g04.s1 NC1_CGAP_P12 Homo sapiens ; vwa, Integrin, A, FG-GAP, none; 2.86; 9.94
 446668; W58353; Hs.285123; Homo sapiens mRNA full length Insert cDN; NDK, PH, Oxysterol_BP; SS=M; 2.85; 14.25
 454080; AI199711; Hs.576; fucosidase, alpha-L-1, tissue; Alpha_L_fucos; TM=M; SS=M; 2.81; 28.84
 432874; W94322; Hs.279551; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 433000; Hs.3144; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4, UBA, Cbl_N, Cbl_N2, Cbl_N3; 2.77; 10.93
 444488; AW192879; Hs.355660; ancient conserved domain protein 4; none, none; 2.77; 12.58
 417904; AI750762; Hs.82911; protein tyrosine phosphatase type IVA, m; Y_phosphatase, DSPc; TM=M; 2.76; 12.78
 425204; NM_002436; Hs.1861; membrane protein, palmitoylated 1 (55kD); SH3, PDZ, Guanylate_kin; SS=M; 2.74; 5.71
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zf-C2H2, SET; 2.73; 12.50
 410793; AW581906; Hs.66392; Intersectin 1 (SH3 domain protein); SH3, ehfand, C2, PH, RhoGEF, M; SS=M; 2.73; 9.84
 446081; AA972412; Hs.13755; f-box and WD-40 domain protein 2; WD40, F-box, Ribosomal_L14; TM=M; 2.71; 12.29
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor ; ig, pkinase; TM=Y; 2.71; 10.53
 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox, none; 2.69; 12.53
 423533; NM_014339; Hs.129751; Interleukin 17 receptor; none; TM=Y; SS=M; 2.67; 8.59
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 2.67; 12.22
 453915; AA588721; Hs.12284; ribosomal protein L4; none, T-box; 2.65; 6.38
 416810; AF035608; Hs.80019; programmed cell death 6; ehfand; TM=M; 2.61; 13.89
 439558; AA332057; Hs.6839; hypothetical protein MGC15440; none; TM=M; SS=M; 2.58; 10.19
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fs, clone H; SH3, none; 2.56; 19.04
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; SS=M; 2.55; 14.99
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP, none; 2.52; 14.71
 409098; AA132672; Hs.7984; pleckstrin homology, Sec7 and coiled/coiled; PH, Sec7; TM=M; 2.51; 14.51
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex; TM=Y; SS=M; 2.49; 9.28
 422070; AF149785; Hs.111126; pituitary tumor-transforming 1 Interact; TCTP; TM=M; SS=Y; 2.45; 12.49
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase; TM=M; 2.44; 6.68
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none; TM=M; 2.43; 7.97
 446287; BE247683; Hs.14611; dual specificity phosphatase 11 (RNA/RNP; DSPc; SS=M; 2.41; 9.51
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none, none; 2.41; 14.01
 424756; AW504657; Hs.125931; lamin B receptor; ERG4_ERG24, FKBP; TM=Y; 2.40; 5.98
 447580; AI953360; Hs.88201; ESTs; none, none; 2.38; 11.63
 426276; AW688141; Hs.169078; hypothetical protein FLJ23018; hormone_rec, zf-C4; TM=M; 2.34; 13.34
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF; 2.33; 12.17
 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase, RGS; TM=M; 2.32; 15.80
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rm, NTF2; TM=M; 2.32; 12.48
 453648; W21493; Hs.28329; hypothetical protein FLJ14005; none, none; 2.31; 13.19
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin, none; 2.31; 8.51
 453327; AW500180; Hs.356109; tryptophanyl-tRNA synthetase; rm, vwa, FG-GAP; 2.30; 13.02
 439256; AA322302; Hs.183302; PCTAIRE protein kinase 2; none, none; 2.28; 10.36
 424457; AI929392; Hs.350026; DnaJ (Hsp40) homolog, subfamily B, member; DnaJ, pkinase, UBA, pkinase_C; SS=M; 2.26; 11.82
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 2.26; 12.54
 456607; AI650190; Hs.106070; cyclin-dependent kinase inhibitor 1C (p5; CDI; TM=M; 2.25; 13.11
 423960; AA164516; Hs.136309; SH3-containing protein SH3GLB1; SH3, none; 2.20; 20.05
 424058; AL121516; Hs.138617; thyroid hormone receptor interactor 12; HECT, WVE; TM=M; 2.20; 13.38
 446544; NM_003272; Hs.15791; transmembrane 7 superfamily member 1 (up; none; TM=Y; SS=M; 2.18; 15.68
 411218; H46440; Hs.180628; dynamin 1-like; dynamin_2, dynamin, GED, none; 2.18; 13.83
 414721; X90392; Hs.77091; ribosomal protein L10; Exo_endo_phos, Ribosomal_L10e, Acyltransferase, SCP; TM=M; SS=M; 2.14; 11.24
 421759; AA027968; Hs.107979; small membrane protein 1; none; TM=Y; SS=M; 2.14; 14.03
 416240; NM_001981; Hs.79095; epidermal growth factor receptor pathway; ehfand, DUF164; TM=M; 2.13; 12.86
 435521; W23814; Hs.6361; mitogen-activated protein kinase kinase ; none, none; 2.12; 11.08
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, P13_P14_kinase, FAT, FATC, BclA, RUN; TM=M; 2.12; 14.05
 453064; R40334; Hs.89483; potassium large conductance calcium-act; none, none; 2.12; 8.96
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP, none; 2.08; 11.60
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 2.06; 14.23
 414496; W73853; Hs.355424; ESTs; pkinase_F5_F8_type_C, adh_short, none; 2.05; 13.45
 450455; AL117424; Hs.25035; chloride intracellular channel 4; none, TNF; 2.05; 19.04
 449906; NM_005638; Hs.24167; synaptobrevin-like 1; synaptobrevin, NTF2; TM=Y; 2.04; 13.34
 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; SS=M; 2.03; 12.60
 434935; BE561824; Hs.273369; uncharacterized hematopoietic stem/proge; none; TM=M; 2.02; 10.52
 433427; AI818449; Hs.171889; cholinephosphotransferase 1; SH2, CDP-OH_P_trans; TM=M; 2.02; 16.87
 410850; X90392; Hs.302738; Homo sapiens cDNA: FLJ21425 fs, clone C; Sulfate_transp, STAS, HMG_box; 2.02; 9.37
 440481; AA182907; Hs.7200; Homo sapiens, clone MGC:16714, mRNA, cont; pkinase, RCC1; TM=M; 2.02; 12.31
 434645; AF255303; Hs.112227; membrane-associated nucleic acid binding; zf-COCH, gpdh, Adeno_E1B_55K, zf-C3HC4; TM=M; 2.00; 9.15
 410113; AW998564; Hs.250824; Homo sapiens cDNA: FLJ23435 fs, clone H; pkinase, none; 1.99; 10.64
 414636; AL120259; Hs.76691; stannin; none; TM=M; SS=Y; 1.95; 7.72
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase, none; 1.95; 14.95
 422690; AU077275; Hs.119222; suppression of tumorigenicity 13 (colon ; TPR; TM=M; 1.94; 10.91
 427881; BE538296; Hs.323834; cytochrome c oxidase subunit Va; none, GKAP; 1.93; 20.57
 433387; L76528; Hs.3260; presenilin 1 (Alzheimer disease 3); Presenilin_7tm_3, oxidored_q5_N; TM=Y; 1.92; 12.58
 453938; AF082569; Hs.36794; D-type cyclin-interacting protein 1; B58; TM=M; 1.90; 12.74
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog); none; TM=M; 1.89; 23.27
 447791; BE241859; Hs.19575; CGI-11 protein; V-ATPase_H, Amadillo_seg; TM=M; 1.88; 12.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fs, clone H; adenylatekinase, none; 1.88; 14.95

- 432650; D00860; Hs.56; phosphoribosyl pyrophosphate synthetase; none; none; 1.88; 12.70
 424250; AF073310; Hs.143648; insulin receptor substrate 2; PH,IRS;TM=M; 1.86; 19.50
 424482; BE268621; Hs.149155; voltage-dependent anion channel 1; Euk_porin;SS=M; 1.85; 11.29
 425335; BE394327; Hs.296267; tollstatin-Era 1; ehfand,kazal,arf,ras,7tm,1;TM=M; 1.85; 13.62
 426122; NM_006925; Hs.166975; splicing factor, arginine/serine-rich 5; rrm;SS=M; 1.83; 10.88
 451579; AW607731; Hs.26670; Human PAC clone RP3-515N1 from 22q11.2-q; kingle;TM=Y;SS=M; 1.63; 20.35
 428901; A1929568; Hs.146668; KIAA1253 protein; 7tm,2,UPF0073,TMS_TDE;TM=Y;SS=M; 1.83; 19.00
 453963; AA040311; Hs.28959; ESTs; pkinase,Activin_rec;none; 1.82; 15.25
 417414; AA434589; Hs.357676; dUTP pyrophosphatase; dUTPase,KRAB; 1.81; 14.20
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 1.81; 22.29
 425356; BE244879; Hs.155939; inositol polyphosphato-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M; 1.80; 18.30
 417733; ALD48678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown prot; none;NA;NA; 1.80; 6.28
 424805; AF230904; Hs.153260; c-Cbl-interacting protein; SH3;TM=M; 1.80; 11.99
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M; 1.79; 25.25
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 1.76; 15.25
 437708; AB033020; Hs.5801; KIAA1194 protein; LRR,Exo_endo_phos;TM=M; 1.77; 11.11
 439877; H37685; Hs.258730; tryptase beta 1; pkinase;SS=M; 1.77; 21.91
 440256; U23841; Hs.18851; hypothetical protein FLJ10875; none,UBA,UBX; 1.76; 12.95
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 1.76; 21.01
 414703; BE243877; Hs.374366; ATPase, Na7 transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 1.75; 20.03
 434693; A1344782; Hs.349261; DnaJ (Hsp40) homolog, subfamily C, member; rrm,DnaJ,TPR;TM=M; 1.75; 13.29
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C138 (fr; ABC_tran,GTP_EFTU,ABC_membrane,none; 1.75; 8.75
 413798; AW408094; Hs.75545; Interleukin 4 receptor; fn3,granulin;TM=M;SS=M; 1.74; 14.73
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyrosine kinase; pkinase,SH2,adenylatekinase,none; 1.73; 24.10
 429655; AW4959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,jg,none; 1.73; 31.59
 421456; AW579842; Hs.104557; hypothetical protein FLJ10697; zf-C2H2,DUF18,ehfand,C2,PI-PLC-Y,PI-PLC-X;TM=M; 1.73; 16.87
 444252; R21135; Hs.54985; ESTs; none;none; 1.71; 10.40
 442819; BE622721; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; none,pkinase,PBD; 1.69; 14.02
 447918; A1129320; Hs.115175; ESTs, Highly similar to JC5818 gamma-act; pkinase,SAM,none; 1.69; 17.14
 429279; AB018271; Hs.198689; KIAA0728 protein; Myosin_tail,ehfand,spectrin,GAS2,Myosin_tail; 1.68; 14.21
 450440; AB024334; Hs.25001; tyrosine 3-monooxygenase/tryptophan 5-mo; 14-3-3;TM=M; 1.67; 24.67
 413423; AU076684; Hs.75350; vinculin; Vinculin,none; 1.65; 29.28
 420972; AW814616; Hs.31431; hypothetical protein FLJ12171; Fructosamin_kin;SS=M; 1.65; 10.75
 416884; M60484; Hs.80350; protein phosphatase 2 (formerly 2A), cat; Metallophos;SS=M; 1.63; 24.55
 436719; Y11192; Hs.52599; aldehyde dehydrogenase 5 family, member; lipocalin,aldedh,ubiquitin,IRK;SS=M; 1.61; 11.20
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 1.61; 14.93
 414176; BE140638; Hs.75794; EDG-2 (endothelial differentiation, lys; 7tm,1,CRCB;TM=Y; 1.61; 8.03
 431746; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;SS=M; 1.60; 24.37
 412347; AW970026; Hs.73818; ubiquinol-cytochrome c reductase hinge p; UCR_hinge,G-alpha,arf;TM=M; 1.59; 18.09
 423804; AW403448; Hs.1708; Interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M; 1.59; 10.99
 426552; BE297660; Hs.170328; moesin; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasm,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 1.58; 25.97
 428216; M18458; Hs.183037; protein kinase, cAMP-dependent, regulator cNMP_binding,R1a;SS=M; 1.56; 10.58
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;SS=M; 1.56; 13.51
 448581; NM_002079; Hs.21537; protein phosphatase 1, catalytic subunit; none;none; 1.55; 12.33
 417098; AB017365; Hs.173859; frizzled (Drosophila) homolog 7; Frizzled,Fz,7tm,2,loxin,2;TM=Y;SS=M; 1.55; 13.77
 437076; AA961260; Hs.5443; BCL2-associated athanogene 5; BAG,Hanta_nucleocap;TM=M; 1.54; 10.93
 426653; AA530892; Hs.171695; dual specificity phosphatase 1; Rhodanese,DSPE_Y_phosphatase;TM=M; 1.54; 11.88
 421143; AB024538; Hs.102171; immunoglobulin superfamily containing 1e; lg,LRR,LRRNT,LRRCT;TM=M;SS=M; 1.53; 23.05
 414457; AW514320; Hs.76159; ATPase, H transporting, lysosomal (vacuol; pkinase,ATP-synt_L;none; 1.53; 32.59
 414382; AW380339; Hs.8068; hematopoietic PBX-interacting protein; M;TM=M; 1.52; 8.66
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm;TM=M; 1.52; 11.74
 402705; ; activator of S phase kinase; AhpC-TSA;TM=M;SS=M; 1.51; 26.85
 426258; AW083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;SS=M; 1.50; 24.04
 414604; AU076649; Hs.76556; growth arrest and DNA-damage-inducible 3; none;TM=M; 1.50; 14.35
 445584; AF217518; Hs.8360; PTD012 protein; none;SS=M; 1.49; 12.00
 407232; X04526; ; gb:Human liver mRNA for beta-subunit elg; WD40;TM=M; 1.49; 19.32
 424208; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 1.48; 13.21
 458761; AF090922; Hs.152738; mitochondrial ribosomal protein L11; ER_lumen_recept,Ribosomal_L11,Ribosomal_L11_N;TM=Y;SS=M; 1.48; 12.50
 426340; Z97989; Hs.169370; FYN oncogene related to SRC, FGR, YES; BNR,SH2,SH3,pkinase;TM=Y;SS=M; 1.48; 17.75
 414166; AW688941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rm,Mdr,Cys_knot,TIL,vwa,vwc,vwd,IQ,R1a,abhydrolase,TGF-beta,DUF139,TPR,DSPE,tsp,1,Ribosomal_S21,rp;TM=M; 1.46; 20.47
 452516; AA058630; Hs.29759; RNA POLYMERASE I AND TRANSCRIPT RELEASE; ;none;SS=M; 1.46; 12.72
 414240; AL046742; Hs.75842; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;SS=M; 1.45; 14.38
 420532; AA248016; Hs.194110; hypothetical protein PRO2730; pkinase,WD40;SS=M; 1.43; 13.92
 402575; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.43; 13.71
 414765; X07854; Hs.77269; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M; 1.41; 24.62
 448423; BE390905; Hs.21198; translocase of outer mitochondrial membr; TPR;TM=M;SS=M; 1.41; 10.70
 422587; A1879352; Hs.118625; hexokinase 1; hexokinase,hexokinase2;TM=M; 1.41; 19.31
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X;TM=M; 1.40; 11.21
 446108; AL036596; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmin;TM=M; 1.40; 13.98
 427721; A1582843; Hs.180455; RAD23 (S. cerevisiae) homolog A; ubiquitin,UBA,integrin_B;SS=M; 1.39; 15.01
 417891; W79410; Hs.82887; protein phosphatase 1, regulatory (inhib; none;TM=M; 1.39; 15.97
 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; enk;TM=M; 1.39; 14.49
 446334; U52427; Hs.14839; polymerase (RNA) II (DNA directed) polyp; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,catreticuln,7tm,2,rm,PAP_assoc;TM=Y;SS=M; 1.38; 12.58
 447042; AB035863; Hs.182217; succinate-CoA ligase, ADP-forming, beta; ligase-CoA,ATP-grasp,Zip,CPSase_L_D2,GARS_B;TM=Y;SS=M; 1.37; 11.37
 427705; A1870421; Hs.180394; signal recognition particle 14kD (homolo; SRP14,TNFR_c6;SS=M; 1.37; 22.05
 425969; AW576265; Hs.301763; KIAA0554 protein; SH3,FCH,HR1;TM=M; 1.37; 13.68
 433572; AL046859; Hs.3407; protein kinase (cAMP-dependent, catalytic; PKI;SS=M; 1.35; 12.43
 410697; W16518; Hs.279518; amyloid beta (A4) precursor-like protein; Kunitz_BPTLA4_EXTRA,Coprogen_oxidas;TM=Y;SS=M; 1.35; 22.54
 418424; Y13622; Hs.85087; latent transforming growth factor beta b; EGF,TB,spidertoxin,granulin,ANF_receptor;SS=M; 1.34; 12.09
 442603; AL035719; Hs.303091; pleckstrin homology, Sec7 and coiled-coil; PH,Sec7;TM=M; 1.34; 11.40
 418043; AW377752; Hs.83341; AXL receptor tyrosine kinase; fn3,jg,pkinase;TM=Y;SS=M; 1.31; 10.79

	439278; AF077046; Hs.6518; ganglioside expression factor 2; MAP1_LC3,aminotran_3;TM=M; 1.31; 15.89
	425875; AU077333; Hs.160483; erythrocyte membrane protein band 7.2 (s; PBP,Band_7;TM=M; 1.31; 17.93
	407744; AB020629; Hs.38095; ATP-binding cassette, sub-family A (ABC1; ABC_tran,PRK;TM=Y;SS=M; 1.29; 10.95
5	420679; X57152; Hs.99853; fibrillarin; CK_IL_beta,Fibrillarin,WD40;TM=M; 1.29; 18.69
	427397; AI929885; Hs.177656; calmodulin 1 (phosphorylase kinase, delta; ehband,RnaAD;SS=M; 1.29; 15.68
	424661; M29551; Hs.151531; protein phosphatase 3 (formerly 2B), cat; Metallophos;TM=M; 1.28; 13.39
	428950; BE311879; Hs.194673; phosphoprotein enriched in astrocytes 15; DED;TM=M; 1.27; 11.15
	440820; AL031846; Hs.356416; plakophilin 4; none,none; 1.26; 10.65
10	448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae; NusG;SS=M; 1.25; 12.07
	447386; NM_006289; Hs.375001; KIAA1027 protein; Band_411_LWEQ,Apolipoprotein,IRS;SS=M; 1.22; 10.65
	433053; BE301909; Hs.279952; glutathione S-transferase subunit 13 hom; HCCA_isomerase;TM=M; 1.20; 15.78
	440708; AF038962; Hs.7381; voltage-dependent anion channel 3; Euk_porin,Enteroloxin_A,PHO4,none; 1.20; 14.06
	417069; AA442192; Hs.374980; cytochrome c oxidase subunit VIII; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,catreticuln,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 1.18; 16.91
15	402559; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.16; 15.49
	426636; BE242634; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT;TM=M; 1.14; 10.99
	428773; BE256238; Hs.193163; bridging integrator 1; BAR,SH3;SS=M; 1.14; 11.38
	405906; Z25424; ; gb:H.sapiens protein-serine/threonine kt; none,none; 1.13; 12.97
20	443932; AW888222; Hs.9973; lensin; SH2,WW,PID,none; 1.07; 15.41
	421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61
	414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 22.96; 4.57
	442573; H93366; Hs.7567; branched chain aminotransferase 1, cytos; aminotran_4,none; 21.41; 1.15
	451035; AU076785; Hs.430; plastin 1 (I isoform); ehband,CH,Adaptin_N;SS=M; 19.25; 3.53
25	408243; Y00787; Hs.624; interleukin 6; HLH,PAS,IL6;TM=M; 15.53; 4.34
	421340; F07783; Hs.1369; decay accelerating factor for complement; susht;SS=M; 14.84; 19.59
	422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c;SS=M; 14.71; 2.89
	430280; AA361258; Hs.237868; interleukin 7 receptor; tn3,none; 14.28; 11.47
	412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1;TM=Y;SS=M; 12.71; 12.56
30	451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 10.18; 2.67
	418693; AI750878; Hs.87409; thrombospondin 1; EGF,bsp_1,vcv,TSPN,bsp_3;SS=M; 9.72; 6.94
	448105; AW591433; Hs.298241; Transmembrane protease, serine 3; kdl_recept_L,trypsin;TM=Y;SS=M; 9.67; 4.06
	456266; L29073; Hs.198728; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
	413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none,START; 9.15; 2.18
35	417933; X02308; Hs.82962; thymidylate synthetase; thymidylat_synt,MR_MLE,MR_MLE_N;SS=M; 8.97; 5.01
	433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
	418030; BE207573; Hs.83321; neuromedin B; Bombasin;TM=M;SS=Y; 8.38; 1.55
	433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20;SS=M; 8.31; 4.23
	449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.26; 5.49
40	428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
	449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
	453459; BE047032; Hs.257789; ESTs; none,none; 7.40; 0.60
	436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78
	426761; AI015709; Hs.172089; PORIMIN Pro-oncogene receptor inducing me; none;TM=Y;SS=M; 7.25; 7.22
45	426158; NM_001992; Hs.199087; v-erb-b2 avian erythroblastic leukemia v; Furin-like,ptkinase,Recep_L_domain,Furin-like,ptkinase,Recep_L_domain,Peptidase_M24; 7.13; 3.97
	419686; X04430; Hs.93913; interleukin 6 (interferon, beta 2); IL6;SS=Y; 6.93; 3.43
	457133; M54968; Hs.351221; v-K-ras2 Kirsten rat sarcoma 2 viral on; ras,ldh;SS=M; 6.90; 2.85
	420344; BE483721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 6.88; 3.10
	417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y; 6.42; 2.26
50	427969; NM_001963; Hs.2230; epidermal growth factor (beta-urogastron; EGF,kdl_recept_L,EB;TM=M;SS=M; 6.37; 1.07
	430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,krtgla,trypsin,Nebulin,LLM;SS=M; 5.77; 1.24
	427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh;SS=M; 5.71; 3.83
	418283; S79895; Hs.83942; cathepsin K (pycnodysostosis); Peptidase_C1;SS=M; 5.59; 38.68
	458471; AV648609; Hs.194240; ESTs; none,none; 5.23; 1.05
55	433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
	433293; AF007835; Hs.32417; hypothetical protein MGC4309; none;TM=M; 4.56; 4.98
	410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); EGF,TB,wnt,EB,TIL;SS=M; 4.32; 26.87
	417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD;TM=Y;SS=M; 4.26; 9.04
	414825; X06370; Hs.77432; epidermal growth factor receptor (avian; Furin-like,ptkinase,Recep_L_domain;TM=M;SS=M; 3.94; 1.16
60	439180; AI933742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,ptkinase,Recep_L_domain,Furin-like,ptkinase,Recep_L_domain,Peptidase_M24; 3.76; 2.21
	419508; AW997939; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 3.47; 2.24
	419749; X73608; Hs.93029; sparco/osteonectin, cwcv and kazal-like d; kazal,thyroglobulin_1;SS=M; 3.37; 7.10
	436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.15; 3.27
	428093; AW594506; Hs.104830; ESTs; none,none; 2.81; 3.40
65	459583; AI674906; Hs.199460; gb:wc7302.x1 NCI_CGAP_Pan1 Homo sapiens; none;TM=Y; 2.77; 1.38
	414443; AU077268; Hs.76144; platelet-derived growth factor receptor.; lg,ptkinase;TM=Y; 2.71; 10.63
	430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase;SS=M; 2.28; 14.59
	428953; AA306610; Hs.348183; tumor necrosis factor receptor superfam; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 2.21; 6.33
	435496; AW840171; Hs.265398; PAR-6 beta; none,none; 2.17; 2.00
70	418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin,Reprolysin,Pep_M12B_propep,EGF;TM=Y;SS=M; 1.91; 13.06
	414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 1.81; 22.29
	419452; U33635; Hs.90572; PTYK7 protein tyrosine kinase 7; lg,ptkinase;TM=Y;SS=M; 1.52; 8.40
	452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fell_Oxy;TM=M; 1.49; 3.29
	432199; AI693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 1.23; 1.60
75	453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,kdl_recept_a,none; 1.00; 3.92
	445418; AW139377; Hs.127179; cryptic gene; none,none; 1.00; 2.45
	451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M; 1.00; 1.87
	447993; AW139525; Hs.170362; ESTs; none,none; 1.00; 1.30

TABLE 42B

Pkey: Unique Eas probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5

Pkey:CAT NumberAccession

4066850_0M18728

4140871632850_1W19712 BE247277

4001519575_21BC006850 U07418 NM_000249 U07343 AL574783 BI090482 BG684481 AA385302 BG196167 BI091720 BG195132 AI680106 AI457552 AA402478

418546242836_1T59708 AA224827 T59843 BE155903

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TABLE 42C

15

Pkey:Unique number corresponding to an Eos probeset

Ref:Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand:Indicates DNA strand from which exons were predicted.

Nt_position:Indicates nucleotide positions of predicted exons.

20

PkeyRefStrandNt_position

4063999256288Minus63448-63554

4051028076881Minus120922-121296

4033448569726Plus70823-70990

4055551552511Plus153405-153564,154623-154876,155272-15540

4055561552511Plus163497-163623,164715-164968,165369-16550

4052047230116Plus126569-126754

4063669256126Minus10639-10800,10890-11023,11113-11293

4005397574902Plus8559-8721

4032087630829Minus147706-147903,148667-148804

4052037230116Plus125295-125463

4027058782736Plus89961-90114,90773-90895,91131-91261

4025759884830Minus109742-109883

4025599864273Plus33539-33715

35

TABLE 43A: 43 genes upregulated in pancreatic cancer relative to normal body tissues

40

Table 43A lists about 43 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins particularly useful for diagnostic or prognostic applications. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

45

Pkey:Unique Eos probeset Identifier number

ExAccn:Exemplar accession number, GenBank accession number

UniGeneID:UniGene number

Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).

50

UniGene Title:UniGene gene title

R190th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs

R290th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

55

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1; R2

60

446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin); Osteopontin;SS=M; 44.95; 2.17

421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;SS=M; 35.40; 29.13

411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M; 30.10; 13.59

446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cy; IL8;SS=Y; 29.33; 16.08

413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8;SS=M; 24.64; 7.21

452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide,TGF-beta,none; 23.81; 10.74

407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagonist; TGF-beta,DAN;SS=Y; 22.33; 10.20

404682; ; C9001188;gij12738842[ref]NP_073725.1] p; none;TM=M; 17.72; 1.40

413554; AA319146; Hs.75426; secretogranin II (chromogranin C); Granin;TM=M;SS=Y; 17.36; 2.01

426392; H10233; Hs.2265; secretory granule, neuroendocrine protet; none;TM=M;SS=M; 16.82; 1.70

408243; Y00787; Hs.624; interleukin 8; IL8,PAS,IL8;TM=M; 15.53; 4.34

419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8;SS=M; 15.40; 3.70

428242; H55709; Hs.2250; leukemia inhibitory factor (cholinergic; LIF_OSM;SS=M; 14.85; 6.58

421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59

409757; NM_001898; Hs.123114; cystatin SN; cystatin;SS=M; 14.61; 12.75

425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 14.35; 17.22

414812; X72755; Hs.77367; monokine induced by gamma interferon; IL6;TM=M;SS=Y; 13.81; 7.69

409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin 100kD); kallini; laminin_B,laminin_EGF;SS=M; 13.05; 7.72

432596; AJ224741; Hs.278461; matrilin 3; EGF_vwa;SS=M; 12.80; 9.91

422109; S73265; Hs.1473; gastrin-releasing peptider; Bombesin,Defensin_propep;TM=M;SS=M; 12.79; 4.69

421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 11.36; 2.22

428547; AW009168; Hs.99376; FGENESH predicted novel secreted protekin; none,none; 10.25; 5.62

422424; AI186431; Hs.296538; prostate differentiation factor; TGF-beta;SS=M; 9.96; 1.88

428505; AL035461; Hs.2281; chromogranin B (secretogranin I); Granin;SS=M; 9.40; 3.46

409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;SS=M; 9.19; 16.46

418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55

452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB;SS=M; 7.46; 4.96

- 5 421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estrogen; trefoil, Gastrin; SS=M; 7.08; 21.61
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none; TM=M; SS=M; 6.78; 12.19
 428486; AW563497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.29; 3.51
 443646; AI085198; Hs.164226; ESTs; EGF, tsp_1, vwc, TSPN, tsp_3, none; 6.17; 4.25
 457489; AI693815; Hs.127179; cryptic gene; none; TM=M; SS=M; 5.19; 2.79
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; none; SS=M; 5.01; 7.43
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3, EGF; SS=M; 4.87; 9.40
 426322; J05068; Hs.2012; transcobalamin I (vitamin B12 binding pr; Cobalamin_bind; SS=M; 4.71; 11.74
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringla, trypsin, plant_thionins; SS=M; 4.24; 6.91
 10 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA; TM=Y; 3.52; 8.43
 422048; NM_012445; Hs.288126; spondin 2, extracellular matrix protein; tsp_1; TM=M; SS=M; 3.45; 7.69
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; tn2, hemopexin, Peptidase_M10; SS=M; 3.43; 10.37
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil; SS=M; 2.98; 9.65
 15 445417; AK001058; Hs.12680; Homo sapiens cDNA FLJ10196 fis, clone HE; tsp_1, Reprolysin, Pep_M12B_propep, none; 2.97; 5.74
 432674; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precu; none, none; 2.70; 1.99

TABLE 43C

20	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
25	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
	404682	9797231	Minus	40977-41150

30

TABLE 44A: 754 GENES UP-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

35 Table 44A lists about 754 genes up-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymatrix/Eos Hu01 GeneChip.

40	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigenelD:	Unigene number		
	Unigene Title:	Unigene gene title		
	Pkey	ExAccn	UnigenelD	Unigene Title
	100042	M10098		AFFX control - HUMRGE/M10098_3
45	101577	M34353	Hs.1041	v-ros avian UR2 sarcoma virus oncogene h
	103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa
	104743	AA021157	Hs.33519	Homo sapiens cDNA FLJ20098 fis, clone CO
	104996	AA112307	Hs.105894	hypothetical protein FLJ21919
	105437	AA252191	Hs.25199	hypothetical protein
50	108258	AA063269		gb:zm02a09.s1 Stratagene corneal stroma
	109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfami
	109279	AA196625	Hs.86080	ESTs
	109779	F10527	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur
	111794	R32647	Hs.23545	ESTs
55	112531	R69798	Hs.29036	ESTs
	112784	R96306	Hs.191290	ESTs
	113293	T67026	Hs.187403	ESTs
	115416	AA283893	Hs.337079	ESTs
	116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa
60	116565	D45533	Hs.129691	hypothetical protein FLJ21603
	118104	N55332	Hs.39785	ESTs
	119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa
	119336	T55340	Hs.208238	ESTs
	120101	W95414	Hs.55497	EST
65	120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GC81 Homo sapiens
	120872	AA357993	Hs.96996	ESTs
	121010	AA398355	Hs.97330	ESTs
	121509	AA412092	Hs.97888	ESTs
	121722	AA419482	Hs.98874	similar to proline-rich protein 48
70	122265	AA436838	Hs.98906	EST
	123205	AA489681	Hs.102248	Homo sapiens cDNA: FLJ22105 fis, clone H
	123490	AA599723		gb:ag11c07.s1 Gessler Wilms tumor Homo s
	124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha
	124294	H90573	Hs.102298	EST
75	125067	T86429	Hs.111725	ESTs
	125153	W38294		
	125330	AA401804	Hs.114574	ESTs
	125335	T86620	Hs.16230	hypothetical protein FLJ20619
	125361	T90348	Hs.183404	ESTs
80	125439	AA826305		gb:PMO-LT0017-031299-001-c07 LT0017 Homo
	125535	R17430	Hs.22215	secretogranin III
	125583	R22272	Hs.86022	ESTs
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
	125742	H81181	Hs.261023	hypothetical protein FLJ20958

	125795	T98190	Hs.7756	proteasome (prosome, macropain) 26S subu
	125858	H11549	Hs.31066	ESTs
	125865	H12876	Hs.283078	hOAT4
5	126039	AA160575	Hs.181102	p30 DBC protein
	126143	N29315	Hs.266331	hypothetical protein MGC4595
	126177	H93164	Hs.129750	hypothetical protein FLJ10546
	126219	N36368	Hs.293483	ESTs, Weakly similar to similar to C. el
	126221	A1248169	Hs.172965	ESTs
10	126262	C75147	Hs.143764	ESTs, Weakly similar to unknown [H.sapi
	126277	N39132	Hs.15441	Crm (Cramped Drosophila)-like
	126292	AA491328		gb:aa65d09.r1 NCI_CGAP_GC81 Homo sapiens
	126293	Z18870	Hs.248121	G protein-coupled receptor 22
	126353	A1243114	Hs.94031	ESTs
15	126556	AA491325	Hs.112227	membrane-associated nucleic acid binding
	126559	R15866	Hs.170263	tumor protein p53-binding protein, 1
	126609	W87435	Hs.186802	ESTs
	126616	AA348581	Hs.134605	ESTs
	126828	A1357886	Hs.170994	hypothetical protein MGC10946
20	126636	AA001527		gb:zf56g09.r1 Soares retina N2b4HR Homo
	126861	AA742428	Hs.144432	ESTs
	126990	AA215510	Hs.191650	ESTs
	127017	AA740146	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I
	127049	AA235866	Hs.291811	ESTs
25	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil
	127331	F20186		gb:HSPD05873 HM3 Homo sapiens cDNA clone
	127357	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	127368	AA434362	Hs.193326	fibroblast growth factor receptor-like 1
	127374	AA448728	Hs.312110	ESTs, Weakly similar to I38022 hypothet
30	127429	AA961490	Hs.293751	ESTs, Moderately similar to TPTE_HUMAN P
	127490	W52891	Hs.7278	cryptochrome 2 (photolyase-like)
	127502	AA614422	Hs.183502	ESTs
	127647	A1087279	Hs.148410	ESTs
	127650	AA873776	Hs.261957	ESTs
35	127676	D31237	Hs.279938	HSPC067 protein
	127746	A1239495	Hs.120189	ESTs
	127812	AA749094	Hs.291434	ESTs
	127824	A1208365	Hs.127811	ESTs
	127933	AA811102	Hs.303581	ESTs, Moderately similar to ALU1_HUMAN A
40	128006	AA058693	Hs.129908	KIAA0591 protein
	128011	A1347067	Hs.124636	ESTs
	128038	AA868782	Hs.137024	ESTs
	128058	A126617	Hs.132449	ESTs
	128199	A1073548	Hs.164597	ESTs
45	128308	A1079496	Hs.134169	ESTs
	128389	A1142639	Hs.146662	ESTs
	128410	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	129199	H90914	Hs.200332	hypothetical protein FLJ20651
50	130998	C00810	Hs.293981	guanine nucleotide binding protein (G pr
	134409	AA281600	Hs.164915	small nuclear RNA activating complex, p
	134578	AA194724	Hs.224137	hypothetical protein
	134644	S83308	Hs.87224	SRY (sex determining region Y)-box 5
	100262	D38500	Hs.278468	postmeiotic segregation increased 2-like
	100676	HG3044-HT3742	Hs.287820	fibronectin 1
55	100704	HG3242-HT3419	Hs.166110	calcium channel, voltage-dependent, alph
	100787	HG3872-HT4142	Hs.302063	immunoglobulin heavy constant mu
	100873	HG4333-HT4603	Hs.17364	zinc finger protein 79 (pT7)
	100943	HG880-HT880		gb:PMO-SN0019-280300-001-D11 SN0019 Homo
	100996	J03909	Hs.14623	interferon, gamma-inducible protein 30
60	101046	K01160		
	101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi
	101461	M22430	Hs.76422	phospholipase A2, group IIA (platelets,
	101697	M64358		gb:Human rhom-3 gene, exon.
	101909	S69265		
65	102199	U21128	Hs.79914	lumican
	102275	U30998	Hs.17752	phosphatidylserine-specific phospholipas
	102295	U32581	Hs.168052	KIAA0421 protein
	102319	U34587	Hs.66578	corticotropin releasing hormone receptor
	102383	U40622	Hs.150930	X-ray repair complementing defective rep
70	102470	U49835	Hs.154138	chitinase 3-like 2
	102544	U57721	Hs.169139	kynureninase (L-kynurenine hydrolase)
	102649	U68133		gb:U68133 Human cell line PCI-O6A Homo s
	102798	U88898		gb:Human endogenous retrovirus H proteas
	102804	U89942	Hs.83354	lysyl oxidase-like 2
75	102851	V00532	Hs.93907	interferon, alpha 14
	102852	V00571	Hs.75294	corticotropin releasing hormone
	102860	X00368		gb:Human prolactin gene 5' region.
	103262	X78555	Hs.289114	hexabrachion (tanascin C, cytolactin)
	103484	Y08374	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	103559	Z19585	Hs.75774	thrombospondin 4
80	103658	Z74615	Hs.172928	collagen, type I, alpha 1
	103719	AA054109	Hs.4273	hypothetical protein FLJ13159
	103876	AA226865	Hs.8203	endomembrane protein emp70 precursor iso
	103897	AA248870	Hs.55058	EH-domain containing 4

5	103906	AA249437	Hs.317403	hypothetical protein MGC2744
	103985	AA313880	Hs.99872	fetal Alzheimer antigen
	104056	AA397529	Hs.58297	CLL8 protein
	104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy
	104386	H41895	Hs.144164	ESTs, Moderately similar to ALU8_HUMAN A
10	104398	H53555	Hs.36790	ESTs, Weakly similar to putative p150 [H
	104422	H86858	Hs.132909	ESTs
	104561	R60100	Hs.323817	DKFZP547E1010 protein
	104593	R81267	Hs.98640	hypothetical protein FLJ21069
	104643	AA004701	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K
15	104673	AA007633	Hs.20010	ESTs
	104681	AA009832	Hs.34500	ESTs
	104711	AA017254	Hs.32794	ESTs
	104812	AA034111	Hs.124187	ESTs
	104877	AA047437	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
20	104886	AA053348	Hs.339699	growth differentiation factor 11
	104924	AA058532	Hs.28774	ESTs, Weakly similar to I38022 hypotheli
	105071	AA136532	Hs.29475	ESTs
	105105	AA151872	Hs.87016	hypothetical protein FLJ22938
	105203	AA195660	Hs.7882	ESTs
25	105317	AA233926	Hs.52620	Integrin, beta 8
	105617	AA280687	Hs.4069	glucocorticoid modulatory element bindin
	105707	AA291012	Hs.37617	ESTs, Weakly similar to A53933 myosin I
	105754	AA302657	Hs.192028	ESTs
	105770	AA347954	Hs.269873	Homo sapiens clone IMAGE:297403, mRNA se
30	105882	AA400292	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	105883	AA400490	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com
	105890	AA400766	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,
	106080	AA418046	Hs.35124	ESTs
	106090	AA418909	Hs.169333	hypothetical protein DKFZp761E2110
35	106096	AA419509	Hs.170121	protein tyrosine phosphatase, receptor I
	106124	AA423987	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106308	AA436186	Hs.30662	ESTs
	106438	AA449199	Hs.21342	ESTs
	106660	AA460936	Hs.27056	KIAA1284 protein
40	106731	AA465657	Hs.29205	alpha Integrin binding protein 63
	106880	AA488889	Hs.32425	ESTs
	107055	AA600152	Hs.29419	ESTs
	107151	AA621169	Hs.8687	ESTs
	107183	C20974	Hs.12114	vanin 1
45	107231	D59299	Hs.34727	ESTs, Moderately similar to I38759 zinc
	107490	W74158	Hs.103189	lipopolysaccharide specific response-68
	107572	AA001903	Hs.59962	ESTs
	107620	AA005039	Hs.60171	ESTs
	107801	AA019433	Hs.285803	Homo sapiens cDNA FLJ10674 fis, clone NT
50	107817	AA020781	Hs.60847	ESTs
	107823	AA021057	Hs.60836	ESTs
	107857	AA024687	Hs.61208	ESTs
	107882	AA025630	Hs.231967	ALL1 fused gene from 5q31
	108005	AA037769	Hs.194293	ESTs, Weakly similar to I54374 gene NF2
55	108092	AA045961	Hs.184029	hypothetical protein DKFZp761A052
	108115	AA047291	Hs.165216	ESTs
	108214	AA058661	Hs.60764	ESTs
	108382	AA074885	Hs.67726	macrophage receptor with collagenous str
	108409	AA075578		gb:zm88h03.r1 Stratagene ovarian cancer
60	108436	AA078801		gb:zm94a09.s1 Stratagene colon HT29 (937
	108625	AA101983	Hs.283022	triggering receptor expressed on myeloid
	108631	AA102553	Hs.334337	ESTs
	108763	AA127539	Hs.281397	hypothetical protein AD034
	108852	AA133131		gb:zm25d03.s1 Stratagene pancreas (93720
65	108931	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
	108976	AA151480	Hs.91202	ESTs
	109028	AA157811		gb:zo35d07.s1 Stratagene colon (937204)
	109170	AA180352	Hs.191472	ESTs, Weakly similar to ALU1_HUMAN ALU
	109303	AA206126	Hs.269291	ESTs
70	109326	AA210719		gb:zr68e04.s1 NCL_CGAP_GC81 Homo sapiens
	109345	AA213774	Hs.203396	ESTs
	109404	AA224594	Hs.86941	ESTs
	109473	AA233151	Hs.81796	ESTs
	109725	F10003	Hs.79658	casein kinase 1, epsilon
75	109794	F10684	Hs.23687	ESTs
	109835	H00615	Hs.170044	ESTs
	109896	H04794	Hs.30489	ESTs
	109918	H05641	Hs.216701	Homo sapiens mRNA; cDNA DKFZp564I0816 (f
	109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos
80	110078	H15054	Hs.318773	KIAA1836 protein
	110182	H20402	Hs.31746	hypothetical protein DKFZp547F072
	110213	H23216	Hs.86905	ATPase, H+ transporting, lysosomal (vacu
	110310	H38209	Hs.32728	EST
	110354	H41280	Hs.22586	ESTs
	110413	H48124	Hs.279454	ESTs
	110422	H48467	Hs.36094	EST
	110433	H49425	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp

	110434	H49446	Hs.26299	ESTs
	110553	H58934	Hs.124990	ESTs
	110750	N20522	Hs.30981	ESTs
5	110827	N30077	Hs.14855	ESTs
	110829	N30198	Hs.28625	ESTs
	110917	N46363	Hs.5170	ESTs
	111100	N62522	Hs.20450	BCM-like membrane protein precursor
	111112	N63281	Hs.35452	ESTs
10	111179	N67239	Hs.10760	asporin (LRR class 1)
	111185	N67551	Hs.12844	EGF-like-domain, multiple 6
	111223	N68921	Hs.334838	KIAA1866 protein
	111275	N70970	Hs.35006	ESTs
	111443	R01801		gb:Homo sapiens endogenous retrovirus W
15	111573	R10305	Hs.185683	ESTs
	111590	R11157	Hs.75425	ubiquitin associated protein
	111671	R19368	Hs.229084	Homo sapiens cDNA FLJ11666 fis, clone H
	111732	R25153	Hs.163813	ESTs
	111809	R33616	Hs.24688	EST
20	111829	R36070		gb:Homo sapiens full length insert cDNA
	111944	R40606	Hs.21263	suppressor of potassium transport defect
	112015	R42836	Hs.23198	ESTs
	112023	R43020	Hs.236223	EST
	112055	R43621	Hs.26139	ESTs
25	112334	R56239	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S
	112340	R56602	Hs.8904	Ig superfamily protein
	112353	R58986	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (I
	112467	R65706		gb:yi16g12.s1 Soares placenta Nb2HP Homo
	112478	R66067	Hs.28664	ESTs
30	112533	R69886		gb:yi47i03.s1 Soares placenta Nb2HP Homo
	112588	R77302		gb:yi75h08.s1 Soares placenta Nb2HP Homo
	112595	R77783	Hs.22404	protease, serine, 12 (neurotrypsin, moto
	112676	R86976	Hs.34060	ESTs
	112744	R93206	Hs.293762	ESTs, Weakly similar to I38022 hypothei
35	112777	R95869	Hs.35467	EST
	112817	R98491	Hs.14584	ESTs
	112902	T09262	Hs.129190	Human DNA sequence from clone RP5-1046G1
	113009	T23699	Hs.7246	ESTs
	113151	T51620	Hs.9326	EST
40	113297	T67161	Hs.13059	ESTs
	113398	T82280	Hs.87016	hypothetical protein FLJ22938
	113484	T87795	Hs.187543	ESTs
	113769	U55966	Hs.22985	alpha2,8-sialyltransferase
	113794	W37382	Hs.11090	membrane-spanning 4-domains, subfamily A
45	113971	W86760	Hs.269172	ESTs
	114066	Z38152	Hs.26920	ESTs
	114178	Z39063	Hs.17930	chromosome 6 open reading frame 11
	114206	Z39294	Hs.27339	EST
	114371	Z41835	Hs.27810	ESTs
50	114428	AA017130	Hs.84790	KIAA0225 protein
	114466	AA026970	Hs.135150	lung type-4 cell membrane-associated gly
	114625	AA084362		gb:zn05b10.r1 Stratagene hNT neuron (937
	114862	AA235174	Hs.106432	Homo sapiens cDNA FLJ13410 fis, clone PL
	114908	AA236545	Hs.54973	cadherin-like protein VR20
55	114973	AA250845	Hs.87762	ESTs
	115009	AA251561	Hs.48689	ESTs
	115055	AA253005	Hs.61753	ESTs
	115098	AA256161	Hs.161729	ESTs
	115321	AA280805	Hs.191540	ESTs
60	115385	AA282540	Hs.109694	KIAA1451 protein
	115466	AA287008	Hs.285655	ESTs
	115479	AA287596	Hs.278188	ESTs, Moderately similar to I54374 gene
	115663	AA405838	Hs.40507	ESTs
	115689	AA410645	Hs.199014	ESTs, Moderately similar to ALU7_HUMAN A
65	115748	AA418835	Hs.90286	ESTs
	115810	AA426026	Hs.187615	ESTs
	115827	AA427890	Hs.83583	actin related protein 2/3 complex, subun
	115881	AA435577	Hs.184942	G protein-coupled receptor 64
	116148	AA460708	Hs.62905	hypothetical protein FLJ14834
70	116257	AA481493	Hs.88537	ESTs
	116365	AA521080	Hs.46765	ESTs
	116941	H77395	Hs.39749	ESTs
	116982	H81933	Hs.312582	ESTs
	116995	H83928		gb:ys64b03.s1 Soares retina N2b4HR Homo
75	116997	H84214	Hs.40594	ESTs
	117016	H87171	Hs.52170	ESTs
	117097	H93608	Hs.41919	EST
	117101	H94043	Hs.24341	transcriptional co-activator with PDZ-bi
	117238	N20815	Hs.173337	ESTs
80	117303	N22776	Hs.264079	ESTs
	117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3
	117503	N31963	Hs.44286	ESTs
	117544	N33222	Hs.44451	ESTs
	117594	N34929	Hs.171984	ESTs

	117627	N36113	Hs.44789	ESTs, Weakly similar to B34087 hypothet
	117653	N38970	Hs.194214	ESTs
	117695	N40953	Hs.45093	EST
5	117697	N40976		gb:yy80b06.s1 Soares_multiple_sclerosis_
	117766	N47807	Hs.46767	EST
	117807	N48701	Hs.46523	EST
	117816	N48872		gb:yy77a05.s1 Soares_multiple_sclerosis_
10	117882	N50101	Hs.301406	hypothetical protein PP3501
	117987	N51935	Hs.47374	Homo sapiens cDNA FLJ13561 fls, clone PL
	118074	N54188	Hs.130323	Homo sapiens, clone IMAGE:3960432, mRNA
	118114	N56875	Hs.143212	cystatin F (leukocystatin)
	118151	N58276	Hs.229119	EST
	118270	N62868	Hs.48653	ESTs
15	118291	N63076	Hs.138746	EST
	118358	N64017	Hs.144633	hypothetical protein DKFZp434F2322
	118383	N64529	Hs.49001	EST
	118412	N64856	Hs.97437	centrosomal protein 1
	118433	N66248	Hs.141609	EST
20	118600	N69222	Hs.238936	ESTs, Weakly similar to (define not av
	118641	N70298	Hs.49829	ESTs
	118643	N70324	Hs.49840	ESTs
	118695	N71781	Hs.50081	KIAA1199 protein
	118915	N91481	Hs.54713	ESTs
25	119041	R02591	Hs.284294	Breakpoint cluster region protein, uteri
	119069	R27619	Hs.231046	EST
	119105	R42357	Hs.91453	ESTs
	119154	R61293		gb:yh07a05.s1 Soares infant brain 1N18 H
	119241	T12559		gb:CHR90079 Chromosome 9 exon II Homo sa
30	119269	T16367	Hs.65327	EST
	119310	T40427		gb:ya01a06.s2 Stratagene lung (937210) H
	119345	T63474	Hs.90696	EST
	119353	T66867	Hs.187402	ESTs
	119390	T89122	Hs.249712	ESTs, Weakly similar to ALU1_HUMAN ALU
35	119423	T99544	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU
	119428	W02129	Hs.55242	EST
	119529	W38053		ESTs, Highly similar to S03917 fibronect
	119795	W73370	Hs.339722	ESTs
	119817	W74257	Hs.159690	DKFZP586L2024 protein
40	119831	W78050	Hs.58419	hypocretin (orexin) receptor 2
	119930	W86471	Hs.151624	ESTs
	120039	W92548	Hs.94985	hypothetical protein
	120256	AA169801		gb:zp54e11.s1 Stratagene NT2 neuronal pr
	120284	AA182626		KIAA0627 protein; Drosophila multiple as
45	120350	AA211300	Hs.108614	gb:DKFZp434B1822_r1 434 (synonym: hles3)
	120379	AA227849		FSH primary response (LRPR1, rat) homolo
	120383	AA228030	Hs.123122	spinal cord-derived growth factor-B
	120420	AA236031	Hs.112885	novel protein with MAM domain
	120437	AA243427	Hs.104311	ESTs
50	120461	AA251301	Hs.293369	ring finger protein 10
	120594	AA282054	Hs.5094	homeo box A10
	120611	AA284178	Hs.110637	EST
	120626	AA285064	Hs.104485	ESTs
	120696	AA291503	Hs.97249	ESTs
55	120747	AA302976	Hs.96672	ESTs
	120749	AA303235		gb:EST14544 Testis tumor Homo sapiens cD
	120752	AA311972	Hs.22895	hypothetical protein FLJ23548
	120851	AA349862	Hs.174248	ESTs
	120866	AA350718	Hs.291272	ESTs
60	120849	AA397830	Hs.98347	ESTs, Weakly similar to JC5308 testis-sp
	120996	AA398281	Hs.308114	ESTs
	121038	AA398536	Hs.97365	ESTs
	121055	AA398658	Hs.97300	ESTs
	121067	AA398662	Hs.97302	ESTs
65	121071	AA398678	Hs.139355	ESTs
	121082	AA398722		gb:zl75h07.s1 Soares_testis_NHT Homo sap
	121172	AA400013	Hs.97750	EST, Weakly similar to MPL3 RAT MICROTUB
	121191	AA400205	Hs.104447	ESTs
	121354	AA405384	Hs.193737	ESTs
70	121393	AA405981	Hs.262643	ESTs
	121399	AA406059	Hs.332700	EST
	121479	AA411911	Hs.98110	ESTs
	121498	AA412033	Hs.178045	ESTs
	121704	AA418743	Hs.98308	KIAA1862 protein
	121736	AA421131	Hs.148515	Human clone Z3564 mRNA sequence
75	122198	AA435892	Hs.97541	ESTs
	122220	AA436011	Hs.98187	ESTs
	122250	AA436692	Hs.98892	EST
	122279	AA437209	Hs.234016	ESTs
	122286	AA437259	Hs.104944	ESTs
80	122330	AA442870	Hs.98628	Homo sapiens, clone IMAGE:4214491, mRNA,
	122338	AA443311	Hs.98998	ESTs
	122355	AA443789	Hs.19978	CGI-30 protein
	122590	AA453264	Hs.99310	ESTs

5	122746	AA458791		gb:aa68c02.s1 Stratagene fetal retina 93
	122805	AA460702	Hs.82772	collagen, type XI, alpha 1
	122841	AA461536	Hs.288908	WAS protein family, member 2
	122899	AA469960	Hs.178420	ESTs, Highly similar to WASP interacting
	122933	AA476728	Hs.107537	chromosome 7 open reading frame 2
	123005	AA479726	Hs.52620	Integrin, beta 8
	123142	AA487504	Hs.105718	EST
	123153	AA488349	Hs.334808	hypothetical protein MGC4189
10	123168	AA488881	Hs.105218	EST
	123188	AA489092	Hs.177726	ESTs
	123276	AA491270	Hs.187946	ESTs
	123305	AA496133		gb:zv51e12.s1 Soares_testis_NHT Homo sapi
	123328	AA496968		gb:aa42g03.s1 Soares_NhHMPu_S1 Homo sapi
15	123450	AA598913	Hs.111207	ESTs
	123464	AA599014	Hs.153321	Homo sapiens cDNA FLJ10577 fls, clone NT
	123650	AA609332	Hs.180696	ESTs
	123700	AA609606	Hs.191956	ESTs
	123858	AA620821	Hs.112911	EST
20	123863	AA620873	Hs.112916	ESTs
	124046	F10243		gb:HSC3CC122 normalized infant brain cDN
	124059	F13673	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124196	H52617	Hs.144167	ESTs
	124197	H52921		gb:yq76c09.s1 Soares fetal liver spleen
25	124229	H62793	Hs.268945	ESTs
	124230	H63111	Hs.6655	Homo sapiens EST from clone 208499, full
	124241	H65947	Hs.165355	ESTs, Moderately similar to ZN91_HUMAN Z
	124251	H68286	Hs.107924	ESTs
	124400	N30597	Hs.179152	loli-like receptor 7
30	124416	N34042	Hs.271674	ESTs
	124570	N67117	Hs.102808	ESTs
	124575	N58168		gb:za11c01.s1 Soares fetal liver spleen
	124588	N69197	Hs.191361	ESTs, Weakly similar to 138022 hypotheti
	124598	N70294	Hs.269137	ESTs, Weakly similar to A56194 thromboxa
35	124655	N93176	Hs.102914	ESTs
	124706	R07499	Hs.193612	ESTs, Weakly similar to ALU8_HUMAN ALU
	124848	R60135	Hs.203498	EST
	124882	R74041	Hs.101539	ESTs
	124898	R82846	Hs.273789	ESTs
40	125086	T91161	Hs.173880	Interleukin 1 receptor accessory protein
	125145	W38001		
	125216	W73409	Hs.103185	ESTs
	125342	A055916	Hs.133552	ESTs
45	125351	T96520	Hs.324746	alpha-2-HS-glycoprotein
	125419	A076822	Hs.134544	ESTs
	125424	T99667	Hs.18564	ESTs
	125526	R14487	Hs.17110	Homo sapiens mRNA; cDNA DKFp434C2016 (f
	125539	R17870	Hs.248120	G protein-coupled receptor 21
50	125633	AA908225	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA
	125689	R48940	Hs.108043	Friend leukemia virus integration 1
	125707	C14616	Hs.284122	Wnt inhibitory factor-1
	125790	AA858325	Hs.99982	proteoglycan 2, bone marrow (natural kil
	125876	AA324967	Hs.7298	blphenyl hydrolase-like (serine hydrolas
55	125969	R94247	Hs.88414	BTB and CNC homology 1, basic leucine zi
	125970	A1400964	Hs.177518	high density lipoprotein binding protein
	125976	AA495891	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv
	125985	H54857	Hs.35981	ESTs
	126018	H54866	Hs.167583	ESTs
60	126032	H59735	Hs.269065	ESTs, Highly similar to KIAA0349 (H.sapi
	126059	H66582	Hs.308488	ESTs
	126107	H79155	Hs.93361	ESTs
	126154	A1004105	Hs.190488	Homo sapiens, Similar to nuclear localiz
	126199	A1000492	Hs.125829	ESTs
	126207	W77936	Hs.83583	actin related protein 2/3 complex, subun
65	126227	N27236	Hs.269034	ESTs
	126269	AA830432	Hs.44701	ESTs
	126373	F11606	Hs.6079	B cell RAG associated protein
	126378	AA347842		gb:yy62a11.s1 Soares_multiple_sclerosis_
70	126383	AA885594	Hs.8298	KIAA1151 protein
	126403	N73388	Hs.125976	ESTs, Weakly similar to S71949 metallopr
	126525	AA884833	Hs.168432	ESTs
	126527	AA548559	Hs.103853	hypothetical protein FLJ20043
	126566	W67245	Hs.103142	ESTs
	126583	W92895	Hs.279746	vanilloid receptor-like protein 1
75	126610	AA460338	Hs.191391	ESTs
	126622	AA699443	Hs.193213	ESTs
	126633	AA206993	Hs.315367	Homo sapiens, Similar to hypothetical pr
	126727	AA037230	Hs.135084	cystatin C (amyloid angiopathy and cereb
	126762	AA064671		gb:czn13b04.s1 Stratagene pancreas (93720
80	126775	S86382	Hs.957	putative opioid receptor, neuromedin K (
	126783	AA126047		gb:zn09d10.s1 Stratagene hNT neuron (937
	126882	AA761143	Hs.250581	SWI/SNF related, matrix associated, acti
	126945	R51877	Hs.25845	ESTs
	126968	A1311457	Hs.99472	ESTs

5	127070	AA541812	Hs.190037	ESTs
	127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor
	127187	AA297138	Hs.207422	ESTs, Weakly similar to S71949 metallopro
	127215	AI246377	Hs.127675	ceroid-lipofuscinosis, neuronal 8 (epila
	127229	AA316181	Hs.61635	sbx transmembrane epithelial antigen of
10	127278	AA342715		gb:EST48309 Fetal spleen Homo sapiens cD
	127299	AA360710	Hs.158480	ESTs
	127325	AA393073	Hs.126099	ESTs
	127347	AA428350	Hs.58389	hypothetical protein MGC4090
	127401	AA921944	Hs.127639	ESTs
15	127420	AA699582	Hs.82171	Homo sapiens clone 19187 placenta expres
	127438	AI224421	Hs.77100	general transcription factor IIE, polype
	127441	AA835684	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH
	127449	AI421866	Hs.75722	ribophorin II
	127493	AA808081	Hs.291701	ESTs
20	127505	AA594244	Hs.292245	ESTs, Weakly similar to ALU1_HUMAN ALU S
	127620	AI025699	Hs.116200	ESTs
	127623	AA773234	Hs.271877	angiotensin-like 2
	127633	AI339609	Hs.268538	potassium voltage-gated channel, Isk-rel
	127701	AA935466		gb:z84c06.s1 Soares_pineal_gland_N3HPG
25	127713	AA688322	Hs.150683	ESTs
	127722	AA700444	Hs.189186	ESTs, Weakly similar to ALUD_HUMAN !!!!
	127733	AA704680	Hs.169005	ESTs
	127816	AA743646	Hs.120604	ESTs, Weakly similar to YAO2_HUMAN HYPOT
	127966	AI493406	Hs.292514	ESTs
30	127973	AI336794	Hs.129117	ESTs
	127989	AA909267	Hs.132413	ESTs
	127997	AI281549	Hs.311054	Homo sapiens mRNA full length insert cDN
	128016	N92597	Hs.82689	tumor rejection antigen (gp96) 1
	128037	AA888394	Hs.181129	ESTs, Weakly similar to S18968 cytoesit
35	128053	T65605	Hs.65377	ESTs, Moderately similar to KIAA1399 pro
	128066	AA884838	Hs.189171	ESTs
	128071	AA889398	Hs.189241	ESTs
	128091	AA904569	Hs.129329	ESTs
	128113	AI341423	Hs.288433	neurotrophin
40	128145	AI498467	Hs.166669	solute carrier family 4, sodium bicarbon
	128167	AA932961	Hs.85752	uncharacterized hematopoietic stem/proge
	128195	AI143866	Hs.127778	ESTs
	128265	T95851	Hs.17691	ESTs
	128283	AI076570	Hs.134053	ESTs
45	128309	AI457235	Hs.166479	ESTs
	128313	AI051250	Hs.167775	ESTs
	128346	AI088907	Hs.160189	ESTs
	128359	AI096526	Hs.270244	ESTs, Weakly similar to I38022 hypotheti
	128369	F12581	Hs.30445	Homo sapiens cDNA FLJ14687 fis, clone NT
50	128371	H12876	Hs.283078	hOAT4
	128421	T77876	Hs.268589	ESTs
	128453	X02761	Hs.287820	fibronectin 1
	128496	T83496	Hs.32944	inositol polyphosphate-4-phosphatase, ty
	128514	H84261	Hs.301693	Homo sapiens, clone IMAGE:3638994, mRNA,
55	128551	H09058	Hs.278398	KIAA1117 protein
	128583	AA316862	Hs.9605	cleavage and polyadenylation specific fa
	128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor
	128843	AA234141	Hs.275675	katanin p80 (WD40-containing) subunit B
	128988	AA411040	Hs.294140	ESTs
60	129016	W84524	Hs.184194	transmembrane 4 superfamily member 5
	129021	AA426406	Hs.173081	KIAA0530 protein
	129095	L12350	Hs.108823	thrombospondin 2
	129171	AA234048	Hs.7753	calumenin
	129188	M30257	Hs.109225	vascular cell adhesion molecule 1
65	129410	U25987	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	129467	AA410311	Hs.44208	hypothetical protein FLJ23153
	129518	AA369807	Hs.112238	ESTs
	129534	R73640	Hs.11260	hypothetical protein FLJ11264
	129632	L27213	Hs.1176	solute carrier family 4, anion exchanger
70	129691	X06700	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl
	129881	AA458952	Hs.181406	hypothetical protein FLJ22301
	129990	N30316		gb:yrw75b05.s1 Soares_placenta_8to9weeks_
	130049	V01515	Hs.1460	glucagon
	130171	AA454177	Hs.245257	ESTs, Weakly similar to A46010 X-linked
75	130411	AA505009	Hs.169910	KIAA0173 gene product
	130479	R44163	Hs.12457	hypothetical protein FLJ10814
	130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	130521	U82971	Hs.194351	coagulation factor II (thrombin) recepto
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA
80	130655	N92934	Hs.17409	cysteine-rich protein 1 (intestinal)
	130656	Z20481	Hs.330988	Homo sapiens, Similar to Bicucalinal D (Dro
	130889	D57622	Hs.20985	sin3-associated polypeptide, 30kD
	131064	AA598441	Hs.22583	DKFZP434K2235 protein
	131070	F13694	Hs.22607	ESTs
	131189	L16782	Hs.240	M-phase phosphoprotein 1
	131318	X51699	Hs.2558	bone gamma-carboxyglutamate (gla) protei
	131506	W47579	Hs.5801	KIAA1194 protein

5	131551	AA127867	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H
	131553	C20547	Hs.302810	Novel human gene mapping to chromosome 20
	131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro
	131879	AA017161	Hs.33782	ESTs
	132017	W67251	Hs.267659	vav 3 oncogene
10	132025	U58516	Hs.3745	milk fat globule-EGF factor 8 protein
	132095	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence
	132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi
	132164	U84573	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132180	AA405569	Hs.418	fibroblast activation protein, alpha
15	132223	R77451	Hs.4245	chromosome 11 hypothetical protein ORF3
	132238	AA453446	Hs.42673	ESTs
	132406	F09979	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
	132945	N40559	Hs.6129	ATP-binding cassette, sub-family B (MDR/
	133185	AA481404	Hs.6686	hypothetical protein DKFZp564O1664
20	133193	C14015	Hs.303075	EST
	133370	AA156897	Hs.72157	DKFZP564I1922 protein
	133406	U22172	Hs.179697	Human DNA damage repair and recombination
	133409	U65918	Hs.73078	deleted in azoospermia-like
	133591	T82292	Hs.75111	protease, serine, 11 (IGF binding)
25	133899	X00588	Hs.77432	epidermal growth factor receptor (avian
	134137	F10045	Hs.79347	KIAA0211 gene product
	134339	AA478971	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	134421	AA122386	Hs.82985	collagen, type V, alpha 2
	134462	U11037	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-
30	134515	C20737	Hs.84469	ESTs
	134527	T40835	Hs.322978	EST
	134711	X04011	Hs.86974	cytochrome b-245, beta polypeptide (chro
	134824	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor
	134854	J03464	Hs.179573	collagen, type I, alpha 2
35	134921	W60186	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f
	135003	H42527	Hs.26102	trichorhinophalangeal syndrome 1
	135210	W90522	Hs.93589	hypothetical protein DKFZp564B1162
	135348	AA442054	Hs.268177	phospholipase C, gamma 1 (formerly subty
	100547	HG2149-HT2219		gb:Homo sapiens mucin (mucin) mRNA, part
40	100572	HG2271-HT2367	Hs.73995	flaggrin
	100687	HG3115-HT3291		gb:Human Goli-mbp gene, exon 2.
	100695	HG315-HT315	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	101447	M21305		gb:Human alpha satellite and satellite 3
	102329	U35407	Hs.158084	peroxisome receptor 1
45	102892	X05232	Hs.83326	matrix metalloproteinase 3 (stromelysin
	103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial
	103206	X72755	Hs.77367	monokine induced by gamma interferon
	103260	X78416	Hs.3155	casein, alpha
	103751	AA082824		gb:zo08b08.s1 Stratagene neuroepithelium
50	104113	AA427510	Hs.181202	hypothetical protein FLJ10038
	104316	D61871	Hs.330821	EST
	104453	M19169	Hs.123114	cystatin SN
	104668	AA007312		gb:EST376458 MAGE resequences, MAGH Homo
	104916	AA056588	Hs.155489	NS1-associated protein 1
55	106151	AA424958	Hs.294132	ESTs
	106899	AA490107	Hs.21753	JM5 protein
	107379	U93868	Hs.333861	polymerase (RNA) III (DNA directed) (32k
	107412	W26105	Hs.287797	integrin, beta 1 (fibronectin receptor,
	107652	AA010195	Hs.52642	ESTs, Weakly similar to ALUF_HUMAN IIII
60	107754	AA017462	Hs.269244	ESTs
	107897	AA026240		gb:zo77e05.s1 NCL CGAP_AA1 Homo sapiens
	108238	AA059473	Hs.66783	EST
	108497	AA083070		gb:zm85e05.r1 Stratagene ovarian cancer
	108710	AA121960		gb:zm24g09.r1 Stratagene pancreas (93720
65	109012	AA155576	Hs.5947	mel transforming oncogene (derived from
	109043	AA159605	Hs.72580	ESTs
	109560	F01778	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H
	110572	H60523	Hs.37844	EST
	110687	H83005	Hs.177311	ESTs
70	111418	R01084	Hs.19081	ESTs
	111507	R07728	Hs.268668	ESTs
	111644	R16539	Hs.223649	EST, Moderately similar to Cd-7 Metallo
	111919	R39926	Hs.21031	ESTs, Weakly similar to I78885 serine/th
	112102	R44840	Hs.326475	ESTs
75	112229	R50938	Hs.24949	ESTs
	112309	R55021		gb:yf76d05.s1 Soares breast 2NbHbSt Homo
	112358	R59371	Hs.26653	ESTs
	112397	R60822	Hs.26805	ESTs, Weakly similar to putative p150 [
	112532	R69824	Hs.28313	ESTs
80	112858	T02963	Hs.4454	ESTs
	113170	T54342	Hs.270373	ESTs, Weakly similar to S65657 alpha-1C
	113321	T70580	Hs.13759	RAB3A interacting protein (rabln3)-like
	113404	T82323	Hs.70337	immunoglobulin superfamily, member 4
	113420	T83964	Hs.15400	ESTs, Weakly similar to S65824 reverse
	113613	T93337	Hs.17167	ESTs, Highly similar to LRR FLJ4 intera
	113663	T95909		gb:yo47g07.s1 Soares fetal liver spleen
	113790	W33178	Hs.26912	ESTs

113889	W72720		gbzd61c03.s1 Soares_fetal_heart_NbHH19W
114016	W90671	Hs.11087	ESTs
114251	Z39898	Hs.21948	ESTs
115187	AA261805	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,
115722	AA417297	Hs.59609	ESTs
115775	AA424030	Hs.46627	ESTs
116380	AA588455	Hs.66817	ESTs
116551	D20458	Hs.229071	EST
117009	H85422	Hs.108556	ESTs
117329	N23680	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone H
117623	N32626	Hs.145532	ESTs, Weakly similar to FV1 MOUSE FRIEND
118387	N64579		gb:yz51d11.s1 Morton Fetal Cochlea Homo
118456	N66580		gb:yy69f01.s1 Soares_multiple_sclerosis_
118741	N74042	Hs.50421	KJAA0203 gene product
118771	N74690	Hs.50547	ESTs
119075	R36451	Hs.287820	fibronectin 1
119217	R95778	Hs.237309	EST
119306	T26914	Hs.132785	EAP30 subunit of ELL complex
119347	T64349		gb:yc10d08.s1 Stratagene lung (937210) H
120006	W90108	Hs.10848	KJAA0187 gene product
120441	AA243588	Hs.190035	ESTs
120651	AA287286	Hs.99657	ESTs
120811	AA346854	Hs.52788	fragile X mental retardation, autosomal
121186	AA400156	Hs.339808	hypothetical protein FLJ10120
121599	AA416770	Hs.98255	EST
122146	AA435584	Hs.250173	hypothetical protein FLJ13158
122261	AA436830	Hs.98902	ESTs
122352	AA443725	Hs.159677	ESTs
122433	AA447417	Hs.285491	ESTs
122489	AA448342	Hs.178551	ribosomal protein L8
122554	AA451886	Hs.154654	cytochrome P450, subfamily I (dioxin-ind
122857	AA463879	Hs.99606	EST, Weakly similar to STK2_HUMAN SERIN
122889	AA465704	Hs.287687	Homo sapiens cDNA: FLJ21960 fis, clone H
123399	AA521274	Hs.105516	EST
123662	AA609385	Hs.112703	ESTs, Moderately similar to AF171102.1 r
123762	AA610013		gb:zf18d04.s1 Soares_testis_NHT Homo sap
123792	AA620333	Hs.112857	ESTs
123900	AA621223	Hs.112953	EST
123981	C20797	Hs.95481	ESTs
124126	H18517	Hs.164568	fibroblast growth factor 7 (keratinocyte
124404	N31998	Hs.164256	hypothetical protein FLJ20657
124557	N66025	Hs.141604	ESTs, Moderately similar to ALU1_HUMAN A
124703	R07294	Hs.300076	solute carrier family 22 (organic cation
124867	R68971	Hs.168500	ESTs
125092	T92544	Hs.137548	CD84 antigen (leukocyte antigen)
125111	T96240	Hs.178658	RAD23 (S. cerevisiae) homolog B
125331	AI422996	Hs.161378	ESTs
125349	T87826	Hs.164480	ESTs, Weakly similar to T50609 hypotheti
125426	R43983	Hs.184029	hypothetical protein DKFZp761A052
125436	R64472	Hs.16131	hypothetical protein FLJ12876
125465	AI375276	Hs.158732	ESTs
125515	R13353		gb:zf76c04.r1 Soares Infant brain 1NIB H
125626	AI038854	Hs.180789	S164 protein
125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ
125743	H17151		gb:ym37a05.r1 Soares Infant brain 1NIB H
125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass
125760	W03020	Hs.40300	calpain 3, (p94)
125804	R79519	Hs.16899	ESTs
125967	AI341206	Hs.173770	ESTs
126068	AI190171	Hs.144413	ESTs
126081	AI346024	Hs.227835	KJAA1049 protein
126150	AA018427	Hs.64816	chromosome 12 open reading frame 3
126171	AA704771	Hs.191942	ESTs
126198	AI469355	Hs.127310	ESTs
126224	AI097280	Hs.44493	Human DNA sequence from clone 462023 on
126289	AA194603	Hs.73451	ESTs, Weakly similar to S55024 nebulin,
126343	AA628890	Hs.158701	ESTs
126406	AA034096		gb:yy41h02.r1 Soares fetal liver spleen
126419	AA451775	Hs.129064	Homo sapiens chromosome 19, cosmid F2216
126479	T78141	Hs.12285	ESTs, Weakly similar to I55214 salivary
126500	AA885308	Hs.184376	synaptosomal-associated protein, 23kD
126520	AA292988	Hs.72071	hypothetical protein FLJ20038
126701	AA515212	Hs.339670	ESTs, Weakly similar to AF147790.1 trans
126718	AA322718	Hs.309435	ESTs, Weakly similar to KJAA0927 protein
126739	AI160709	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE
126745	AA057506		gb:zf49g04.r1 Soares retina N2b4HR Homo
126846	AA663527	Hs.116910	ESTs
126872	AA136653		gb:UH-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
126952	AA195575	Hs.85962	hyaluronan synthase 3
127036	AI688598	Hs.276916	nuclear receptor subfamily 1, group D, m
127039	AA233366	Hs.168103	prp28, US snRNP 100 kd protein
127067	F06732		gb:HSC1JA051 normalized infant brain cDN
127083	Z44079	Hs.91608	otoferlin

5	127116	AA278492	Hs.288304	Homo sapiens cDNA FLJ11529 fis, clone HE
	127282	AA347547	Hs.185780	ESTs
	127349	AA412108	Hs.269350	ESTs
	127352	AA416577	Hs.189105	ESTs, Weakly similar to NBR13 [Hs]sapiens
	127482	AI337294	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I
	127543	AI364367	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO
	127553	AA282433		gb:aa63g02.r1 NCI_CGAP_GC81 Homo sapiens
10	127556	AA679831	Hs.190228	ESTs
	127859	AA808837	Hs.291559	ESTs
	127993	AA847856	Hs.124565	ESTs
	128277	AI018275	Hs.269791	ESTs
	128285	AA634569	Hs.13351	LanC (bacterial lantibiotic synthetase c
	128317	AI051960	Hs.303754	ESTs
15	128334	AI080130	Hs.134207	ESTs
	128428	AI185718	Hs.143900	ESTs
	128582	U22963	Hs.101840	major histocompatibility complex, class
	128592	AA470056	Hs.113994	Homo sapiens cDNA FLJ20796 fis, clone CO
	128751	AA442274	Hs.183176	ESTs
20	129105	AA224351	Hs.108681	Homo sapiens brain tumor associated prot
	129161	N27334	Hs.181780	hypothetical protein FLJ20241
	129246	N99174	Hs.206063	ESTs
	129361	X64229	Hs.110713	DEK oncogene (DNA binding)
	129577	AA424952	Hs.82906	CDC20 (cell division cycle 20, S. cerevi
25	129600	N78980	Hs.271599	hypothetical protein MGC10500
	129989	AF005887	Hs.247433	activating transcription factor 6
	130024	U15197	Hs.113271	ABO blood group (transferase A, alpha 1-
	130292	U70136	Hs.218791	proteoglycan 4, (megakaryocyte stimulat
	130589	AA234308	Hs.16441	DKFZP434H204 protein
30	130736	T99385		gb:ow69g07.s1 Soares_fetal_liver_spleen_
	131238	R82327	Hs.24625	ESTs
	131378	AA463886	Hs.203910	small glutamine-rich tetrapeptide r
	131601	M31165	Hs.29352	tumor necrosis factor, alpha-induced pro
	131605	AA256220	Hs.29383	Homo sapiens mRNA; cDNA DKFZp434E2321 (f
35	131676	C20785	Hs.30514	ESTs
	131861	D11925	Hs.184245	KIAA0929 protein Mx2 interacting nuclea
	131873	H39997	Hs.166852	KIAA1683 protein
	132023	F01927	Hs.3743	matrix metalloproteinase 24 (membrane-in
	132273	AA489716	Hs.43658	DKFZP586L151 protein
40	132770	AA425647	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL
	132859	D20925	Hs.69235	transportin-SR
	133052	R40166	Hs.106826	KIAA1696 protein
	133373	S72487	Hs.73946	endothelial cell growth factor 1 (platelet
	133446	M25322	Hs.73800	selectin P (granule membrane protein 140
45	134693	N70361	Hs.8854	Human transcription unit PVT gene, exons
	134733	U03644	Hs.89421	CBF1 Interacting corepressor
	134965	J05480	Hs.272458	protein phosphatase 3 (formerly 2B), cat
	135327	AA477989	Hs.98800	ESTs
50	135377	C21382	Hs.99766	Homo sapiens mRNA; cDNA DKFZp564J0323 (f
	135398	AA194075	Hs.287270	rel proto-oncogene (multiple endocrine

TABLE 44B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
108497	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA055148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065061 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070580 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA059220 AA070940 AA075968 AA074563 AA084027 AA115929
107897	91776_1	AA604872 AA026240
130736	611414_1	AI168326 T99385
108710	133560_1	AA121959 AA121960
100943	45976_1	AW884944 L07517 AW889606
124575	1666649_1	N68168 N69188 N90450
125439	465590_1	AW835829 AA826305 R01759
117697	499877_1	N40976 AA902795
125515	181_2	R13353 R13890 H11359
118387	65081_5	N64579
126292	327512_1	AA491328 N42312
102798	34524_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
125378	244444_1	N58924 AA347842
125743	5025_5	H17151 H11956
126406	95703_1	N76683 AA034096 AA034082

127067	1534978_1	F06732 Z43705
119243	1774795_1	T12603 T12604
111443	31528_18	AF072503 AF208161 AA613238 H12439 N76991 D78692 BE019603 AA776439 R37932 T93615 AF072508 R00744 R01948 R68685
5		AI128496 AA865193 AI797629 H13302 AF072506 NM_014590 AF072505 R00743 T93661 T39519 R68740 H13097 N58614 N77302
		H01372 N41878 H04136 AA426511 AW971553 AW900030 R76136 T52094 AI598135 AA781423 R76086 R77278 AI393478 AA837267
		AI570707 R01901 R27412 N53177 AI379210 AI128526 AA250958 R79323 R27389 H01325 N55091 T69704 AA868777 T47345 R27591
		AA860368 AA729556 H04137 T87297 C17420 AA293243 AA419144
10	127278 240640_1	AA342715 AA367634
	103751 118557_1	AA131367 AA082824
	126636 80804_1	AA057531 AA001527
	127331 379388_1	F20186 AA622352
	127357 288073_1	AA424107 AA452788
	126745 104479_1	AA047854 AA057506 AA053841
15	126762 110350_1	AA064613 AA064671
	126783 113388_1	AA083531 AA126047 AA074915 AA148649
	112309 1576900_1	R55021 H26613
	126872 142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
20	120284 158963_1	BE011368 BE011362 BE011215 BE011365 BE011363
	111829 46636_1	AA179656 AA182626 AA182603
	104668 82752_1	AF074991 R36070
	127553 202308_2	AW964385 AA007312 AI081711 AA318253 AW891655 T99192
	120379 34624_3	AA505046 AW969109 AA505047
25		AL042725 BE063316 AW975810 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849
		AA216700 AI696002 AA101867 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757
		AW818104 AW392886 AA584918 AA099408 AW856396 AW861859 AA053045
30	127701 405284_1	AA679064 AA935466
	128410 288073_1	AA424107 AA452788
	114625 111686_1	AA081507 AA070071 AA070840 AA084362
	109026 150431_1	AA157811 AA836869
	108409 113869_1	AA075631 AA075578
	100687 tigr_HT3291	L18862
	109326 genbank_AA210719	AA210719
	123762 genbank_AA610013	AA610013
35	116548 genbank_D20433	D20433
	125145 entrez_W38001	W38001
	125153 entrez_W38294	W38294
	116995 genbank_H83928	H83928
	102649 genbank_U68133	U68133
40	118456 genbank_N66580	N66580
	102860 entrez_X00368	X00368
	120715 genbank_AA292700	AA292700
	120749 genbank_AA303235	AA303235
	113663 genbank_T95909	T95909
45	113889 genbank_W72720	W72720
	108258 genbank_AA063269	AA063269
	101046 entrez_K01160	K01160
	129990 genbank_N30316	N30316
	122746 genbank_AA458791	AA458791
50	124046 genbank_F10243	F10243
	108436 genbank_AA078801	AA078801
	124197 genbank_H52921	H52921
	101447 entrez_M21305	M21305
	108852 genbank_AA133131	AA133131
55	101697 entrez_M84358	M84358
	108931 genbank_AA147186	AA147186
	101909 entrez_S69265	S69265
	117816 genbank_N48872	N48872
	119154 genbank_R61293	R61293
60	119241 genbank_T12559	T12559
	119310 genbank_T40427	T40427
	119347 genbank_T64349	T64349
	119529 entrez_W38053	W38053
	112467 genbank_R65706	R65706
65	112533 genbank_R69886	R69886
	112588 genbank_R77302	R77302
	121082 genbank_AA398722	AA398722
	123305 genbank_AA496133	AA496133
	123328 genbank_AA496968	AA496968
70	100547 tigr_HT2219	M57417
	123490 genbank_AA599723	AA599723

75 TABLE 45A: 90 GENES DOWN-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 45A lists about 90 genes down-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

80 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title

	Pkey	ExAccn	UnigeneID	Unigene Title
5	100137	D13627	Hs.15071	chaperonin containing TCP1, subunit 8 (i
	100240	D31767	Hs.75416	DAZ associated protein 2
	100289	D45248	Hs.179774	proteasome (prosome, macropain) activato
	100558	HG2855-HT2995	Hs.75452	heat shock 70kD protein 2
	100763	HG3597-HT3800		gb:Human major histocompatibility comple
10	100779	HG3731-HT4001	Hs.302063	immunoglobulin heavy constant mu
	101091	L06132	Hs.149155	voltage-dependent anion channel 1
	101155	L13972	Hs.301698	sialyltransferase 4A (beta-galactosidase
	102223	U24658		gb:Homo sapiens immunoglobulin heavy cha
	102282	U31383	Hs.79126	guanine nucleotide binding protein 10
15	102378	U40369	Hs.28491	spermidine/spermine N1-acetyltransferase
	102386	U40998	Hs.81728	unc119 (C.elegans) homolog
	102389	U41371	Hs.75916	splicing factor 3b, subunit 2, 145kD
	102480	U50327	Hs.1432	protein kinase C substrate 80K-H
	102565	U59752	Hs.303091	pleckstrin homology, Sec7 and coiled/coi
20	102605	U64444	Hs.181369	ubiquitin fusion degradation 1-like
	102693	U73824	Hs.183684	eukaryotic translation initiation factor
	102710	U77827	Hs.113207	G protein-coupled receptor 30
	102920	X12451	Hs.78056	cathepsin L
	102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc
25	103166	X67951	Hs.180909	peroxiredoxin 1
	103283	X80199	Hs.83422	MLN51 protein
	103463	Y00281	Hs.2280	ribophorin I
	103835	AA172215	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT
	104796	AA029388	Hs.33026	hypothetical protein PP2447
30	105714	AA291429	Hs.12211	GDP-fucose transporter 1
	105927	AA402988	Hs.332040	hypothetical protein MGC13010
	105945	AA404512	Hs.14453	interferon consensus sequence binding pr
	106001	AA410986	Hs.8963	Homo sapiens mRNA full length insert cDN
	106027	AA412119	Hs.234799	breakpoint cluster region
35	106227	AA429262	Hs.19613	ESTs
	106295	AA435664	Hs.8583	similar to APOBEC1
	106417	AA448008	Hs.261828	G protein-coupled receptor kinase 7
	107391	W02877	Hs.284294	Breakpoint cluster region protein, uteri
	109107	AA169180	Hs.269280	ESTs
40	109685	F09325	Hs.28102	ESTs
	110021	H11252	Hs.31037	ESTs
	110738	H99370	Hs.139648	kinesin family member 1C
	112746	R93237	Hs.74170	metallothionein 1E (functional)
	113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (a
45	113822	W47350	Hs.17466	retinoic acid receptor responder (tazaro
	113859	W67225	Hs.13273	KIAA0592 protein
	113909	W78127	Hs.9956	hypothetical protein FLJ20259
	114693	AA122158	Hs.300683	Homo sapiens cDNA FLJ12825 fis, clone NT
	115399	AA283182	Hs.92023	core histone macroH2A2.2
50	116606	D80217	Hs.259842	protein kinase, AMP-activated, gamma 2 n
	116633	F02702	Hs.268726	ESTs, Highly similar to ZN91_HUMAN ZINC
	119254	T15937	Hs.279009	matrix Gla protein
	119493	W35364	Hs.50477	RAB27A, member RAS oncogene family
	120108	W95696	Hs.16803	LUC7 (S. cerevisiae)-like
55	120886	AA365566	Hs.301342	hypothetical protein MGC4342
	120953	AA397911	Hs.97499	ESTs, Weakly similar to unknown [H.sapi
	121303	AA402441	Hs.303197	B-cell CLL/lymphoma 7C
	121547	AA412448	Hs.104777	ESTs
	123495	AA599850	Hs.106747	serine carboxypeptidase 1 precursor prot
60	123608	AA609144	Hs.112651	ESTs
	123749	AA609949	Hs.112790	EST
	124763	R39610	Hs.76288	calpain 2, (mII) large subunit
	125368	H60192	Hs.76853	Homo sapiens mRNA; cDNA DKFZp434N1728 (f
	125657	AA481719	Hs.150540	Homo sapiens, clone IMAGE:3954961, mRNA,
65	125670	AI432621	Hs.82685	CD47 antigen (Rh-related antigen, integr
	125882	H45538	Hs.101448	metastasis associated 1
	126541	AA204913	Hs.7854	zinc-finger regulated transporter-like
	126715	R70160	Hs.241552	KIAA0268 protein
	126817	AA478642	Hs.291623	ESTs, Weakly similar to unnamed protein
70	127112	AI143906	Hs.125103	ESTs
	127273	AA335263	Hs.144950	ESTs
	127615	AA718919		gb:zv88a04.s1 Soares_NhHMPu_S1 Homo sapi
	127635	AA766903	Hs.116346	ESTs, Highly similar to A46297 beta-1,6-
	128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.s
75	129398	AA437374	Hs.234573	Homo sapiens mRNA for TL132
	129521	AA489459	Hs.301005	purine-rich element binding protein B
	131037	AA256171	Hs.22391	chromosome 20open reading frame 3
	131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131631	AA486868	Hs.29802	sliit (Drosophila) homolog 2
80	132079	H67964	Hs.38694	ESTs
	132455	T15774	Hs.4892	Homo sapiens clone 24841 mRNA sequence
	132582	AA318547	Hs.278712	eukaryotic translation initiation factor
	132610	AA443114	Hs.5326	amino acid system N transporter 2; porc
	132755	AA609201	Hs.182635	ESTs
	133192	AA393804	Hs.67052	vacuolar protein sorting 26 (yeast homol

133437	R57419	Hs.7370	phosphatidylinositol transfer protein, b
133449	AA094989	Hs.7381	voltage-dependent anion channel 3
133649	AA479139	Hs.75393	acid phosphatase 1, soluble
133814	M33882	Hs.76391	myxovirus (influenza) resistance 1, homo
134378	AF006088	Hs.82425	actin related protein 2/3 complex, subun
134419	L08044	Hs.82961	trefoil factor 3 (intestinal)
134548	U41515	Hs.333495	Deleted in split-hand/split-foot 1 regio
134776	J05582	Hs.89603	mucin 1, transmembrane
135032	AA243497	Hs.173685	hypothetical protein FLJ12619

TABLE 45B

15	Play:	Unique Eos probeset Identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
20	Play	CAT number	Accessions
	127615	380951_1	AA626215 AA718919
	100763	tigr_HT3800	X12432 Y08693
	102223	221_265	AF013616 AA300945 X65907 AF062264 AF062250 Z47228 Z75389 Z75374 AF062152 AF062146 Z75398 X64153 AF062101 AF062218 SS9161
25			Z75392 AF062196 AF062192 X65904 U24685 AF062181 Z47241 Z75376 AF062217 Z47234 X64152 AF062187 AF062173 AF062158 Z47229
			M74018 M74021 X54441 M84512 L29115 M84508 Z75384 AJ244983 AJ245240 AJ245030 AJ245042 M26998 L03635 S64473 AJ244997 AJ245013
			AJ279535 U89768 AF174049 AF174085 AF174086 U97246 AJ245011 AJ245017 AJ245028 AJ245041 AJ245051 AJ245065 AJ245236 U22391
			Z49143 Z74655 AF087428 S66098 Z70650 AJ244929 AF006528 AF022004 AF021983 U00556 AJ245035 Z70617 Z70605 AJ245052 AJ245046
			AF087424 AF174054 S67110 U21257 U21267 U21268 Z35492 U71103 AF021991 L23518 Z70644 AJ245036 Z49141 AF089001 Z74695 Z46304
			AF021957 AF021990 AF022005 AF052527 AF021947 Z70604 Z70610 AF062104 Z49135 X64235 Z46341 Z46305 Z46307 Z49136 AJ244996
30			Z46342 AJ244931 AJ244935 AJ244937 AJ244938 L12192 AJ244939 AJ244940 AJ244941 Z46308 AJ244962 AF062234 AJ244973 AJ244984
			AJ244985 AF174088 AJ279519 AJ279521 AJ279526 AJ245009 AJ279531 AJ245008 AJ244994 AJ244991 AJ244990 AJ244988 AJ244987 X87440
			AJ245238 Z70625 Z70626 Z70641 Z70640 Z70643 AJ244975 Z70616 Z70637 AJ244982 AJ244967 AJ239377 AJ245057 AF021948 AF107239
			AJ245040 L34163 AF062231 Z70627 AF062113 AF006527 AF174041 AJ279537 Z70642 U00497 Z70639 AJ245054 AJ244960 AJ279524 AJ244943
			AJ249631 AF035041 AJ245039 AJ245050 AF107233 AJ239362 AJ244969 Z46278 Z46290 Z46274 Z46281 AJ239351 L25293 AJ244944 AJ244951
35			Z46280 Z46270 AJ245043 Z46276 AF107241 Z46271 Z46277 AJ245034 Z46273 AJ244992 Z46282 Z70638 Z46275 AJ244972 Z46272 Z46279
			Z46269 AF087422 M74469 X64159 AF103243 X64156 AJ244942 Z46316 AJ222547 Z46322 Z46324 Z46326 Z46327 AJ222556 Z46329 Z46330
			Z46302 AJ222561 AJ222549 AJ222568 AJ222570 AJ222571 Z49139 AJ222578 AJ222562 AJ222577 Z46323 AJ222576 AJ222566 Z46315
			AJ222557 AJ222564 AJ222559 AJ222573 AJ222575 Z46318 AJ222548 Z46319 AJ222552 AJ222550 AJ222567 AJ222558 AJ222563 Z46317
40			X87438 AJ222555 AJ240581 AF103161 AJ240580 AJ240594 Y17929 AJ240553 AJ240573 AJ240558 AJ240555 Y17927 Y17949 AJ240561 Y17948
			Y17933 Y17947 Y17944 Y17928 Y17931 Y17934 AJ240595 Y17943 Y17932 Y17930 AJ240590 AJ240560 Y17945 AJ240556 S79918 AF103278
			AW364256 AF103299 AF103122 X75022 AF004937 Z30557 Z30677 Z30573 Z30576 Z30561 Z30674 Z30562 Z30675 AW403129 AJ203192
			AW404253 AW237246 A1654630 H61354

Table 46A lists about 714 genes upregulated in esophageal cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix HuO3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 47A lists about 113 genes upregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix HuO3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 48A lists about 162 genes downregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix HuO3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

TABLE 46A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of esophageal tumor AIs divided by the 70th percentile of normal tissue AIs, where the 15th percentile of the normal tissue AIs was subtracted from both the numerator and denominator.

70	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	31.57
	411243	AB039886	Hs.69319	CA11	26.06
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	25.65
	401781			Target Exon	23.23
75	424098	AF077374	Hs.139322	small proline-rich protein 3	21.35
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	20.37
	417368	BE185289	Hs.1076	small proline-rich protein 18 (cornilin)	20.33
	401780			NM_005557*:Homo sapiens keratin 16 (foca	18.94
	421948	L42583	Hs.334309	keratin 6A	18.13
80	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	18.01
	429538	BE182592	Hs.11261	small proline-rich protein 2A	17.31
	400668			NM_002425:Homo sapiens matrix metallopro	17.28
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	16.96

	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	16.35
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	16.22
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	15.64
5	421582	AI910275		trefoil factor 1 (breast cancer, estroge	14.86
	425679	X05997	Hs.159177	lipase, gastric	14.53
	421773	W69233	Hs.112457	ESTs	14.26
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	14.26
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	13.93
10	444325	AW152618	Hs.16757	ESTs	13.24
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFp564B2062 (f	13.19
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	11.98
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.99
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	10.77
15	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	10.31
	446292	AF081497	Hs.275682	Rh type C glycoprotein	9.69
	421978	AJ243662	Hs.110196	NICE-1 protein	9.68
	448811	AI590371	Hs.199460	ESTs	9.38
	453331	AJ240665		ESTs	9.37
20	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	9.28
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.18
	406687	M31126		matrix metalloproteinase 11 (stromelysin	9.13
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	9.04
	450701	H39960	Hs.288467	hypothetical protein XP_098151	8.77
25	418685	Z36830	Hs.87268	annexin A8	8.76
	421110	AJ250717	Hs.1355	cathepsin E	8.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.42
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.38
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	8.18
30	427666	AJ791495	Hs.180142	calmodulin-like skin protein (CLSP)	8.11
	450375	AA009647		a disintegrin and metalloproteinase doma	8.03
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	7.97
	445891	AW391342	Hs.199460	DPCR1 protein	7.95
	437053	AJ077018	Hs.3235	keratin 4	7.93
35	423271	W47225	Hs.126256	Interleukin 1, beta	7.80
	409757	NM_001898	Hs.123114	cystatin SN	7.74
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	7.64
	452638	U65011	Hs.30743	preferentially expressed antigen in mela	7.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	7.55
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.26
	448045	AJ297436	Hs.20166	prostate stem cell antigen	7.14
	408243	Y00787	Hs.624	interleukin 6	7.13
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	7.08
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	7.04
45	407366	AF026942	Hs.17518	gb:Homo sapiens c1g33 mRNA, partial sequ	7.04
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.98
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	6.89
	414774	X02419	Hs.77274	plasminogen activator, urokinase	6.85
	439926	AW014875	Hs.137007	ESTs	6.84
50	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.82
	429259	AA420450	Hs.292911	Plakophilin	6.77
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	6.71
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	6.67
55	429228	AI553633	Hs.326447	ESTs	6.61
	426312	AF026939	Hs.181874	Interferon-induced protein with tetratri	6.60
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.58
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.55
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	6.54
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.53
60	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.51
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.49
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.48
	428471	X57348	Hs.184510	stratfin	6.46
	422511	AI076442	Hs.117938	collagen, type XVII, alpha 1	6.45
65	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.44
	401747			Homo sapiens keratin 17 (KRT17)	6.42
	421508	NM_004833	Hs.105115	absent in melanoma 2	6.42
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	6.42
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.41
70	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11348 fis, clone PL	6.38
	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	6.38
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	6.36
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	6.35
	407811	AW150902	Hs.40098	cysteine knot superfamily 1, BMP antagon	6.33
75	425415	M13903	Hs.157091	involucrin	6.32
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	415989	AI267700		ESTs	6.23
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.21
	449228	AJ403107	Hs.148590	protein related with psoriasis	6.21
80	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	6.18
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	6.06
	418663	AK001100	Hs.41690	desmocollin 3	6.04
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	5.96

5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.93
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	5.92
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.92
	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	5.84
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.76
	400665			NM_002425:Homo sapiens matrix metallopro	5.75
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.72
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	5.72
10	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.71
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	5.70
	439606	W79123	Hs.58561	G protein-coupled receptor 87	5.70
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	5.68
	433447	U29195	Hs.3281	neuronal pentraxin II	5.67
15	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.64
	408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	5.62
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	5.60
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.53
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.50
20	416250	AA581386	Hs.73452	hypothetical protein MGC10791	5.48
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	5.47
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	5.44
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	5.42
25	402994			NM_002463:Homo sapiens myxovirus (infl	5.40
	447333	BE090580	Hs.70704	hypothetical protein dJ616B8.3	5.40
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	5.36
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	5.33
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	5.32
30	449722	BE280074	Hs.23960	cyclin B1	5.31
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.30
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	5.29
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	5.29
	417720	AA205625	Hs.208067	ESTs	5.29
35	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	5.28
	419216	AU078718	Hs.164021	small inducible cytokine subfamily B (Cy	5.27
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	5.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	5.25
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	5.24
40	402075			ENSP00000251056:Plasma membrane calcium	5.24
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	5.24
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	5.22
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.22
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domain	5.21
45	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	5.20
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	5.20
	406663	U24683	Hs.293441	immunoglobulin heavy constant mu	5.19
	409178	BE393948	Hs.50915	kallikrein 5	5.15
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.14
50	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	5.10
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	5.09
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.09
	412471	M83193	Hs.73946	endothelial cell growth factor 1 (platelet	5.08
	411274	NM_002776	Hs.69423	kallikrein 10	5.07
55	407756	AA116021	Hs.38260	ubiquitin specific protease 18	5.03
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	5.03
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	5.02
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	5.02
	416530	U82801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.02
60	429058	AF138863	Hs.35254	hypothetical protein FLB6421	5.00
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	5.00
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.97
	405770			NM_002362:Homo sapiens melanoma antigen,	4.96
	444783	AK001468	Hs.62180	anillin (Drosophila Scrapie homolog), act	4.94
65	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.94
	426866	U02330	Hs.172818	neuregulin 1	4.93
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	4.92
	455601	AI368880	Hs.816	SRY (sex determining region Y)-box 2	4.91
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.90
70	427786	BE407863	Hs.256871	ESTs	4.87
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalinin	4.86
	444371	BE540274	Hs.239	forkhead box M1	4.86
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	4.85
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.84
75	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	4.83
	409402	AF208234	Hs.695	cystatin B (stealin B)	4.81
	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.79
	401994			Target Exon	4.77
80	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.74
	421574	AJ000152	Hs.105924	defensin, beta 2	4.69
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.69
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.68
	439453	BE264974	Hs.65666	thyroid hormone receptor interactor 13	4.68
	407944	R34008	Hs.239727	desmocollin 2	4.67

	411296	BE207307	Hs.10114	growth suppressor 1	4.65
	433364	AI075407	Hs.296083	ESTs, Moderately similar to 154374 gene	4.65
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothetical	4.61
5	421335	X99977	Hs.103505	ARS component B	4.60
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.59
	453779	N35187	Hs.43388	28kD interferon responsive protein	4.59
	423575	C18863	Hs.163443	periostin (OSF-2os)	4.59
	417308	H60720	Hs.81892	KIAA0101 gene product	4.58
10	428651	AF196478	Hs.188401	annexin A10	4.58
	424354	NM_014314	Hs.145612	RNA helicase	4.58
	404996			Target Exon	4.56
	404240			NM_018950:Homo sapiens major histocompat	4.56
	453095	AW295660	Hs.252756	ESTs	4.55
15	410407	X66839	Hs.63287	carbonic anhydrase IX	4.55
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	4.55
	450685	L15533	Hs.423	pancreatitis-associated protein	4.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog	4.53
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.52
20	408380	AF123050	Hs.44532	diubiquitin	4.47
	443859	NM_013409	Hs.9914	folistatin	4.46
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	4.44
	412140	AA219691	Hs.73625	RAB6 interacting, kinase-like (rabkines	4.44
	421777	BE562088	Hs.108196	HSPC037 protein	4.44
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.43
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	4.42
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	4.42
	400419	AF084545		Target	4.42
	452571	W31518	Hs.34665	ESTs	4.41
30	430044	AA464510	Hs.152812	ESTs	4.41
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	4.39
	448111	AA053486	Hs.20315	Interferon-induced protein with tetrat	4.39
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.39
	453884	AA355925	Hs.36232	KIAA0186 gene product	4.38
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	4.37
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	4.37
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor	4.37
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	4.36
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	4.36
40	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.34
	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.34
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.34
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	4.32
	402447			C1000201:gi 204416 gb AAA02627.1 (L0519	4.31
45	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	4.28
	432731	R31178	Hs.287820	fibronectin 1	4.27
	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	4.27
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osao	4.25
	425580	L11144	Hs.1907	galanin	4.25
50	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	4.23
	409433	AA074382	Hs.135255	ESTs	4.23
	430630	AW269920	Hs.2621	cystatin A (stefin A)	4.22
	447343	AA266641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	4.21
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4.20
55	432375	BE536069	Hs.2962	S100 calcium-binding protein P	4.20
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.19
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.19
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.18
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	4.17
60	410286	AJ739159	Hs.61898	DKFZP586N2124 protein	4.16
	448844	AJ581519	Hs.177164	ESTs	4.16
	432680	T47364	Hs.278613	Interferon, alpha-inducible protein 27	4.16
	417599	AA204688	Hs.62954	ESTs	4.16
	402992			Target Exon	4.15
65	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	4.14
	422100	AI098988	Hs.111554	ADP-ribosylation factor-like 7	4.13
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.12
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.11
	407137	T97307		gb:53h05.s1 Soares fetal liver spleen	4.10
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	4.10
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.10
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	4.09
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.08
75	418589	AI360883	Hs.274448	hypothetical protein FLJ11029	4.06
	417678	X06560	Hs.82396	2',5'-oligoadenylate synthetase 1 (40-46	4.06
	451541	BE279383	Hs.28557	plakophilin 3	4.06
	433848	AF095719	Hs.93764	carboxypeptidase A4	4.06
	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	4.04
80	429599	AA806106	Hs.123684	ESTs	4.03
	450823	T81223	Hs.22011	complement-C1q tumor necrosis factor-rel	4.02
	423787	AJ295745	Hs.236204	nuclear pore complex protein	4.00
	431250	BE284649	Hs.251377	taxol resistance associated gene 3	4.00
	416091	AF295370	Hs.283082	defensin, beta 3	3.97

	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.97
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.97
	402408			NM_030920: Homo sapiens hypothetical pro	3.97
5	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.95
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	3.95
	452888	AW955454	Hs.30942	ephrin-B2	3.95
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.95
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.94
10	419693	AA133749	Hs.301350	FXRD domain-containing ion transport reg	3.94
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.94
	422094	AF129535	Hs.272027	F-box only protein 5	3.94
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	3.93
	404286			C6001909:gi704441 dbj BAA18909.1 (D298	3.93
15	423961	D13666	Hs.136348	periostin (OSF-2os)	3.92
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	3.91
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	3.91
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	3.91
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (I	3.91
20	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.90
	441553	AA281219	Hs.121296	ESTs	3.90
	428093	AW594506	Hs.104830	ESTs	3.90
	441020	W79283	Hs.35962	ESTs	3.89
	447078	AW885727	Hs.9914	ESTs	3.89
25	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	3.89
	417621	AV654694	Hs.82316	Interferon-induced, hepatitis C-associat	3.87
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.87
	426059	BE292842	Hs.166120	interferon regulatory factor 7	3.86
	419833	AA251131	Hs.220697	ESTs	3.85
30	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	3.85
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.83
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.83
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	3.83
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	3.83
35	442599	AF078037	Hs.324051	RelA-associated inhibitor	3.82
	405387			NM_022170: Homo sapiens Williams-Beuren	3.82
	449539	W80363	Hs.58446	ESTs	3.82
	419079	AW014836	Hs.18844	ESTs	3.81
	410434	AF051152	Hs.63668	toll-like receptor 2	3.81
40	408660	AA525775		ESTs, Moderately similar to PC4259 ferr	3.80
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.80
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.80
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.79
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (I	3.79
45	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.78
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.78
	414561	AI064813	Hs.195155	Homo sapiens amino acid transport system	3.78
	411789	AF245505	Hs.72157	Adican	3.77
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.77
50	449378	AW664026	Hs.59892	ESTs	3.76
	449961	AW265634	Hs.133100	ESTs	3.76
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.75
	407242	M18728		gb:Human nonspecific crossreacting antig	3.75
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.75
55	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.75
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	3.74
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	3.74
	441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	3.74
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	3.73
60	422648	D86983	Hs.118893	Melanoma associated gene	3.72
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	3.71
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	3.71
	428728	NM_016825	Hs.191381	hypothetical protein	3.71
	400245			Eos Control	3.71
65	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.70
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.70
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.70
	440659	AF134160	Hs.7327	claudin 1	3.69
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.67
70	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.66
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	3.65
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.63
	414883	AA926960		CDC28 protein kinase 1	3.63
75	428398	AI249368	Hs.98558	ESTs	3.63
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	3.63
	408482	NM_000676	Hs.45743	adenosine A2b receptor	3.63
	404287			C6001909:gi704441 dbj BAA18909.1 (D298	3.63
80	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.61
	414110	BE251752		gb:601112444F1 NIH_MGC_16 Homo sapiens c	3.61
	427857	AL133017	Hs.2210	hypothetical protein FLJ22865	3.61
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	3.61
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.60
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	3.60

	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.60
	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, com	3.60
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.59
5	437340	AL353935	Hs.135917	hypothetical protein DKFZp761D1823	3.59
	435793	AB037734	Hs.4993	KIAA1313 protein	3.59
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	3.59
	420247	AA256930	Hs.44680	hypothetical protein FLJ20979	3.58
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	3.57
	422282	AF019225	Hs.114309	apolipoprotein L	3.57
10	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.57
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.57
	408015	AW136771	Hs.244349	epidermal differentiation complex protel	3.56
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	3.56
	449039	A1962602	Hs.74284	hypothetical protein MGC2714	3.56
15	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.55
	400297	AJ127076	Hs.306201	hypothetical protein DKFZp564O1278	3.55
	428977	AK001404	Hs.194698	cyclin B2	3.55
	402995			NM_002463*:Homo sapiens myxovirus (infu	3.55
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.54
20	432917	NM_014125	Hs.241517	PRO0327 protein	3.54
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	3.53
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	3.52
	438113	AJ467908	Hs.8882	ESTs	3.52
25	414420	AA043424	Hs.76095	immediate early response 3	3.51
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.50
	447208	BE315291	Hs.237971	hypothetical protein MGC5627	3.50
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.49
	442295	A1827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.49
30	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	3.49
	429249	X81479	Hs.2375	egl-like module containing, mucin-like,	3.48
	413900	AW409747	Hs.75512	stress-induced-phosphoprotein 1 (Hsp70/H	3.48
	424242	AA337476	Hs.347408	hypothetical protein MGC13102	3.48
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.47
35	446480	NM_014578	Hs.15114	ras homolog gene family, member	3.46
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.46
	426865	BE544095	Hs.164960	BarH-like homeobox 1	3.46
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.46
	450506	NM_004460		fibroblast activation protein, alpha	3.46
40	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.45
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.45
	405545			Target Exon	3.45
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.44
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.44
45	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.44
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	3.44
	431228	AB005746	Hs.198282	phospholipid scramblase 1	3.44
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.43
	440502	A1824113	Hs.78281	regulator of G-protein signalling 12	3.43
50	448741	BE614567	Hs.19574	hypothetical protein MGC5469	3.43
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.43
	406646	M33600	Hs.308026	major histocompatibility complex, class	3.42
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.42
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.42
55	430890	X54232	Hs.2699	glypican 1	3.41
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.41
	412429	AV650262	Hs.75765	GRO2 oncogene	3.41
	443211	AJ128388	Hs.143655	ESTs	3.41
	422209	AF005210	Hs.113222	chemokine (C-C motif) receptor 8	3.40
60	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	3.39
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	3.39
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.39
	422101	AW404176	Hs.111611	ribosomal protein L27	3.39
	457670	AF119666	Hs.23449	Insulin receptor tyrosine kinase substra	3.38
65	437033	AW248364	Hs.5409	RNA polymerase I subunit	3.37
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.37
	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.37
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	3.36
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.36
70	436748	BE159107	Hs.159263	collagen, type VI, alpha 2	3.36
	401797			Target Exon	3.36
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.35
	421563	NM_006433	Hs.105806	granulysin	3.35
	402294			Target Exon	3.34
75	414024	AA134712	Hs.22410	gbzm79g08.r1 Stratagene neuroepithelium	3.34
	401961			NM_021626:Homo sapiens serine carboxypep	3.33
	418462	BE001596	Hs.85266	Integrin, beta 4	3.33
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.33
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.33
80	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.33
	404440			NM_021048:Homo sapiens melanoma antigen,	3.33
	432398	AA307808	Hs.2979	trefol factor 2 (spasmolytic protein 1)	3.33
	421677	H64092	Hs.38282	ESTs	3.33
	407792	AJ077715	Hs.39384	putative secreted ligand homologous to f	3.32

5	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.32
	417197	AW994561	Hs.151777	eukaryotic translation initiation factor	3.32
	429569	BE185499	Hs.2471	KIAA0020 gene product	3.32
	409636	AA305729	Hs.18272	amino acid transporter system A1	3.32
	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.32
10	405386			Target Exon	3.32
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.31
	448275	BE514434	Hs.20830	kinesin-like 2	3.31
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.31
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.31
15	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.31
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	3.31
	404171			NM_000636: Homo sapiens superoxide dismu	3.31
	418464	R87580	Hs.144531	gb:ym89h07.r1 Soares adult brain N2b4HB5	3.31
	425568	AW162943	Hs.250618	UL16 binding protein 2	3.31
20	410226	AI831858	Hs.61053	hypothetical protein	3.30
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.30
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.30
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	3.30
	428336	AA503115	Hs.183752	microseminoprotein, beta-	3.29
25	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.29
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.28
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.28
	405778			NM_005361: Homo sapiens melanoma antigen,	3.28
	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmn 3	3.27
30	421150	AI913562	Hs.189902	ESTs	3.27
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	3.27
	455813	BE141577		gb:QV2-HT0083-071299-018-a11 HT0083 Homo	3.27
	426084	BE387014	Hs.166145	Homer, neuronal immediate early gene, 3	3.27
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.27
35	458791	BE615453	Hs.346509	dedicator of cyto-kinesis 1	3.27
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	3.26
	429002	AW248439	Hs.2340	junction plakoglobin	3.26
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	3.25
	407777	AA161071	Hs.71465	squalene epoxidase	3.25
40	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.25
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	3.24
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	3.24
	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	3.24
	447519	U46258	Hs.339665	ESTs	3.24
45	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.24
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.24
	423198	M81933	Hs.1634	cell division cycle 25A	3.23
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.23
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.22
50	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.22
	406901	AK001330	Hs.48855	hypothetical protein FLJ10458	3.22
	425849	AJ000512	Hs.298323	serum/glucocorticoid regulated kinase	3.22
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.22
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.21
55	409197	N54708	Hs.303025	chromosome 11 open reading frame 24	3.21
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	3.21
	413436	AF238083	Hs.68061	sphingosine kinase 1	3.21
	408638	BE294925	Hs.46680	CGI-12 protein	3.21
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.21
60	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.21
	411573	AB029000	Hs.70823	KIAA1077 protein	3.20
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.19
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	3.19
	435014	BE560896	Hs.10026	mitochondrial ribosomal protein L17	3.18
65	401176			Target Exon	3.18
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.17
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.16
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.16
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	3.16
70	452012	AA307703	Hs.279766	kinesin family member 4A	3.16
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.15
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	3.15
	433020	AI375726	Hs.279918	hypothetical protein	3.14
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTERa2D1 teratoca	3.14
75	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.14
	420005	AW271108	Hs.133294	ESTs	3.14
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.13
	412270	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.13
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	3.13
80	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.12
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.11
	431722	AF161528	Hs.268049	hypothetical protein	3.11
	427239	BE270447	Hs.174070	ubiquitin carrier protein	3.11
	413385	M34455	Hs.840	indoleamine-pyrrrole 2,3 dioxygenase	3.10
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.10
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	3.10
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfam	3.10

	439755	AW748482	Hs.77873	B7 homolog 3	3.10
	404170			NM_000636: Homo sapiens superoxide dismutase 1	3.09
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	3.09
5	410006	AW732308	Hs.57783	eukaryotic translation initiation factor 4E	3.09
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.08
	421155	H87879	Hs.102267	lysyl oxidase	3.08
	441224	AU076964	Hs.7753	calumenin	3.08
	424326	NM_014479	Hs.145296	disintegrin protease	3.08
10	429413	NM_014058	Hs.201877	DESC1 protein	3.08
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	3.08
	446510	H58306	Hs.15165	retinoic acid induced 14	3.08
	442620	CO0138	Hs.8535	Homo sapiens mRNA for KIAA1668 protein,	3.07
	409637	AA323948	Hs.55407	Homo sapiens mRNA: cDNA DKFZp434K0621 (f	3.07
15	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polypeptide	3.07
	448853	NM_012204	Hs.22302	general transcription factor III C, polypeptide	3.07
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.07
	408915	NM_016651	Hs.48950	hepatic carcinoma novel gene-3 protein	3.06
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	3.06
20	412577	Z22968	Hs.74076	CD163 antigen	3.06
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.06
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kinase)	3.05
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	3.05
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	3.04
25	451578	NM_016323	Hs.26563	cytochrome E binding protein 1	3.04
	444726	NM_006147	Hs.84981	interferon regulatory factor 6	3.04
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast), human	3.04
	437741	BE591610	Hs.5809	putative transmembrane protein; homolog	3.04
	442643	U82756	Hs.3991	PRP4/STK/WD splicing factor	3.04
30	429358	AB037825	Hs.200317	KIAA1404 protein	3.03
	410068	AI633888	Hs.58435	FYN-binding protein (FYN-120/130)	3.03
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotate	3.03
	409154	U72882	Hs.50842	interferon-induced protein 35	3.02
	442173	N76101	Hs.8127	KIAA0144 gene product	3.02
35	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	3.01
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma autoantigen	3.01
	407634	AW016569	Hs.136414	UDP-GlcNAc:beta-Gal beta-1,3-N-acetylglucosaminyl	3.01
	411387	AW842339	Hs.130815	hypothetical protein FLJ21670	3.01
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific factor	3.01
40	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolog	3.00
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.00
	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	3.00
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.00
	448569	BE382657	Hs.21486	signal transducer and activator of transcription	3.00
45	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.00
	400200			NM_002788: Homo sapiens proteasome (pro	3.00
	403330			Target Exon	2.99
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.99
	403416	AI744626		KIAA0564 protein	2.97
50	403438			NM_031419: Homo sapiens molecule possess	2.96
	447942	F12628	Hs.155470	hypothetical protein MGC16040	2.96
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.95
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	2.94
	440088	NM_005402	Hs.288757	viral simian leukemia viral oncogene homolog	2.94
55	429547	AW009166	Hs.99376	ESTs	2.93
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	2.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit)	2.89
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.89
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.86
60	441633	AW858544	Hs.112242	normal mucosa of esophagus specific 1	2.85
	423425	AA375756	Hs.14449	KIAA1609 protein	2.85
	412851	AI826502	Hs.106149	ESTs	2.85
	400664			NM_002425: Homo sapiens matrix metallopro	2.85
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	2.85
65	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.85
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.84
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.83
	423767	H18283	Hs.132753	F-box only protein 2	2.82
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	2.82
70	441801	AW242799	Hs.86368	ESTs	2.80
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	2.80
	416539	Y07909	Hs.79368	epithelial membrane protein 1	2.79
	428959	AF100779	Hs.194680	WNT1 Inducible signaling pathway protein	2.79
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.75
75	417849	AW291587	Hs.82733	nldogen 2	2.74
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.73
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.72
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.71
	424874	AA347951	Hs.326413	Homo sapiens cDNA FLJ20812 fis, clone AD	2.71
80	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.71
	447854	AW138454	Hs.11594	ESTs	2.71
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.70
	412636	NM_004415		desmoplakin (DPI, DPII)	2.69
	420576	AA297634	Hs.54925	KIAA1858 protein	2.68

	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.68
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.68
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.66
	428598	AA852773	Hs.334838	KIAA1856 protein	2.64
5	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	2.64
	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	2.64
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.63
	406137			NM_000179::Homo sapiens mulS (E. coli) h	2.63
10	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.62
	443054	AJ745185	Hs.8939	yes-associated protein 65 kDa	2.59
	452620	AA436504	Hs.119286	ESTs	2.59
	420552	AK000492	Hs.88806	hypothetical protein	2.59
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.56
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.56
15	448454	NM_005879	Hs.21254	TRAF interacting protein	2.55
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	2.55
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.54
	440576	NM_004987	Hs.112378	LJM and senescent cell antigen-like doma	2.54
20	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.54
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.53
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	2.53
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	2.51
	411908	L27943	Hs.72924	cytidine deaminase	2.49
25	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.48
	430024	AJ808780	Hs.227730	integrin, alpha 6	2.47
	458079	AJ796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.46
	425345	AJ077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.45
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	2.45
30	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	2.45
	457819	AA057484	Hs.35408	ESTs, Highly similar to unnamed protein	2.44
	408298	AL117452	Hs.44155	DKFZP586G1517 protein	2.42
	413048	M93221	Hs.75182	mannose receptor, C type 1	2.40
	403851			CS002154::gi7299015[gb]AAF54217.1[AE0	2.39
35	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	2.37
	423903	M57765	Hs.1721	interleukin 11	2.37
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.36
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.32
	426827	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase	2.31
40	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	2.31
	406974	M57293		gb:Human parathyroid hormone-related pep	2.31
	401924			ENSP00000246632::CDNA FLJ20261 fis, clon	2.30
	444190	AJ878918	Hs.10526	cysteine and glycine-rich protein 2	2.29
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.29
45	436608	AA628980		down syndrome critical region protein DS	2.28
	427509	M82505	Hs.2161	complement component 5 receptor 1 (C5a I	2.27
	434398	AA121098	Hs.3838	serum-inducible kinase	2.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	2.28
	418030	BE207573	Hs.83321	neuromedin B	2.25
50	404927			Target Exon	2.25
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.24
	409038	T97480	Hs.50002	small inducible cytokine subfamily A (Cy	2.23
	411388	X72925	Hs.69752	desmocollin 1	2.21
	445757	AW449065	Hs.13264	KIAA0856 protein	2.18
55	405069			NM_006212::Homo sapiens 6-phosphofructo-	2.17
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.16
	443168	AJ038653	Hs.60500	ESTs	2.15
	444301	AK000136	Hs.10760	asporin (LRR class 1)	2.13
	433345	AJ681545	Hs.152982	hypothetical protein FLJ13117	2.11
60	426471	M22440	Hs.170009	transforming growth factor, alpha	2.10
	445019	AJ205540	Hs.281295	ESTs	2.08
	402021			NM_031891::Homo sapiens cadherin 20, type	2.07
	431866	NM_012098	Hs.8025	angiotensin-like 2	2.05
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.04
65	409571	AA504249	Hs.187685	ESTs	2.03
	450831	R37974	Hs.25255	ESTs	1.99
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.99
	445960	AJ268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN LINE-	1.98
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.97
70	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	1.91
	426850	BE247670	Hs.172766	MAP/microtubule affinity-regulating kina	1.90
	427335	AA448542	Hs.251677	G antigen 7B	1.90
	450649	NM_001429	Hs.25272	E1A binding protein p300	1.88
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.88
75	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.88
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	1.86
	433228	AW503733	Hs.9414	KIAA1488 protein	1.86
	413129	AF292100	Hs.104613	RP42 homolog	1.85
	432608	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.85
80	446620	AA128808	Hs.179902	transporter-like protein	1.81
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	1.79
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.78
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	1.77
	423482	BE280172	Hs.129228	galactokinase 2	1.77

434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.76
419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.75
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	1.74
405102			C15001220*:g[111206958]b[AA021311.1] (AF	1.74
433201	AB040896	Hs.21104	KIAA1463 protein	1.73
420798	WS3774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.65
437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.62
414961	U27266	Hs.927	myosin-binding protein H	1.61
428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	1.61
422170	AJ791949	Hs.112432	anti-Mullerian hormone	1.61
431846	BE019924	Hs.271580	uroplakin 1B	1.58
404468			C3000442*:g[111206958]re[1]NP_068518.1] c	1.57
405779			NM_005367:Homo sapiens melanoma antigen,	1.55
441129	AA074904	Hs.296420	ESTs, Weakly similar to T18651 hypothei	1.55
427244	AA402400	Hs.178045	ESTs	1.52
411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	1.52
417777	AB23763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.51
418367	AA326035	Hs.59236	hypothetical protein DKFZp434L0718	1.51
440340	AW895503	Hs.125276	ESTs	1.48
437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	1.47
424750	D29956	Hs.152818	ubiquitin specific protease 8	1.46
429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	1.44
405374			C16001364:g[11067373]re[1]NP_067689.1] C	1.43
430606	BE256026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	1.40
404405			Target Exon	1.39
401258			NM_030932*:Homo sapiens diaphanous (Dros	1.38
433323	AA805132	Hs.159142	ESTs	1.36
427441	AA412605	Hs.343879	SPANX family, member C	1.33
444707	A188613	Hs.41690	desmocollin 3	1.31
409103	AF251237	Hs.112208	XAGE-1 protein	1.27
451106	BE382701	Hs.25960	N-MYC oncogene	1.27
434804	AA649530	Hs.348148	gb:ns44105.s1 NCI_CGAP_Aiv1 Homo sapiens	1.23
430686	NM_001942	Hs.2633	desmoglein 1	1.21
429325	AW088739	Hs.243770	ESTs	1.19
406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	1.03
418827	BE327311	Hs.47166	HT021	1.01
404104			C6001378*:g[11171748]s[P46530]NOTC_BRAR	1.00

TABLE 46B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

45	Pkey 413808	CAT Number 2905_1	Accession AL570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI926902 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI638062 AI282258 AI580678 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW869709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI858151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767 X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA588276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50895 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663874 AA190993 H01642 BF510304 AA626915 AA746952 AI610114 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035 M31126 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AI128438 BE384458 AI353967 BI857117 BF668525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AI353968 AA191092 BF132635 BE184942 BE184946 AW238414 BE144666
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452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21208 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 B1823519 B1770023 AL554969 B1489506 A1304693 AW295947 BM145642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897218 BF914190 BF903647 S70277 A1569694 AW073296 A1361433 AA564644 AA487429 BE858232 AA838610 A1539114 A1719375 A1829129 BG057675 A423422 AU158860 BE300555 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 B1258544 BF342301 BG875994 AA054458 AA353161 A1940434 BE818522 AL577636 A1479650 AW150377 AU154395 AW951271 A1032220 A1819778 A1346733 AW771150 AW512525 A1249904 AA279809 A1352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 B1819184 AV660190 AL556475 A1620020 AW089888 AW079179 Z21518 AA687601 F04551 A1733961 T57198 A1433367 T78852 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 A1266514 A1538823 A1475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 A1682892 AA830989 AA862356 AA653084 BM009154 A1135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 HB8457 AA627748 B1560216 B1753586 AW975281 AA664986 AA525775 AA056342 A1538978 X79449 BC017853 AL121035 BF196384 AW119044 A1028023 AW451110 A1971911 AW015069 A1079170 A1376367 A1264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 A1074589 A1523475 BE890249 AW406263 BE074258 AV729485 BF809510 BG058619 AA677244 BE179838 AA622264 A1460106 AA740411 A1499168 A1078223 A1582923 BE696559 AW375385 AA908739 BG984978 Z40874 T17054 F09669 AW844043 U10439 B1711870 AW245957 AU158567 AA579305 AA679316 W72510 A1346029 BG059762 AW251062 AA132373 A1925621 A1860230 A1340172 AW192891 A1079790 A1094937 A1042115 A1200901 BE328452 AA644678 AA551209 BE351065 AA970761 N86609 AW002028 AA160826 A1422774 AW873114 AW073597 AW664483 A1218700 AW020550 AW190607 A1984545 A1871921 A1333970 A452887 A1818335 AA398655 A1554424 A1274187 BE465703 AW512940 AW241366 A1923354 AA576649 AW168294 AA813181 AA912168 A1049738 AW514073 AA548255 A1569630 BE710031 AA244182 A1341697 AA563904 A1537990 AW517908 AW172943 Z39498 A1750294 AW150414 A1253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 A1499917 AA054452 H05484 A1828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 B1021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 B1919250 B1253018 AW130996 BE074249 BE895428 B1034862 BE083277 BF952166 AF274943 BG494894 A1719075 AA908739 A1935150 A1422691 AA910644 AA583187 BM272167 A1828996 AA527373 AW972459 A1831360 AA772418 A1033892 A100926 A1154749 A459432 A1423513 A1094597 AA740817 A1991988 A1090262 A1312104 A1256707 AA459522 AA16871 A1075239 A1339996 AA701623 A1139549 A1336880 AA633648 A1989380 A1362835 AA399239 A1146955 BF514270 N92892 A1348243 A1278887 AA459292 A1494230 BF507531 A1492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 A196862 A157100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 A1537692 A1203723 A1857576 AA584410 AW371667 BM172363 BE253764 BE250764 BE255757 BE251752 BE251925 U09278 NM_004460 U76833 AF007822 AL550894 BG203919 AL575714 A1478772 AW022667 AW613820 A1435793 A1051768 A1200109 AA436611 BG208151 A1446661 BG215551 BM449645 AW630055 BG620125 AL550932 AW471133 A1136648 BE925603 BF828688 BE141577 BE141585 BE141587 AL109688 R23665 R26578 BC005265 BG176720 AW006027 BM352064 AW026316 A1635822 A1880584 A1693769 A1092211 B1492387 A1400449 AW166297 BF939910 AA232282 AW021432 A1333893 AA494308 AA854899 A1436795 AW069256 AA682373 A1092748 AA993184 A126077 A1081758 A1240686 A1261663 A1378423 AA465237 A1376096 AA035579 A1087308 AA48162 AA129977 A1090903 A1080686 A1288939 N33004 A1801240 AW021546 A1370773 A1086064 AA669528 A1250053 A1870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 A1582295 A1417525 A1563975 A1093566 A1077743 A1290741 AW073417 BE875418 BM264076 BG876884 A1680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 A1908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 B1438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 B1039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 B1090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 B1036306 BG990973 B1040954 BF919911 AU140155 A951766 A1434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 B1039782 AU140407 BE144243 BE709863 BF958642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE00561 A1695992 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349457 A1190590 A1554403 A1392926 AU158477 B1467252 AU158919 A1760816 BF082516 A1439101 AA451923 A1304326 A1590975 B1791553 A1700963 A1142882 AA039976 AA946936 AA644381 BM314884 AA702424 A147612 AW190555 A120573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026884 A1830049 AW780435 A1078449 A1819984 A1858282 B1468588 A1860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207 A1205263 BF082491 AW021347 A1568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 A1910434 BF082513 A1494069 A1270027 A1635878 AA126330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 B1762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 A1571075 BE067786 AV721320 A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1686869 A1568892 A1915596 A1105614 A1887258 A1565857 BE926474 BE067737 BG319486 AA247685 AW798883 A103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713658 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 A1905927 BF992780 AW853812 BG954443 B170853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 B1089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 B1040941 AA337270 AW384371 AW847442 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 A1284090 BE084323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W83382 A1498487 BC015981 AJ301615 AA628980 A1126603 BF184719
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TABLE 46C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83558,83740-83901,8423

5	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	400666	8118496	Plus	17982-18115,20297-20456
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	400665	8118496	Plus	16879-17023
	402994	2996643	Minus	4727-4969
	402075	8117407	Plus	121907-122035,122804-122921,124019-12416
	405770	2735037	Plus	61057-62075
10	401894	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	404240	5002624	Minus	116132-116407,116653-116922
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	402992	7767907	Minus	42137-42515
15	402408	9796239	Minus	110326-110491
	404286	2326514	Plus	51086-51301
	405387	6587915	Minus	3769-3833,5708-5895
	404287	2326514	Plus	53134-53281
	402995	2996643	Minus	5962-6216
20	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	401797	6730720	Plus	6973-7118
	402294	2282012	Minus	2575-3000
	401961	4581193	Minus	124054-124209
	404440	7528051	Plus	80430-81581
25	405386	6579238	Minus	40959-41297
	404171	9930793	Plus	173667-173783,176876-177055
	405778	7280331	Plus	18748-19757
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	401176	9438469	Minus	20475-20734
30	404170	9930793	Plus	168836-169248

TABLE 47A:

35	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
40	R1:	Maximum of esophageal tumor Als divided by the 98th percentile of the normal esophagus Als			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	31.70
	411243	AB039886	Hs.69319	CA11	30.12
45	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	18.46
	444325	AW152618	Hs.16757	ESTs	18.22
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	16.28
50	400666			NM_002425:Homo sapiens matrix metallopro	15.59
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	15.22
	425679	X05997	Hs.159177	lipase, gastric	14.60
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	13.14
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	12.60
55	445619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.00
	453331	AI240665		ESTs	11.20
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	10.77
	408360	AF123050	Hs.44532	diubiquitin	10.32
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.32
60	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	10.22
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	10.18
	408243	Y00787	Hs.624	interleukin 8	9.80
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	9.75
	450375	AA009647		a disintegrin and metalloproteinase doma	9.12
65	407366	AF026942	Hs.17518	gb:Homo sapiens cig33 mRNA, partial sequ	8.88
	433447	U29195	Hs.3281	neuronal pentraxin II	8.64
	421508	NM_004833	Hs.105115	absent in melanoma 2	8.46
	452852	AW378065	Hs.8687	ESTs	8.34
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	7.92
70	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	7.86
	409757	NM_001898	Hs.123114	cystatin SN	7.62
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.60
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	7.58
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	7.46
75	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.44
	406687	M31126		matrix metalloproteinase 11 (stromelysin	7.24
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.18
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	7.13
	429228	AI553633	Hs.326447	ESTs	7.04
80	421110	AJ250717	Hs.1355	cathepsin E	6.98
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	6.88
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	6.88
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.72
	421582	AI910275		trefoil factor 1 (breast cancer, estroge	6.52

5	447164	AF026941	Hs.17518	Homo sapiens c1g5 mRNA, partial sequence	6.40
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	6.32
	439926	AW014875	Hs.137007	ESTs	6.32
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.12
	411296	BE207307	Hs.10114	growth suppressor 1	6.03
	425312	AF026939	Hs.181874	interferon-induced protein with tetrat	5.86
	413441	AI929374	Hs.75367	Src-like-adaptor	5.86
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIIb, r	5.81
10	417715	AW969587	Hs.86366	ESTs	5.76
	413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	5.63
	400665			NM_002425:Homo sapiens matrix metallopro	5.60
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.53
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	5.44
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.42
15	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.40
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	5.38
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	5.08
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	5.08
20	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	5.04
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.92
	436856	AI469355	Hs.127310	ESTs	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.60
	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	4.53
25	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.48
	404240			NM_018950:Homo sapiens major histocompat	4.36
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	4.34
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.29
	425139	AW630488	Hs.25338	protease, serine, 23	4.24
30	415989	AI267700		ESTs	4.20
	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.11
	450701	H39960	Hs.288467	hypothetical protein XP_098151	4.06
	432271	W47225	Hs.126256	interleukin 1, beta	4.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.96
35	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	3.90
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.86
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.86
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	3.76
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	3.49
40	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	3.44
	431629	AU077025	Hs.265827	Interferon, alpha-inducible protein (clo	3.37
	435370	AI964074	Hs.225838	ESTs	3.29
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.19
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.18
45	409154	U72882	Hs.50842	Interferon-induced protein 35	3.13
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	3.12
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.00
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.76
	402992			Target Exon	2.57
50	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.54
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.52
	413945	NM_000591	Hs.75627	CD14 antigen	2.51
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	2.50
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	2.48
55	416149	X12451	Hs.78056	cathepsin L	2.47
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	2.46
	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	2.45
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.39
60	422562	AI962060	Hs.118397	AE-binding protein 1	2.35
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.28
	444652	BE513613	Hs.11538	.actin related protein 2/3 complex, subun	2.19
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	2.19
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	2.03
65	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.03
	428981	BE313077	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.83
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	1.79
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.70
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	1.69
70	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.66
	414024	AA134712	Hs.22410	gbzm79g08.r1 Stralagena neuroepithelium	1.65
	426530	U24578	Hs.276625	complement component 4A	1.58
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.52

75

TABLE 47B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

80

Pkey	CAT Number	Accession
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147833 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157457 AW663674 AA190993

			H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI350919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
5	450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758
	452410	59661_1	AL133619 AI435410 AA622747 AW272464 AI215594 AI673758 AI476447 AI804128 AI581345 AI026826 AI300820 AW513621 AA256162 AI559724 AI493388 AA614641 AI125754 AI214351 AI567080 AI200813 AI476629 AI685732 AA602400 AA730140 AI565082 AI269603 AI807095 AA905453 AA505909 AI204595 AI582930 AI686077 AA757863 AA730154 AA664048 BI831663 AI734138 AI734130 AI732734 AW043563 AI741241 AI732741 BF111446 BE677727 AA437369 AA426284 AA433997 AA425820 M31125
10	406687	0_0	XD0474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA558312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841768 BF373837 AW863191 BE841705 AW868315 AW868673 AW867311 AA335898 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI868837 AW866622 AI803901 AW005718 AI538062 AI282258 AI580678 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW028395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI510620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236

TABLE 47C

40	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
45	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
	400666	8118496	Plus	17982-18115,20297-20456
	400665	8118496	Plus	16879-17023
	404240	5002624	Minus	116132-116407,116653-116922
50	402992	7767907	Minus	42137-42515

TABLE 48A:

55	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
60	R1:	90th percentile of normal esophagus AIs divided by the 90th percentile of esophageal tumor AIs		
	Pkey	ExAccn	UnigeneID	Unigene Title
	407245	X90568	Hs.172004	titin
	426752	X69490	Hs.172004	titin
65	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com
	407013	U35637		gb:Human nebulin mRNA, partial cds
	400440	X83957	Hs.83870	nebulin
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus
	426087	AA100573	Hs.182421	troponin C2, fast
	417070	Z19077	Hs.172004	titin
70	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu
	405001	U58196		Interleukin enhancer binding factor 1
	418391	NM_003281	Hs.84673	troponin I, skeletal, slow
	418205	L21715	Hs.83760	troponin I, skeletal, fast
	422533	X56832	Hs.118804	enolase 3, (beta, muscle)
75	400499			C10001858.g16679124[re]NP_032759.1] ne
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific
	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,
80	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)
	416373	AA195845	Hs.73680	ESTs, Weakly similar to S12658 cysteine-
	415672	N53097	Hs.193579	ESTs
	409096	AA194412	Hs.50550	sarcomeric muscle protein

	431360	NM_000427	Hs.251680	loricrin	9.42
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcosin)	9.20
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	9.15
5	422069	AJ010063	Hs.343603	titin-cap (teletthonin)	8.96
	409028	AB014513	Hs.49998	Z-band alternatively spliced PDZ-motif	8.64
	437205	AW975934	Hs.283382	ESTs, Weakly similar to I38344 titin, ca	8.48
	421296	NM_002666	Hs.103253	perlepin	8.47
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	8.39
10	434352	AF129505	Hs.86492	small muscle protein, X-linked	8.28
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	7.93
	408591	AF015224	Hs.46452	mammaglobin 1	7.88
	435124	AA725362	Hs.120456	ESTs	7.76
	430681	AW969675	Hs.291232	ESTs	7.70
	454229	AW957744	Hs.278469	lacrimal proline rich protein	7.68
15	424734	AI217685	Hs.96844	ESTs	7.59
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.57
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	7.41
	443727	Z25389	Hs.18459	ESTs	7.21
20	408753	AJ337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	7.04
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	6.98
	424485	AI685069	Hs.272556	peptidylarginine deaminase type I	6.93
	403805			Target Exon	6.87
	429997	NM_006789	Hs.227457	apolipoprotein B mRNA editing enzyme, ca	6.72
25	418532	F00797	Hs.85844	neurotrophic tyrosine kinase, receptor,	6.70
	419711	C02621	Hs.159282	ESTs	6.70
	422640	M37984	Hs.118845	troponin C, slow	6.68
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.55
	405703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	6.34
30	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.27
	446962	AI351421	Hs.279709	muscle specific ring finger protein 1	6.20
	411102	AA401295	Hs.23926	triadin	6.17
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.15
	454059	NM_003154	Hs.37048	statherin	5.95
35	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	5.85
	434360	AW015415	Hs.127780	ESTs	5.57
	420813	X51501	Hs.99949	prolactin-induced protein	5.52
	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	5.46
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	5.42
40	446523	NM_003063	Hs.334629	sarcolipin	5.41
	402270			Target Exon	5.25
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	5.24
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	5.17
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.14
45	410621	AA194329	Hs.172004	titin	5.10
	429134	AA446953	Hs.99004	ESTs	5.06
	436519	AJ278124	Hs.238756	myozenin	5.04
	447023	AA356764	Hs.17109	Integral membrane protein 2A	5.03
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	5.02
50	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	5.00
	433635	AI074502	Hs.134292	hypothetical protein MGC12921	4.98
	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	4.96
	411021	F00055	Hs.172004	titin	4.95
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.93
55	424897	D63216	Hs.153684	frizzled-related protein	4.92
	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.92
	428824	W23624	Hs.173059	ESTs	4.78
	418592	AK000268	Hs.87383	hypothetical protein	4.74
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp5648078 (fr	4.73
60	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.66
	424049	AB014524	Hs.136380	KIAA0624 protein	4.65
	439609	AW971945	Hs.293236	ESTs	4.65
	433122	AB018391	Hs.58049	ESTs	4.62
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	4.59
65	415655	W05433		ESTs	4.59
	442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12228 fis, clone MA	4.58
	452308	AI167560	Hs.61297	ESTs	4.57
	418072	F35210	Hs.86507	Human DNA sequence from clone RP3-353C17	4.56
	429413	NM_014058	Hs.201877	DESC1 protein	4.53
70	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.53
	438704	AI435060	Hs.32825	ESTs	4.50
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	4.49
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	4.48
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	4.46
75	422313	AF045941	Hs.115166	scellin	4.43
	417045	F01180	Hs.332030	Homo sapiens ORF1	4.41
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.39
	435101	AI743156	Hs.131064	ESTs	4.37
	432408	N39127		ESTs, Weakly similar to A46010 X-linked	4.35
80	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	4.35
	429930	AI580809	Hs.99569	ESTs	4.30
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	4.26
	428454	AL039940	Hs.202949	KIAA1102 protein	4.20
	411000	NA0449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	4.11

5	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.99
	429560	AJ243209	Hs.98669	ESTs, Weakly similar to B47411 ADPribosy	3.95
	438328	AJ492261	Hs.32450	ESTs	3.84
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.84
	453976	AW021748	Hs.110405	ESTs, Weakly similar to I38022 hypothe	3.83
	414807	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	3.82
	430171	AF086289	Hs.234766	skin-specific protein	3.80
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	3.75
10	446082	AJ274139	Hs.156452	ESTs	3.74
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.70
	431205	AA194560	Hs.250763	tropomodulin 4 (muscle)	3.68
	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.68
	424747	AA346241	Hs.231887	EST	3.67
15	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	3.63
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.62
	453817	AW755253	Hs.61920	ESTs	3.57
	416431	AW384459	Hs.172004	titin	3.52
	425971	AF135024	Hs.165296	kalikrein 13	3.49
20	412452	AA215731	Hs.79265	suppression of tumorigenicity 5	3.48
	421512	AB007923	Hs.265848	myomegalin	3.41
	413922	AI535895	Hs.221024	ESTs	3.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.36
	418067	AJ127958	Hs.83393	cystatin E/M	3.32
25	426666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.29
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	3.26
	420197	AW139647	Hs.88134	ESTs, Weakly similar to A57291 cytokine	3.23
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	3.21
	404270	F00991	Hs.50889	NM_006061:Homo sapiens specific granule	3.21
30	409169	NM_003245	Hs.2022	(clone PWHLC2-24) myosin light chain 2	3.17
	426350	AB032999	Hs.27566	transglutaminase 3 (E polypeptide, prola	3.13
	452023	D42047	Hs.82432	KIAA1173 protein	3.08
	417713	AB011540	Hs.4930	KIAA0089 protein	2.99
	435538	AL041440	Hs.58210	low density lipoprotein receptor-related	2.97
35	450300	AA847992	Hs.137003	ESTs, Highly similar to ITH4_HUMAN INTER	2.97
	451814	AI742082	Hs.98539	ESTs	2.83
	452360	AA938471	Hs.54431	ESTs	2.67
	431938	AW972927	Hs.293968	specific granule protein (28 kDa); cyste	2.57
	408104	W73753	Hs.209637	ESTs	2.57
40	444329	W67826	Hs.55412	hypothetical protein FLJ12921	2.54
	439652	AA043193	Hs.273186	ESTs, Weakly similar to K1CJ_HUMAN KERAT	2.50
	432191	AF135025	Hs.159679	hypothetical protein, clone Telethon/Ita	2.33
	425855	Z28942	Hs.243960	kalikrein 12	2.32
	430560	NM_003278	Hs.65424	N-myc downstream-regulated gene 2	2.28
45	410677	X72925	Hs.69752	tetranectin (plasminogen-binding protein)	2.25
	411388	AC002115	Hs.159309	desmocollin 1	2.25
	425721	NM_016190	Hs.242057	uroplakin 1A	2.12
	430520	AJ224172	Hs.204096	chromosome 1 open reading frame 10	2.10
	429441	W28657	Hs.5307	lipophilin B (uteroglobin family member)	2.02
50	417405	R13052	Hs.3964	ESTs	2.01
	434560	Z49878	Hs.81131	Homo sapiens clone 24877 mRNA sequence	1.95
	417074	AJ012008	Hs.241586	guanidinoacetate N-methyltransferase	1.79
	430513	AW805749	Hs.318885	G6C protein	1.68
	454478	AI039195	Hs.128060	superoxide dismutase 2, mitochondrial	1.68
55	416559	BE617015	Hs.11006	ESTs	1.66
	447205	W5898	Hs.78846	ESTs, Moderately similar to T17372 plasm	1.64
	415780	AI752244		heat shock 27kD protein 2	1.55
	409702			eukaryotic translation elongation factor	1.50

60 TABLE 48B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

65	Pkey	CAT Number	Accession
	407013	2073_7	U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376
	424982	25362_1	AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26957 F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311 F32380 F25216 F19879 F18658 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940 F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W80691 F16457 F24094 F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012
	415555	15499_1	AJ276240 N70563 F37502 F29200 F27803 F18577 F19683 F20867 Z28857 F30994 F31752 F17375 F15601 F17543 F17411
	432408	2061_18	AV724258 AA247153 BF736219 BF513744 AW058048 AI082691 AA865520 N39127 AV724549 F20776 AA249747 AW970392 AA535433 F36964 F33894
75	409702	38388_1	AK056951 AK026458 BI439120 BM021106 F30243 BM055214 BM054962 BM069667 F37401 AA563621 AJ752243 AJ20773 AI933014 F18984 F35317 F35258 F27772 H39537 AW445222 F19408 H28557 F30608 F31797 F30960 BF837737 BF837688 AL551046 BI758668 BI765038 BI837440 BE392882 BI438801 AI093511 AJ752244 AJ784111 BG450221 BF338974 BG896472 AL576843 AW966769 F25388 F37436 H28558 AI025548 AA782333 F30929 F36002 F21229 AJ720539 AA719449 F21231 F18924 AA626888 F30774 F27704 F31411 F31127 F33381 F36153 F31793 F31138 F31966 F33901 AA298244 BI757347 AI810201 AI692843 F29441 H51409 F21804 AW973249 F18440 F17572 F32499 AA327152 AA534140 AI188088 F18893 F23362 AA010888 F18143 Z28500 H27651 AJ720790 F22425 H13178 H28677 F21098 F37777 F21466 F16598 F23420 AL574723 R75610 F34035 F17845 F18560 F25902 R79117 F35534 F15713 AI612800 F16563 F15645 F33609 F29995 BG939623 F17385 F17384 F18660 F17922 F15523 AI093253 F18359 F31452 F00232 AI583430 BM021353 AA284108 H27650 H29935 BE708208 AA010737 H51451

Z19399 AI678418 AJ952535 F17265 F17826 F37939 F35639 F17367 W75962 R70189 Z28755 R72106 AA335915 R75700 R79116 W72887
 AIS81552 R71403 F23388 C03913 B1756149 B116109 BF790727 AL553994 R82966 W47487 AA455066 AW984608 BE708220 BG490537 W47419

5

TABLE 48C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

10

15

Pkey	Ref	Strand	NL_position
405001	6015406	Minus	104646-104819
400499	9796071	Minus	148495-148806
403805	8140491	Minus	51483-51742,53429-53511
402270	3108020	Plus	117656-117822
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965

Table 49A. 1562 genes upregulated in lung cancer relative to normal body tissues

Table 49A shows 1562 genes upregulated in lung cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 90th percentile of lung tumor AIs divided by the 50th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from the numerator and denominator.

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate), member 2; Ribosomal_L20,Na_PL_cotrans;TM=Y; 24.06
 439335; AA742697; Hs.62492; ESTs, Weakly similar to B39066 proline-rich protein 15 - rat [R.norvegicus]; none;SS=M; 21.70
 406621; X57809; Hs.181125; Immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M; 19.36
 421341; AJ243212; Hs.279611; deleted in malignant brain tumors 1; zona_pellucida,CUB,SRCR;SS=M; 16.99
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine proteinase [H.sapiens]; none,none; 16.67
 429259; AA420450; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 16.50
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member A1; aldedh; 16.24
 408000; L11690; Hs.620; bullous pemphigoid antigen 1 (230/240kD); ehend,spectrin,GAS2,SH3,Plectin,RA,Xylose_Isom,FlitD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M; 14.75
 421798; N74880; Hs.29877; N-acylsphingosine amidohydrolase (acid ceramidase)-like; SAPA,Surfactant_L,none; 14.18
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]; none,none; 13.94
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 13.54
 417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1;SS=M; 12.97
 444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothetical protein YGL050w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]; Collagen;TM=M;SS=M; 12.92
 408243; Y00787; Hs.624; Interleukin 8; HLH,PAS,IL8;TM=M; 12.76
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP;TM=M;SS=M; 12.50
 414809; AA434699; Hs.77356; transferrin receptor (p90, CD71); PA;TM=Y; 12.12
 436553; AW407157; Hs.181125; Immunoglobulin lambda locus; Ig,HSP70,Ppx-GppA;TM=M; 12.00
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none,none; 11.99
 419893; AA133749; Hs.301350; FXD domain-containing ion transport regulator 3; ATP1G1_PLM_MAT8;TM=Y;SS=M; 11.88
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 11.38
 414998; NM_002543; Hs.77729; oxidized low density lipoprotein (lectin-like) receptor 1; lectin_c;TM=Y;SS=M; 11.21
 428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3;TM=Y;SS=M; 11.08
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member B2; aldedh;TM=M;SS=M; 11.01
 425397; J04066; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolV,HATPase_c;SS=M; 10.69
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4); ank; 10.65
 439223; AW238299; Hs.250618; UL16 binding protein 2; kIL_receptLa,PKD,MHC;TM=M;SS=Y; 10.52
 441835; AB036432; Hs.184; advanced glycosylation end product-specific receptor; homeobox,Acyltransferase,notch,EGF,ank,Acyltransferase; 10.47
 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ABC_tran,SRP54;TM=Y;SS=M; 10.33
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 10.21
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; Ig,Rhbd_glycop;TM=Y;SS=M; 10.14
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); PTN_MK;TM=M;SS=Y; 10.13
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_rec;TM=M;SS=Y; 10.12
 454098; W27953; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none,none; 10.05
 414812; X72765; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 9.98
 430832; AT073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]; none,none; 9.79
 422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; none,kinase,fn3,Ig; 9.60
 414887; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 9.54
 439453; BE284974; Hs.6566; thyroid hormone receptor interactor 13; AAA_ABC_tran,CoeE;TM=M; 9.52
 430280; AA361258; Hs.237868; Interleukin 7 receptor; fn3,none; 9.48

- 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); Kunitz_BPTI,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 9.44
- 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-family C (CFTR/MRP), member 1; ABC_membrane,ABC_tran;TM=Y;SS=M; 9.32
- 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid cells 1; Ig;TM=M;SS=M; 9.26
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens]; none:none; 9.18
- 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; ABC_tran,ABC_membrane;TM=Y;SS=M; 9.06
- 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fls, clone HRC00953; 7m_3:none; 8.98
- 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp.FecCD;TM=Y;SS=M; 8.74
- 436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 8.71
- 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 8.71
- 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2delta subunit 2; vwa,Cache;TM=M; 8.66
- 439608; W79123; Hs.58561; G protein-coupled receptor 87; 7m_1;TM=Y;SS=M; 8.63
- 438091; AW373062; nuclear receptor subfamily 1, group I, member 3; hormone_rec,zf-C4:none; 8.60
- 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M; 8.57
- 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;SS=M; 8.56
- 408908; BE295227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 8.52
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plasmin,thionins;SS=M; 8.49
- 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 8.42
- 413011; AW068115; Hs.821; biglycan; LRR,LRRNT;SS=M; 8.40
- 446291; BE397753; Hs.14623; Interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 8.39
- 411089; AA456454; cell division cycle 2-like 1 (PITSLRE proteins); none:none; 8.37
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); BIR;TM=M; 8.34
- 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; none;SS=M; 8.25
- 449019; AI949095; Hs.67776; ESTs, Weakly similar to T2341 hypothetical protein F4788.5 - Caenorhabditis elegans [C.elegans]; none:none; 8.24
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M; 8.22
- 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 8.19
- 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M; 8.16
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; ABC_tran,M,SMC_N,SMC_C,DUF164:none; 8.16
- 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M; 8.14
- 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.14
- 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;SS=Y; 8.10
- 414821; M53835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Ig;TM=Y;SS=M; 8.03
- 439285; AL133916; hypothetical protein FLJ20093; Ig,pkinase,LRR,LRRNT,LRRCT:none; 7.97
- 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B; Sema,PSI,Integrin_B;TM=Y;; 7.86
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2; pkinase;TM=M; 7.85
- 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 7.85
- 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M; 7.84
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); SH3,TPR;TM=M; 7.73
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Ig;TM=Y;SS=M; 7.72
- 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily, member 17; IL2;SS=M; 7.71
- 451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.70
- 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid cells 2; Ig;TM=Y;SS=M; 7.70
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M; 7.70
- 426251; M24283; Hs.168383; Interleukin adhesion molecule 1 (CD54), human rhinovirus receptor; Ig,ICAM_N;TM=M;SS=M; 7.67
- 422282; AF019225; Hs.114309; apolipoprotein L; MoLA_ExtB;TM=Y;SS=M; 7.64
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; SAM_PNT:none; 7.54
- 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding protein; 7m_1;TM=Y;SS=M; 7.52
- 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); Y_phosphatase,DSPC;TM=M; 7.46
- 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen alpha 1(X) chain precursor [H.sapiens]; none;TM=Y;SS=M; 7.40
- 421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 7.39
- 438089; W05391; nuclear receptor subfamily 1, group I, member 3; hormone_rec,zf-C4:none; 7.38
- 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M; 7.36
- 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, epsilon; Neur_chan_LBD,Neur_chan_mem;TM=Y;SS=M; 7.36
- 416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; none;TM=M; 7.31
- 418506; AA084248; Hs.85339; G protein-coupled receptor 39; none:none; 7.25
- 441553; AA281219; Hs.121296; ESTs; none,FG-GAP,Integrin_A; 7.25
- 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3;TM=M; 7.21
- 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-type, Z polypeptide 1; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 7.20
- 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; transferrin,Guanylate_kin,PDZ,SH3; 7.20
- 412723; AA648459; Hs.335951; hypothetical protein AF301222; ncne;TM=M; 7.14
- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 7.14
- 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 7.12
- 418462; BE001596; Hs.85256; Integrin, beta 4; fn3,Integrin_B,Cab-beta,EGF;TM=M;SS=M; 7.08
- 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 7.02
- 426450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M; 7.00
- 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; Ig,Isohd,Ribosomal_L6,F-box;TM=Y;SS=M; 6.98
- 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; Furin-like,pkinase,Recep_L_domain,YLP:none; 6.97
- 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M; 6.96
- 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; ITAM;TM=Y;SS=M; 6.83
- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 6.83
- 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT;TM=M; 6.91
- 451033; AU076785; Hs.430; plasmin 1 (I isoform); eifhand,CH,Adaplin_N;SS=M; 6.86
- 432407; AA221036; gb:z03f12.r1 Stratagene NT2 neuronal precursor 837230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ; mRNA sequence; DEAD,helicase_C,rm,Ndr,Cys_knoI,TIL,vwa,vwd,IQ,Rila,ebhydrolase,TGF-beta,DUF139,TPR,DSPc,isp_1,Ribosomal_S21,rvp;TM=M; 6.84
- 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M; 6.77
- 448243; AW369771; Hs.52620; Integrin, beta 8; Integrin_B:none; 6.76
- 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh;SS=M; 6.75
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.74
- 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; sugar_tr;TM=Y;SS=M; 6.73

- 430397; A1924533; Hs.105607; bicarbonate transporter related protein 1; HCO3_cotransp;TM=Y;; 6.71
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 6.71
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor); FG-GAP,Rhadd_glycop,Integrin_A;TM=Y;SS=M; 6.70
 410434; AF051152; Hs.63658; toll-like receptor 2; LRR,LRRC7,TIR;TM=M;SS=M; 6.69
 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation antigen; PAAD_DAPIN,HIN; 6.69
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor); vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 6.65
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 6.64
 430770; AA765694; Hs.123296; ESTs; none,none; 6.63
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G protein), alpha 15 (Gq class); G-alpha,art;TM=M; 6.59
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA clone EUROMAGE 2005735; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricin_B_lectin; 6.59
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPP;TM=M; 6.59
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 6.58
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 6.58
 416110; Z42262; Hs.322844; hypothetical protein DKFP564A176; Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 6.58
 418883; BE247706; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 6.57
 426746; J03626; Hs.2057; uridine monophosphate synthetase (pyruvate phosphoribosyl transferase and orotidine-5'-decarboxylase); Pribosyltran,OMPdecase;TM=M; 6.57
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA; transcript (F8A), mRNA; pkinase,Fibrillarin,none; 6.56
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide); none;TM=Y;; 6.53
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; Idl_recept_a,PKD,MHC;TM=M;SS=Y; 6.53
 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; inositol_P,lg;TM=M;; 6.52
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;TM=Y;SS=M; 6.52
 432920; U37689; Hs.3128; polymerase (RNA) II (DNA directed) polypeptide H; none;TM=M;; 6.48
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; PLDC;TM=M; 6.48
 409208; Y00093; Hs.51077; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); vwa,FG-GAP,Integrin_A,vwa,Integrin_A,FG-GAP; 6.43
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF; 6.43
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; lg;TM=Y;SS=M; 6.41
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fs, clone PLACE2000103; HLH,death,TNFR_c6,Acyl-CoA_hydro; 6.41
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPP,Y_phosphatase,Ribosomal_S3_N;TM=M; 6.39
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPPase;TM=M; 6.37
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip;TM=M;SS=Y; 6.37
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;SS=M; 6.36
 432636; AA340864; Hs.278562; claudin 7; PMP22, Claudin;TM=Y;SS=M; 6.34
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPPc,Rhodanese,none; 6.34
 451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate, RC3); IQ,7tm_1;TM=M; 6.34
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; none;TM=M;SS=Y; 6.34
 401027; ; Target Exon; none,none; 6.26
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); Integrin_B,EGF,PSI;TM=Y;SS=M; 6.22
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); SH2;SS=M; 6.21
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fs, clone ADKA02377; 7tm_3,none; 6.20
 408771; AWT32573; Hs.47584; potassium voltage-gated channel, delayed-rectifier, subfamily 3, member 3; ehand,ion_trans,K_tetra,none; 6.19
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudogene; LIM,PDZ,pkinase;SS=M; 6.18
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.17
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 6.17
 445019; AJ205540; Hs.281295; ESTs; none,none; 6.16
 438552; AJ245820; Hs.6314; type I transmembrane receptor (seizure-related protein); none,none; 6.16
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLQ_box,tRNA-synt_1b,dynamidin,dynamidin_2,GED,bZIP,M; 6.14
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; PI3_P4_kinase,FAT,FATC;TM=M;; 6.13
 417421; AL138201; Hs.82120; nuclear receptor subfamily 4, group A, member 2; hormone_rec,zf-C4;SS=M; 6.13
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 6.12
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 6.12
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M; 6.12
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.11
 444143; AW747896; Hs.160999; ESTs, Moderately similar to A56194 thromboxane A-2 receptor, endothelial (H.sapiens); Bcl-2,none; 6.10
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y;; 6.10
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y;; 6.09
 411020; NM_006770; Hs.67726; macrophage receptor with collagenous structure; SRCR,Collagen;TM=Y;SS=M; 6.09
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 6.08
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); PAF-AH_1b,Lipase_GDSL;TM=M; 6.07
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-family B (MDR/TAP), member 6; ABC_tran,ABC_membrane;TM=Y;SS=M; 6.07
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gene, complete CDS.; none,none; 6.07
 425849; AJ000512; Hs.296323; serum glucocorticoid regulated kinase; pkinase,pkinase_C;TM=M;SS=M; 6.06
 452363; A1582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; C1q,Collagen;SS=M; 6.05
 414883; AA926960; CDC28 protein kinase 1; CKS; 6.05
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,DSPPc,isp_1,Ribosomal_S21_rvp;TM=M; 6.03
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,in2;TM=Y;SS=M; 6.03
 448782; AL050295; Hs.22039; KIAA0758 protein; 7tm_2,lg,GPS,SEA;TM=Y;; 6.03
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 6.01
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 6.00
 424381; AA285249; Hs.146329; protein kinase Chk2; pkinase,FHA,DnaJ;TM=M; 6.00
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M; 5.99
 439310; AF086120; Hs.102793; ESTs; casein_kappa,pkinase,lg,none; 5.97
 414972; BE263782; Hs.77695; KIAA0008 gene product; GKAP;TM=M; 5.97
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 5.94
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 5.93
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin;TM=M; 5.93
 421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 5.92
 426761; AJ015709; Hs.172089; Homo sapiens mRNA: cDNA DKFZp586i2022 (from clone DKFZp586i2022); none;TM=Y;SS=M; 5.92
 407792; A077715; Hs.39384; putative secreted ligand homologous to fix1; none;TM=M;SS=Y; 5.91
 428771; AB028992; Hs.193143; KIAA1069 protein; C2,Pi-PLC-Y,Pi-PLC-X;TM=M; 5.91
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; lg,MHC_II_alpha,none; 5.91

- 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 5.90
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,ig,Neuregulin;TM=M; 5.90
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, receptor, type 2; Ig,pkinase,LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.89
 413186; AU077141; Hs.75231; solute carrier family 16 (monocarboxylic acid transporters), member 1; sugar_tr;TM=Y;SS=M; 5.89
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C,none; 5.88
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 5.88
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; none;TM=M;SS=Y; 5.88
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor 4 gamma, 1; none,none; 5.86
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222); SH2,SH3,BTB; 5.86
 436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaJ; 5.85
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, calcium-dependent); C2,PLA2_B;TM=M; 5.85
 419881; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 5.83
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily, member 6b, decoy; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 5.83
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 5.82
 451320; AW118072; Hs.150772; diacylglycerol kinase, zeta (104kD); none;TM=M; 5.82
 400991; ; Target Exon; Armadillo_seg,lectin_c,none; 5.81
 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral transforming sequence c; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M; 5.81
 434263; N34895; Hs.44648; ESTs; Ig,none; 5.81
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino acid transporter), member 5; eIF6,SDF;TM=M; 5.78
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; p450;TM=Y;SS=M; 5.78
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain,none; 5.77
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 5.77
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); MIF,sugar_tr,none; 5.75
 409633; AW969543; Hs.21291; mitogen-activated protein kinase kinase kinase 13; Peptidase_C48,none; 5.73
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) receptor; hormone_rec,zf-C4,Metallothio_5;TM=M; 5.73
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); none,none; 5.72
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; SH2,STAT,STAT_bind,STAT_prot;TM=M; 5.72
 452295; BE378936; Hs.28866; programmed cell death 10; serpin,none; 5.72
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; NUDIX;TM=M;SS=M; 5.72
 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter transporter, creatine), member 8; SNF;TM=Y; 5.71
 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox;TM=Y;SS=M; 5.69
 453323; AF034102; Hs.32951; solute carrier family 29 (nucleoside transporters), member 2; Nucleoside_tran;TM=Y;SS=M; 5.69
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 5.69
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 46kD; mm,hormone_rec,zf-C4,sugar_tr; 5.69
 418526; BE019020; Hs.85838; solute carrier family 18 (monocarboxylic acid transporters), member 3; none;TM=Y;SS=M; 5.66
 447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PP2C;TM=M; 5.65
 438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 5.65
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; Ig,none; 5.64
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; Sm,pkinase; 5.64
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 Gt; MutS_C,PWWP,MutS_N;TM=M; 5.63
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P4_kinase,PI3Ka;TM=M; 5.62
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; PABP,mm,pkinase,14-3-3; 5.62
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; SH3,PH,RhoGEF;TM=M; 5.61
 446872; X97058; Hs.16362; pyrimidnergic receptor P2Y, G-protein coupled, 6; 7tm_1;TM=Y;SS=M; 5.59
 433662; W07162; Hs.150826; CATX-8 protein; ras,ABC_tran,arf;TM=M;SS=M; 5.59
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; aa-permeases;TM=Y;SS=M; 5.58
 431238; AV656840; Hs.285115; Interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 5.57
 430508; AI015435; Hs.104637; ESTs; SDF;TM=Y;SS=M; 5.56
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; 7tm_1;TM=Y;SS=M; 5.55
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.54
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M; 5.54
 429563; BE619413; Hs.2437; eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD); hexapep,W2,hormone2,DUF29;TM=M; 5.52
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subunit, non-ATPase, 2; PC_rep;TM=M; 5.51
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; pkinase;TM=M; 5.51
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (from clone DKFZp547C136); ABC_tran,GTP_EFTU,ABC_membrana,none; 5.50
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 5.48
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); SH3,PX;TM=M; 5.48
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fs, clone HEMBB1001304; Nucleoside_tra2,none; 5.48
 426591; NM_006201; Hs.171834; PCTAIRE protein kinase 1; pkinase;TM=M; 5.48
 453905; NM_002314; Hs.35566; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M; 5.48
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor 1 gamma; none,none; 5.44
 430486; BE062109; Hs.241551; chloride channel, calcium activated, family member 2; none;TM=Y;SS=M; 5.43
 430066; AI929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synt; 5.40
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; kinesin,fn3,Y_phosphatase;TM=M; 5.40
 411825; AK000334; Hs.72289; hypothetical protein FLJ20327; SNF,Zip;TM=Y; 5.36
 400205; ; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA.(APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; DUF173;SS=M; 5.35
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 5.34
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 5.34
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,Mخان_ur_permease,HCO3_cotransp;TM=M; 5.32
 400210; ; Eos Control; Adap_comp_sub,Clat_adaptor_s;TM=M; 5.32
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 5.31
 414035; Y00630; Hs.75718; serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; serpin;SS=M; 5.30
 416000; R82342; Hs.78856; ESTs; Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; none,sugar_tr; 5.30
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE; 5.29
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; SH2,SH3,pkinase;TM=M; 5.29
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; none,none; 5.29
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, complete cds; none,PK,PK_C,myosin_head,RhoGAP; 5.28
 410068; AI633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3;TM=M; 5.28
 456629; AW891865; Hs.279789; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD,none; 5.27
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); pkinase,Sema,PSI,TIG,Integrin_B;TM=Y;SS=M; 5.26
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none,none; 5.26

- 404083; ; C6002159;g[628027]p[4]A53593 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor ty; none;SS=M; 5.26
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; mito_carr;TM=M; 5.26
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,kinase;TM=M; 5.26
 427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 5.25
 425921; NM_007231; Hs.162211; solute carrier family 6 (neurotransmitter transporter), member 14; SNF;TM=Y;SS=M; 5.25
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A, member 4A; none;TM=Y;SS=M; 5.24
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3lg;TM=M; 5.23
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 5.23
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M; 5.23
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazarotene induced) 3; none;TM=Y; 5.21
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; SH3,HS1_rep;TM=M; 5.20
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M; 5.19
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; Troponin,Exo_endo_phos,IQ;TM=M; 5.19
 446536; AC002563; Hs.15767; citron (rho-interacting, serine/threonine kinase 21); CNH,DAG_PE-bind,PH,Involucrin,M;TM=M; 5.19
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.19
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, subfamily J, member 15; IRX;TM=Y; 5.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; Ribosomal_S14,ank,kinase,death,none; 5.18
 442200; AW590572; Hs.235766; ESTs; none,none; 5.18
 446566; H55741; Hs.17914; membrane-spanning 4-domains, subfamily A, member 6A; none;TM=Y;SS=M; 5.18
 426900; AI536070; Hs.15085; ESTs; pou,homeobox,lig_chan,ANF_receptor; 5.18
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR,JTPR,RyR,MIR;TM=Y; 5.17
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 5.16
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 5.16
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta (Liddle syndrome); ASC;TM=Y;SS=M; 5.15
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytotactin); EGF,fn3,fibrinogen_C,toxin_2,Keratin_B2;TM=M;SS=Y; 5.15
 411984; NM_005419; Hs.72988; signal transducer and activator of transcription 2, 113kD; SH2,STAT,STAT_bind,STAT_prot;TM=M; 5.15
 433470; AW960564; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 5.14
 425817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; kinase,PBD;TM=M; 5.14
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.14
 427792; BE3928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; SRP14,TNFR_c6;SS=M; 5.14
 430563; AA481269; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; ABC_tran,GTP_EFTU,ABC_membrane,none; 5.13
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y; 5.12
 431183; NM_005855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3; ER_lumen_recept;TM=M;SS=M; 5.12
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarotene induced) 1; none,none; 5.11
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase 1; kinase,CNH;TM=M; 5.11
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily, member 13; TNF;TM=Y;SS=M; 5.11
 436856; AI469355; Hs.127310; ESTs; kinase,rm;TM=M; 5.09
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy;TM=M;SS=M; 5.09
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rm;TM=M; 5.09
 404440; ; NM_021048;Homo sapiens melanoma antigen, family A, 10 (MAGEA10), mRNA, VERSION NM_021049.1 Gt; MAGE;TM=M; 5.08
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fls, clone KAT05581; none,none; 5.08
 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; arf,ras;TM=M; 5.07
 452222; AW806287; Hs.21432; SEX gene; Sema,TIG,PSI,GDI; 5.07
 430300; U60805; Hs.238648; oncostatin M receptor; fn3;TM=Y;SS=M; 5.07
 408369; R38438; Hs.182575; solute carrier family 15 (H777 transporter), member 2; PTR2;TM=Y; 5.07
 422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;SS=M; 5.06
 449961; AW265634; Hs.133100; ESTs; kinase,Furin-like,Recep_L_domain,none; 5.06
 430024; AI808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 5.06
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; HSP90,HATPase_c;TM=M; 5.05
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; kinase,RIO1,none; 5.05
 400296; AA305627; Hs.139333; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y; 5.04
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3,none; 5.04
 425262; D87119; Hs.155418; GS3955 protein; kinase;SS=M; 5.04
 414703; BE243877; Hs.76941; ATPase, Na? transporting, beta 3 polypeptide; Na_K-ATPase;TM=Y;SS=M; 5.03
 434808; AF155108; Hs.258150; Homo sapiens, Similar to RIKEN cDNA 2810027019 gene, clone MGC:14827, mRNA, complete cds; none;TM=M; 5.03
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member 21; death,TNFR_c6;TM=Y;SS=M; 5.03
 449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fls, clone KAT05581; none,none; 5.03
 448913; AA194422; Hs.22584; myosin VI; rm,zf-RanBP,kinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIIS,AT_hook,SAM;TM=M; 5.02
 413441; AI929374; Hs.75367; Src-like-adapter; SH2,SH3;TM=M; 5.02
 427618; NM_000760; Hs.2175; colony stimulating factor 3 receptor (granulocyte); fn3;TM=M;SS=M; 5.02
 417666; AI345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M; 5.02
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); CDK5_activator,none; 5.01
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; ras,arf,TK;SS=M; 5.01
 426285; U20620; Hs.343581; karyopherin alpha 1 (importin alpha 5); Armadillo_seg,IBB;TM=M; 5.01
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4;TM=Y;SS=M; 5.01
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fls, clone MAMMA1000643; SH2,STAT,STAT_bind,STAT_prot,none; 5.00
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-receptor type 1; Y_phosphatase,DSPT;TM=M;SS=M; 5.00
 446946; AI878932; Hs.317; topoisomerase (DNA) I; Topoisomerase_I,Topoisomer_I_N,RnaAD,Hania_nucleocap;TM=M; 4.99
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); TPR,PDZ,WV,Guanylate_kdn;TM=M; 4.98
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor); 7tm_1;TM=Y;SS=M; 4.98
 400792; AA635062; ; Homo sapiens mRNA; cDNA DKFZp434O0515 (from clone DKFZp434O0515); zf-C3HC4,CARD,BIR;TM=M; 4.98
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related oncogene homolog; SH2,SH3,kinase;TM=M; 4.98
 427247; AW504221; Hs.174103; Integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 4.98
 442080; AW444761; Hs.44565; ESTs; ank; 4.97
 454042; H22570; ; hypothetical protein FLJ20093; ig,kinase,LRR,LRRNT,LRRCT,none; 4.97
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 4.96
 416276; U41060; Hs.79136; LIV-1 protein, estrogen regulated; Peptidase_C4,Osteopontin,Zip;TM=Y;SS=M; 4.96
 408847; AW290997; Hs.30348; ESTs; kinase,lg,none; 4.96
 419452; U33633; Hs.90572; PTK7 protein tyrosine kinase 7; ig,kinase;TM=Y;SS=M; 4.95
 450737; AW007152; Hs.203330; ESTs; trypsin_kd_recept_a,none; 4.95
 443354; AW970572; Hs.9247; protein kinase, AMP-activated, alpha 1 catalytic subunit; kinase,RIO1;TM=M; 4.94

- 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese, DSPc, Y-phosphatase; TM=M; 4.94
 424247; X14008; Hs.234734; lysosyme (renal amyloidosis); lys, Ig, FAD_Synth, Idh, Idh_C, pkinase; SS=M; 4.94
 434206; AW136973; Hs.180479; ESTs, Weakly similar to S69890 milogen inducible gene mig-2 [H.sapiens]; PH; TM=M; 4.93
 5 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); 7tm_1, 7tm_2; TM=Y; SS=M; 4.93
 408716; AJ567639; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, partial cds; UvrD-helicase, RNB, Runt; TM=M; 4.93
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 4.92
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; Els, SAM_PNT; TM=M; 4.92
 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; In2, CIMR; TM=M; SS=M; 4.92
 10 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; Ig; TM=Y; SS=M; 4.92
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; DEAD, helicase_C, CARD; TM=M; 4.91
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); Ig, ITAM, Zn_dus; TM=Y; SS=M; 4.91
 404289; ; NM_002944; Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; In3, pkinase, DUF139; TM=Y; SS=M; 4.90
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; Nramp; TM=Y; 4.90
 15 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 4.89
 432179; X75208; Hs.2913; EphB3; EPH_1bd, In3, pkinase, SAM; TM=Y; SS=M; 4.89
 401083; ; NM_016582; Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 GI; PTR2; TM=Y; SS=M; 4.89
 402211; AA811738; ; KIAA0430 gene product; ion_trans, K_tetra; TM=Y; 4.88
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polypeptide 4; pkinase, pkinase_C; TM=M; 4.87
 431810; X67155; Hs.270845; kinesin-like 5 (mitotic kinesin-like protein 1); kinesin; TM=M; 4.86
 20 425295; AA431366; Hs.37251; ESTs; pkinase, none; 4.86
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase; 4.86
 419168; AJ336132; Hs.33718; Homo sapiens cDNA FLJ12641 fis, clone NT2RM4001953; none, none; 4.86
 442675; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequence; K_tetra, DUF51, none; 4.86
 25 425465; L18964; Hs.1904; protein kinase C, Iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; 4.86
 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; 4.86
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; C1q, Collagen; SS=M; 4.85
 445903; AI347487; Hs.132781; class I cytokine receptor; In3; TM=Y; 4.85
 427509; M82505; Hs.2161; complement component 5 receptor 1 (C5a ligand); 7tm_1; TM=Y; SS=M; 4.85
 30 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); vwa, Integrin_A, FG-GAP; TM=Y; SS=M; 4.84
 445143; U29171; Hs.75852; casein kinase 1, delta; zf-C3HC4, Filamin, zf-B_box, NHL, pkinase, zf-MIZ; TM=M; 4.82
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; 4.81
 427857; AL133017; Hs.2210; hypothetical protein FLJ22865; myosin_head, IQ, zf-MYND; TM=M; SS=M; 4.81
 35 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); aldedh, aakine; TM=M; 4.81
 414280; BE410769; Hs.75873; zyxin; LIM, Ig, pkinase; TM=M; SS=M; 4.81
 424570; AA343306; Hs.133511; ESTs; SH3, ank, none; 4.80
 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c, none; 4.80
 402705; AA214618; ; activator of S phase kinase; AhpC-TSA; TM=M; SS=M; 4.80
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M; 4.80
 40 419972; AL041465; Hs.182882; golgin-67; none, none; 4.80
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C, none; 4.80
 413476; U25849; Hs.75393; acid phosphatase 1, soluble; LMWPc; TM=M; SS=M; 4.80
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, receptor for (CD32); Ig; TM=Y; 4.79
 402233; ; NM_030760; Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA; 7tm_1; TM=Y; SS=M; 4.79
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; NusG; SS=M; 4.79
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB; TM=M; 4.79
 405370; ; NM_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA; pkinase, LIM, PDZ; SS=M; 4.79
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1 (TWIK-1); ion_trans; TM=Y; SS=M; 4.78
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COL1TSPN, laminin_G, CorA; SS=M; 4.78
 50 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase; TM=M; 4.78
 433133; AB027249; Hs.104741; PDZ-binding kinase; T-cell originated protein kinase; pkinase; TM=M; 4.78
 431629; AU077025; Hs.258927; Interferon, alpha-inducible protein (clone IFI-6-16); none; TM=M; SS=Y; 4.78
 417929; R27219; Hs.74847; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Ig, abhydrolase; 4.78
 55 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y; SS=M; 4.78
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase; SS=M; 4.77
 409744; AW675258; Hs.56255; Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321); none; NA; NA; 4.77
 446196; AJ744888; Hs.149470; ESTs; zf-C3HC4, Sulfate_transp, STAS; 4.77
 429305; AF095727; Hs.287832; myelin protein zero-like 1; Ig, transmembrane4; TM=Y; SS=M; 4.77
 60 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chloride transporters), member 7; none; TM=Y; 4.77
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); Armadillo_seg, IBB, DEAD, helicase_C, Sec63, DDT, PHD, bromodomain; TM=M; 4.77
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; DSPc; TM=M; 4.77
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702; GDI, 7tm_1, none; 4.76
 447207; AA442233; Hs.17731; hypothetical protein FLJ12892; none; TM=M; 4.76
 65 400848; ; sortilin-related receptor, L(DLR class) A repeats-containing (SORL1); EGF, In3, Idl_recept_a, Idl_recept_b, granuln, BNR; TM=Y; SS=M; 4.76
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; 4.75
 406809; AF000574; Hs.22405; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; Ig, Gemini_mov; TM=M; SS=M; 4.75
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE; TM=M; 4.75
 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHITE), member 1; ABC_tran, PRK, GBP; TM=Y; 4.74
 70 410408; AJ969703; Hs.1466; glycerol kinase; FGGY, FGGY_C; TM=M; 4.73
 411653; AF070578; Hs.71168; Homo sapiens clone 24674 mRNA sequence; none; NA; NA; 4.73
 437667; BE616412; Hs.286218; junctional adhesion molecule 1; none, HLH; 4.73
 417781; BE279380; Hs.82563; KIAA0153 protein; TTL_Acyl_transf; 4.73
 453968; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin, Idl_recept_a, none; 4.73
 75 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr virus) receptor 2; sush1; TM=Y; SS=M; 4.73
 418255; AW135405; Hs.37251; ESTs; pkinase, none; 4.73
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; SDF; TM=Y; SS=M; 4.73
 406906; Z25424; ; qbH.sapiens protein-serine/threonine kinase gene, complete CDS; none, none; 4.73
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; Metallophos; TM=M; 4.72
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; SS=M; 4.72
 80 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; NDK, PH, Oxysterol_BP; SS=M; 4.71
 426138; AW957239; ; gbEST369309 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence; PP2C, none; 4.71
 446203; Z47553; Hs.14286; flavin containing monooxygenase 5; FMO-like, pyr_redox; TM=Y; SS=M; 4.71
 451295; AJ557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase, DAG_PE-bind, pkinase_C, OPR, none; 4.71

- 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y;; 4.70
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; lkh,ldh_C,SH3,pkinase,UBA;TM=M;; 4.70
 427206; NM_004586; Hs.173965; ribosomal protein S6 kinase, 90kD, polypeptide 3; none;none; 4.70
 421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; EGF,F5_F8_type_C,laminin_G,Sulfate_transp,STAS,7tm_3,xan_ur_permease;TM=Y;SS=M; 4.70
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); UQ_con;TM=M; 4.70
 405484; ; C3002124;g1j2737280[re]XP_006682.2] keratin 18 [Homo sapiens]]6633; none;SS=M; 4.70
 401345; M83738; ; protein tyrosine phosphatase, non-receptor type 9; none;TM=M; 4.70
 416602; NM_008159; Hs.79389; nel (chicken)-like 2; EGF,wvc,TSPN;SS=Y; 4.69
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 4.69
 437897; AA770561; Hs.146170; hypothetical protein FLJ22569; zf-DHHC;none; 4.69
 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M; 4.69
 400843; ; NM_003105;Homo sapiens sortilin-related receptor, LQDLR class) A repeats-containing (SORL1), mRNA;
 EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.68
 433409; A1278802; Hs.25661; ESTs; pkinase,pkinase; 4.68
 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; none;TM=Y;SS=M; 4.68
 430259; BE550182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.68
 425761; AW664214; Hs.196729; ESTs; SH3,Ribosomal_S3Ae; 4.68
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone COL04544; pkinase,Furin-like,Recep_L_domain;none; 4.68
 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subunit, non-ATPase, 11; CDK5_activator,PCI;none; 4.67
 425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C;TM=M; 4.67
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 4.67
 453476; A1640500; Hs.24633; SAM domain, SH3 domain and nuclear localisation signals, 1; SH3,SAM;SS=M; 4.67
 412926; A1879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; MARCKS;SS=M; 4.67
 424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fis, clone PLACE1001076; pkinase,Furin-like,Recep_L_domain;none; 4.66
 446051; BE048061; Hs.37054; ephrin-A3; Ephrin,A_deamin,dsrm,z-elpha; 4.66
 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.66
 408024; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, member 3; Y_phosphatase;TM=M; 4.66
 435542; AA687376; ; ESTs; SH3,jg,pkinase,PH,spectrin,RhoGEF;none; 4.66
 429682; NM_006306; Hs.211602; SMC1 (structural maintenance of chromosomes 1, yeast)-like 1; ABC_tran,SMC_N,SMC_C,KID;TM=M; 4.66
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 4.66
 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_CAT_hook,SNF2_N;TM=M; 4.65
 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1;TM=M; 4.65
 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;SS=M; 4.65
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M; 4.64
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-family A (ABC1), member 4; ABC_tran,SRP54;TM=Y;SS=M; 4.64
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M; 4.63
 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M; 4.63
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 (aryltrold potentiating activity, collagenase inhibitor); TIMP,pkinase,DAG_PE-bind,RBD; 4.63
 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGK;TM=M; 4.63
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ehand,ldl_recept_a;SS=M; 4.62
 442590; AJ002688; Hs.130313; ESTs; none,Y_phosphatase,Band_41,connexin; 4.62
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding domain; ehand;SS=M; 4.62
 423740; U07701; Hs.293007; aminopeptidase puromycin sensitive; Peptidase_M1,Armaddillo_seg; 4.61
 429300; AB011108; Hs.198891; serine/threonine-protein kinase PRP4 homolog; pkinase;TM=M; 4.60
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.60
 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activated protein kinase 2; pkinase;TM=M; 4.60
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPC; 4.59
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); EGF,lectin_c,sushi;TM=M;SS=M; 4.59
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 4.59
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;SS=M; 4.59
 447312; AL434345; Hs.36908; activating transcription factor 1; rrm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIA,AT_hook,SAM;TM=M; 4.58
 435254; AW194689; Hs.30778; ESTs; pkinase,Bacterial_PQO;none; 4.58
 426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone HRC06741; Esterase,anolase,Peptidase_S8;TM=M; 4.58
 421685; AF189723; Hs.106778; ATPase, Ca transporting, type 2C, member 1; Cation_ATPase_C,Cation_ATPase_N,E1-E2_ATPase,Hydrolase,XPG_N;TM=Y;; 4.58
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; fn3,jg,Y_phosphatase,MAM;TM=Y;SS=M; 4.58
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frtzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.57
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200; none;none; 4.57
 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; pkinase;SS=M; 4.57
 423184; NM_004428; Hs.1624; ephrin-A1; Ephrin;TM=M;SS=M; 4.56
 443920; AL037764; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 4.56
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced, 68kD; Fasclidin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.56
 418869; AW516655; ; gb:cx01d05.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone 3' similar to contains Alu repetitive element ;contains element MER11 repetitive element ;, mRNA sequence; none,RasGAP,WW,IQ; 4.56
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus receptor; SPX,EXS;TM=Y;; 4.56
 437157; BE048860; Hs.120655; ESTs; IRK;none; 4.55
 422769; AA938905; Hs.120017; olfactory receptor, family 7, subfamily E, member 38 pseudogene; none;none; 4.55
 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc;TM=M; 4.55
 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PLACE1002962; 7tm_1;none; 4.55
 421140; AA298741; Hs.102135; signal sequence receptor, delta (translocon-associated protein delta); none;TM=Y;SS=M; 4.55
 406364; ; Target Exon; hexapep;TM=M; 4.55
 434682; AA827165; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig;none; 4.54
 438939; H21012; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5_F8_type_C,pkinase,Ets;none; 4.54
 433433; BE545277; Hs.340959; Tc translation elongation factor, mitochondrial; EF_TS,UBA; 4.54
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiose;SS=M; 4.54
 408958; AK001868; Hs.49344; hypothetical protein FLJ11006; ion_trans;TM=Y;; 4.54
 416847; L43321; Hs.80261; enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related); SH3;TM=M; 4.53
 410226; A1831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M; 4.53
 422753; BE528995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); Sm;SS=M; 4.52
 418355; L42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; E1-E2_ATPase,Cation_ATPase_N,Hydrolase;TM=Y;; 4.52
 400261; ; Eos Control; ig,MHC_IL_beta;TM=Y;SS=M; 4.52
 444633; AF111713; Hs.285218; junctional adhesion molecule 1; ig;TM=Y;SS=M; 4.52
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo sapiens cDNA, mRNA sequence; Sec7,PH,ANF_receptor,Ilg_chan,WD40,IRK; 4.52

- 400303; AA242758; Hs.79135; LIV-1 protein, estrogen regulated; none;none; 4.51
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M; 4.51
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin;TM=M; 4.51
 5 457906; AW975939; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 4.51
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 4.51
 429690; AW956329; Hs.23721; ESTs; none,sugar_tr,Ribosomal_S25; 4.50
 424618; L29472; Hs.1802; major histocompatibility complex, class II, DO beta; Ig,MHC_II_beta;TM=Y;SS=M; 4.50
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 4.50
 10 405490; ; NM_031414;Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA.; pkinase,TUDOR;TM=M; 4.50
 424494; U78575; Hs.149255; phosphatidylinositol-4-phosphate 5-kinase, type I, alpha; PIP5K;SS=M; 4.50
 441031; AJ110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 4.50
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22_Claudin;none; 4.50
 410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; SH2_Y_phosphatase,DSPc;TM=M; 4.50
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 4.50
 15 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y; 4.49
 425209; AL049781; Hs.155140; casein kinase 2, alpha 1 polypeptide; pkinase,ABC1;TM=M; 4.49
 425695; NM_005401; Hs.159238; protein tyrosine phosphatase, non-receptor type 14; Y_phosphatase,Band_41,DSPc;TM=M; 4.49
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 4.49
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanesa,DSPc;SS=M; 4.48
 20 400755; AA635062; ; Homo sapiens mRNA; cDNA DKFp434O0515 (from clone DKFp434O0515); zf-C3HC4,CARD,BIR;TM=M; 4.48
 425566; AW162943; Hs.250618; UL16 binding protein 2; ktl_recept_aPKD,MHC_1;TM=M;SS=Y; 4.48
 410151; X15723; Hs.59242; paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein); Peptidase_S8,P;TM=Y;SS=M; 4.48
 423536; L22075; Hs.1666; guanine nucleotide binding protein (G protein), alpha 13; UCR_hinge,G-alpha,arf;TM=M; 4.48
 25 424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2,HRM;TM=Y;SS=M; 4.48
 427878; C05766; Hs.181022; CGI-07 protein; none,zf-C2H2; 4.48
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 4.48
 422605; H16646; Hs.118666; hypothetical protein PP591; PAPS_reduct,MoCF_biosynth.; 4.47
 410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]; SH3,PDZ,Guanylate_kin;none; 4.47
 30 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc;TM=M; 4.47
 410032; BE065985; ; gb:RC3-BT0319-120200-014-a09 BT0319 Homo sapiens cDNA, mRNA sequence; abhydrolase_2;none; 4.46
 423078; M35198; Hs.123125; integrin, beta 6; Integrin_B,EGF_pp-binding;TM=Y;SS=M; 4.46
 400263; ; Eos Control; GTP_EFTU,EGF_C,GTP_EFTU_D2,serpin;TM=M; 4.46
 441406; Z45957; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M; 4.45
 35 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; none;TM=M; 4.45
 413227; M79082; ESTs; none;none; 4.45
 441321; H17182; Hs.7771; B-cell associated protein; Band_7;TM=M; 4.45
 457194; H20669; Hs.35406; ESTs, Highly similar to unnamed protein product [H.sapiens]; none,pkinase,PBD; 4.45
 414745; AA160511; Hs.5326; amino acid system N transporter 2; porcupine; none;none; 4.45
 40 404276; ; NM_002944;Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; tn3,pkinase,DUF139;TM=Y;SS=M; 4.45
 426966; AJ493134; ; sclerostin; DAN;TM=M;SS=M; 4.45
 408873; AL046017; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none;none; 4.44
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFp586B0220 (from clone DKFp586B0220); pkinase;none; 4.44
 432798; AA565309; Hs.194015; ESTs; Integrin_B,Sema,PSI,TIG;none; 4.44
 439668; AJ091277; Hs.302634; fizzled (Drosophila) homolog 6; Fizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.44
 45 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor;none; 4.43
 452098; AI858183; ; gb:W46a12.x1 NCL_CGAP_U1 Homo sapiens cDNA clone 3' similar to contains Alu repetitive element, mRNA sequence; SH3;none; 4.43
 426874; M67325; Hs.347487; ESTs; SH3,TonB_boxC;none; 4.43
 422714; AB018335; Hs.119387; KIAA0792 gene product; DUF221;TM=Y;SS=M; 4.42
 50 410741; Z11695; Hs.324473; mitogen-activated protein kinase 1; pkinase;none; 4.42
 432193; AA372264; Hs.273193; hypothetical protein FLJ10706; pkinase;TM=M; 4.41
 409506; NM_006163; Hs.54689; NCK adaptor protein 1; SH2,SH3;TM=M; 4.41
 429390; AB040942; Hs.201500; KIAA1509 protein; none;TM=M; 4.41
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArlGap;SS=M; 4.41
 55 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none;none; 4.41
 421748; NM_014718; Hs.107809; KIAA0726 gene product; cadherin;TM=Y; 4.40
 410416; BE410072; Hs.63304; protein phosphatase methyltransferase-1; none;TM=M; 4.40
 460457; AA367701; Hs.6639; KIAA1624 protein; none;TM=M;SS=M; 4.40
 433029; NM_014322; Hs.279926; opsin 3 (encephalopsin); 7tm_1,Monoxygenase;TM=Y;SS=M; 4.40
 60 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase;TM=M; 4.40
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1;TM=Y;SS=M; 4.40
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; SPRY,BAG,UPF0001; 4.40
 451154; AA015879; Hs.33536; ESTs; TIMP;none; 4.40
 433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase kinase 4; pkinase,zf-C4,CNH,ERM;TM=M; 4.40
 65 422034; AC008488; Hs.333069; Ets2 repressor factor; Ets;TM=M; 4.39
 444009; AJ380792; Hs.135104; ESTs; TNFR_c6,TIL;none; 4.39
 420020; BE295866; Hs.94382; adenosine kinase; ptkB;SS=M; 4.39
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, complete cds; none;TM=Y;SS=M; 4.39
 417655; AA780791; Hs.14014; hypothetical protein FLJ14813; pkinase,pkinase_C;TM=M; 4.39
 70 402915; ; ENSP00000202587; Bicarbonate transporter-related protein BTR1.; HCO3_cotransp;TM=Y; 4.39
 453199; AJ336266; Hs.32353; mitogen-activated protein kinase kinase kinase 4; pkinase;TM=M; 4.38
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 4.38
 453672; U73531; Hs.34528; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.38
 437852; BE001838; Hs.256897; ESTs, Weakly similar to dJ365012.1 [H.sapiens]; GPS,7tm_2;TM=Y; 4.38
 420039; NM_004605; Hs.94581; sulfotransferase family, cytosolic, 2B, member 1; Sulfotransfer;SS=M; 4.38
 75 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23005 fis, clone LNC00414; 7tm_1;none; 4.38
 452203; X57522; ; transporter 1, ATP-binding cassette, sub-family B (MDR/TAP); ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 4.37
 425317; AW205118; Hs.210546; interleukin 21 receptor; none;TM=Y;SS=M; 4.37
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.37
 80 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fs, clone Y79AA1001384, highly similar to Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA; none;none; 4.37
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M; 4.37
 412596; AA161219; Hs.799; diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor); EGF;TM=Y;SS=M; 4.38
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; tn3;SS=M; 4.36

- 432987; A1864771; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none; TM=Y; SS=M; 4.36
- 436943; AA773838; Hs.5353; caspase 10, apoptosis-related cysteine protease; ICE_p10, ICE_p20, DED; TM=M; 4.36
- 457897; A1356125; Hs.345168; ESTs; Weakly similar to HXA2_HUMAN HOMEBOX PROTEIN HOX-A2 [H.sapiens]; homeobox; NA; NA; 4.36
- 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); Sema, pkinase, TIG, PSI; none; 4.36
- 5 413969; X14034; Hs.75548; phospholipase C, gamma 2 (phosphatidylinositol-specific); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; SS=M; 4.35
- 408101; AW958504; Hs.123073; CDC2-related protein kinase 7; none; none; 4.35
- 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); Man-6-P_recep; TM=M; SS=M; 4.35
- 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; aldo_kal_red; none; 4.35
- 438937; AW952654; Hs.244624; ESTs; EPH_b, pkinase, fn3, SAM; none; 4.35
- 10 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; none; lectin_c; 4.35
- 436540; BE397032; Hs.14468; hypothetical protein MGC14226; rrm, 7tm_1, SNF; TM=M; 4.34
- 435267; N23797; Hs.110114; ESTs; none; Syja_N, Exo_endo_phos; 4.34
- 405616; ; Target Exon; none; SH3, BAR; 4.34
- 432141; BE410964; Hs.272738; nuclear receptor binding protein; pkinase; TM=M; 4.33
- 15 417927; R73095; Hs.24122; ESTs; none; pkinase; 4.33
- 429849; U33053; Hs.2499; protein kinase C-like 1; pkinase, pkinase_C, HR1; TM=M; 4.33
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y; 4.33
- 453863; X02544; Hs.572; orosomucoid 1; lipocalin, oxidized, ubiquitin, JRC; SS=M; 4.33
- 20 400847; ; NM_003105; Homo sapiens soritin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, Jld_recep, Ldl_recep, b, granulin, BNR; TM=Y; SS=M; 4.33
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT, FATC, PI3, PI4_kinase; TM=M; 4.33
- 413858; NM_001610; Hs.75589; acid phosphatase 2, lysosomal; acid_phosphat; TM=Y; SS=M; 4.33
- 442539; AL119506; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP, adenylylatekinase; 4.33
- 25 419507; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4; TM=M; 4.32
- 436703; AW880614; Hs.146381; RNA binding motif protein, X chromosome; rrm, SH3, PH, CH, RhoGEF; 4.32
- 414899; AW975433; Hs.36288; ESTs; pkinase, SH2, SH3; none; 4.32
- 444895; A1674383; Hs.22691; solute carrier family 7 (cationic amino acid transporter, y system), member 8; ASC, death, TNFR_c6; 4.31
- 30 415135; AW673559; Hs.78040; KDE1 (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; ER_lumen_recept; none; 4.31
- 444070; NM_015367; Hs.10267; MIL1 protein; Bcl-2; TM=Y; 4.31
- 422611; AA158177; Hs.118722; fucosyltransferase 8 (alpha (1,6) fucosyltransferase); SH3, K-box; TM=M; SS=Y; 4.31
- 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; bromodomain; TM=M; 4.30
- 440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; sugar_tr; TM=Y; SS=M; 4.30
- 35 414080; AA135257; Hs.47783; B aggressive lymphoma gene; A1pp; TM=M; 4.30
- 415072; BE253687; Hs.77876; Homo sapiens, clone IMAGE:3461982, mRNA, partial cds; Metallophos, Armadillo_seg; TM=M; 4.30
- 442994; A1026718; Hs.16954; ESTs; ank, pkinase, death, Ribosomal_S14; 4.30
- 432328; AJ572739; Hs.195471; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3; PGAM, 6PF2K; TM=M; 4.29
- 439490; AW249197; Hs.100043; ESTs; Weakly similar to A46302 PTB-associated splicing factor, long form [H.sapiens]; none; TM=M; 4.29
- 422005; BE266558; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212); none; Na_H_Exchange; 4.29
- 40 415214; A445236; Hs.125124; EphB2; fn3, pkinase, SAM, EPH_b; TM=Y; SS=M; 4.29
- 430316; NM_000875; Hs.239176; insulin-like growth factor 1 receptor; fn3, Furin-like, pkinase, Recep_L_domain; TM=M; SS=M; 4.29
- 429099; BE439952; Hs.196177; phosphotyrosine kinase, gamma 2 (latis); pkinase, Bac_DNA_binding; TM=M; 4.29
- 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 4.28
- 437603; AW979259; Hs.293673; ESTs; death; none; 4.28
- 45 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triphosphate pyrophosphatase); Ham1p_like; TM=M; 4.28
- 424512; X53002; Hs.149846; Integrin, beta 5; Integrin_B, EGF; TM=Y; SS=M; 4.28
- 442980; AA857025; Hs.8878; kinesin-like 1; Kinesin, Luteo_ORF3, DUF164; TM=M; 4.28
- 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetraspan NET-7); transmembrane4; TM=Y; SS=M; 4.27
- 50 409582; R27430; Hs.271565; ESTs; none; Neur_chan_LBD, Neur_chan_memb; 4.27
- 439096; AA830185; ; ESTs; ras; none; 4.27
- 414561; A1064813; Hs.195155; Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds; Aa_trans; TM=Y; 4.27
- 411835; U29343; Hs.72550; hyaluronan-mediated motility receptor (RHAMM); bZIP; SS=M; 4.27
- 428781; AF164789; Hs.193384; putative 28 kDa protein; pkinase, DAG_PE-bind, pkinase_C, OPR; SS=M; 4.27
- 55 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4, zf-RanBP, pkinase; 4.27
- 415149; X12451; Hs.78056; calthopsin L; Peptidase_C1; SS=M; 4.26
- 444838; AV651680; Hs.208558; ESTs; Integrin_A, FG-GAP; none; 4.26
- 402328; ; Target Exon; pkinase; TM=M; 4.26
- 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none; none; 4.26
- 60 420942; H03514; Hs.15589; ESTs; none; pkinase; 4.26
- 453902; BE502341; Hs.3402; ESTs; none; none; 4.26
- 425505; AL036458; ; gb-DKFZp564D2062_r1 564 (synonym: hibr2) Homo sapiens cDNA clone DKFZp564D2062.5, mRNA sequence; arf, G-alpha; none; 4.26
- 427344; NM_000859; Hs.2142; 5-hydroxytryptamine (serotonin) receptor 3A; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 4.26
- 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met-related tyrosine kinase); pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 4.26
- 65 417007; AF224741; Hs.80768; chloride channel 7; CBS, voltage_CLC; TM=Y; 4.26
- 447980; AW954377; Hs.26412; ring finger protein 26; zf-C3HC4; TM=Y; SS=M; 4.26
- 442300; A1765908; Hs.129166; ESTs; none; SS=M; 4.25
- 421856; NM_016447; Hs.108931; MAGUK protein p57; Protein Associated with Lns 2; SH3, PDZ, Guanylate_kin, L27; TM=M; 4.25
- 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PLACE1010076; pkinase, Activin_recp; none; 4.25
- 70 422451; AA310753; Hs.42491; ESTs; Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; PDZ, SH2, STAT, STAT_bind, STAT_prot; none; 4.25
- 453955; AW579207; Hs.304666; ESTs; Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; fn3, Ig, MAM; none; 4.25
- 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substrate; SH3; TM=M; 4.25
- 419133; U46116; Hs.89627; protein tyrosine phosphatase, receptor type, G; fn3, Y_phosphatase, carb_anhydrase, DSPc; TM=Y; SS=M; 4.25
- 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; aa_permeases; TM=Y; SS=M; 4.25
- 75 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; 4.24
- 416440; A1823912; Hs.79335; Homo sapiens, Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1, clone MGC:15280, mRNA, complete cds; SWIB; TM=M; 4.24
- 419169; AW851980; Hs.262346; ESTs; Weakly similar to S72482 hypothetical protein [H.sapiens]; none, spectrin, SH3, PH, CH; 4.24
- 449444; AW818436; Hs.23590; solute carrier family 16 (monocarboxylic acid transporters), member 4; none; TM=Y; SS=M; 4.24
- 80 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carb_OpepL_Propep_M14; SS=M; 4.24
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glucose transporter), member 10; sugar_tr; TM=Y; SS=M; 4.24
- 412681; AW983555; Hs.172004; Ulin; fn3, Jg, SGXSG, pkinase; TM=M; 4.24
- 424653; AW977534; Hs.151469; calcium/calmodulin-dependent serine protein kinase (MAGUK family); none; none; 4.24
- 421066; AU076725; Hs.101408; branched chain aminotransferase 2, mitochondrial; aminotran_4; 4.23

- 428338; AF147765; Hs.232093; ESTs; fn2, C1MR; TM=M; SS=M; 4.23
 443329; BE262943; Hs.9234; hypothetical protein MGC1936; none; TM=Y; SS=M; 4.23
 432314; AA533447; Hs.312989; ESTs; Xlink; none; 4.23
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none; TM=M; 4.23
 454166; AW93356; Hs.265814; sprouty (Drosophila) homolog 4; SH2, SH3; TM=M; SS=M; 4.23
 442596; A457102; Hs.347970; Human glucose transporter pseudogene; none; none; 4.23
 442549; A1751601; Hs.8375; TNF receptor-associated factor 4; MATH, zf-TRAF, zf-C3HC4; SS=M; 4.22
 424154; AF026004; Hs.141660; chloride channel 2; voltage, CLC, CBS, EPO, TPO, PC, rep; 4.22
 433419; A1830342; Hs.211272; ESTs; transmembrane4; none; 4.22
 421921; H83363; Hs.6820; translocase of inner mitochondrial membrane 10 (yeast) homolog; zf-Tim10, DDP, ethand, CH, spectrin, serpin; TM=M; 4.22
 445633; A453386; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK; none; 4.22
 424812; AF059252; Hs.153299; DOM-3 (C. elegans) homolog 2; none; TM=M; 4.22
 410668; BE379794; Hs.65403; hypothetical protein; death, TNFR, c6; TM=Y; SS=M; 4.22
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic acid transporters), member 6; none; none; 4.22
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; 4.21
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; none; none; 4.21
 400208; ; Eos Control; FCH, RhoGAP, SH3; TM=M; 4.21
 405369; ; NM_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA; pkinase, LIM, PDZ; SS=M; 4.21
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase, 2; TM=M; 4.21
 441208; A1339704; Hs.150401; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ion, trans, RYDR, TPR, MIR; none; 4.21
 427217; AA399272; Hs.144341; ESTs; ANP, GHMP, kinases; none; 4.21
 400845; ; NM_003105; Homo sapiens sortilin-related receptor, L (OLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.21
 422667; H25642; ; ESTs; FMO-like, FMO-like; 4.21
 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus]; ABC, tran, ABC, membrane, Ig, MHC, IL, beta, SRP54, proteasome, ABC, membrane, ABC, tran; 4.20
 448950; AF288887; Hs.9275; CG-152 protein; E1-E2, ATPase, Hydrolase; TM=Y; 4.20
 408634; AW407254; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none; none; 4.20
 422335; AA375957; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none; none; 4.20
 426754; NM_014264; Hs.172052; serine/threonine kinase 18; pkinase; TM=M; 4.20
 435810; BE349853; Hs.2785; keratin 17; zf-Tim10, DDP, SH2, SH3, pkinase, PH, BTK, Ribosomal, L44; 4.20
 446143; BE245342; Hs.306079; sec61 homolog; NUDD, secY, E1, dehydrog, transket, pyr; TM=Y; SS=M; 4.20
 426626; A124572; Hs.323879; inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; zf-C2H2; TM=M; 4.20
 403716; ; Target Exon; Adap, comp, sub, PDZ, DEP, DIX, Dishevelled, hexapep, W2, ABC, tran; 4.19
 415749; BE262529; Hs.78771; phosphoglycerate kinase 1; PGK; none; 4.19
 434599; AB002313; Hs.3989; plexin B2; PSI, Sama, TIG; NA; 4.19
 412600; L28824; Hs.74101; spleen tyrosine kinase; SH2, pkinase; 4.19
 416738; N29218; Hs.40290; ESTs; ABC, tran, ABC, membrane; none; 4.19
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD, helicase, C, PRK, AIP3; TM=M; 4.19
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none; none; 4.19
 407305; AA715284; ; gbnv35f03.r1 NL_CGAP_Br5 Homo sapiens cDNA clone similar to contains Alu repetitive element, mRNA sequence; pkinase, integrin, B, Sama, PSI, TIG; none; 4.18
 452880; AA029332; Hs.87549; ESTs; none; integrin, B; 4.18
 428245; AF151046; Hs.183180; anaphase promoting complex subunit 11 (yeast APC11 homolog); none; SS=M; 4.18
 421964; X73079; Hs.288579; polymeric immunoglobulin receptor; Ig, Cobalamin, bind; TM=M; SS=M; 4.18
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2, SH3, pkinase; TM=M; 4.18
 421790; AW986201; Hs.22654; sodium channel, voltage-gated, type I, alpha polypeptide; ion, trans, IQ, PEP-utilizers, C; TM=Y; 4.18
 429668; AA626142; Hs.179991; ESTs, Weakly similar to S28942 protein kinase C [H.sapiens]; none; none; 4.18
 443068; A188710; ; ESTs; Endonuclease, pkinase, Activin, recp; none; 4.18
 418827; BE327311; Hs.47166; HT021; none; TM=M; 4.18
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine protease; ICE, p10, ICE, p20, DED; TM=M; 4.18
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3, OPR, PX; TM=M; 4.18
 422083; NM_001141; Hs.111258; arachidonate 15-lipoxygenase, second type; none; none; 4.18
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; SS=M; 4.18
 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like 1; SH2, SAM, Exo, endo, phos; SS=M; 4.18
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53, WD40, IRK; TM=M; 4.17
 421838; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none; none; 4.17
 431544; AK000770; Hs.299329; Homo sapiens cDNA FLJ20763 fis, clone COL09911; none; none; 4.17
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; CBS, IMPDH, C, IMPDH, N, NP; TM=M; 4.17
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin, DNA, topoisom, V, K-box; TM=M; 4.17
 425606; U52112; Hs.158331; renin-binding protein; none; 4.16
 416817; AA398045; Hs.104679; ESTs; Furin-like, pkinase, Recep, L, domain, fn3; none; 4.16
 402447; ; C1000201.gil204416[gb]AAA02627.1 [L05195] fructose transporter [Rattus norvegicus] p144; none; TM=Y; SS=M; 4.16
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; Euk, porin; TM=M; SS=M; 4.15
 426395; BE151985; Hs.5722; hypothetical protein FLJ23316; pkinase; none; 4.15
 404140; ; NM_006510; Homo sapiens ret finger protein (RFP), transcript variant alpha, mRNA; zf-C3HC4, SPRY, zf-B, box; SS=M; 4.15
 432268; BE311856; Hs.274230; 3-phosphoadenosine 5-phosphosulfate synthase 2; APS, kinase, ATP-sulfurylase; TM=M; 4.15
 405516; ; ENSP00000200457; Thyroid receptor interacting protein 6 (TRIP6) (OPA-interacting protein 1) (Zyrd related protein 1) (ZRP-1); LIM; TM=M; 4.15
 448390; AL035414; Hs.21068; hypothetical protein; FGGY, C; TM=M; 4.15
 435732; AF229178; Hs.123136; leucine rich repeat and death domain containing protein; none; none; 4.15
 414108; A1267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxysterol, BP, pkinase; TM=M; 4.15
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor, pi; Neur, chan, LBD, Neur, chan, memb; TM=Y; SS=M; 4.14
 424339; BE257148; Hs.145416; endoglycan; none; TM=Y; SS=M; 4.14
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog; Ig, pkinase; TM=Y; SS=M; 4.14
 440524; R71264; Hs.16798; ESTs; SH3, Ig, pkinase, PH, spectrin, RhoGEF; none; 4.14
 436115; AW512033; Hs.102004; ESTs; pkinase; none; 4.14
 447050; NM_016314; Hs.17200; STAM-like protein containing SH3 and ITAM domains 2; SH3, VHS, UIM; SS=M; 4.14
 418529; AW005695; Hs.250897; TRK-fused gene; Band, 41, ERM, pkinase, LRR, LRRCT, JAM, Nucleoplasm, Tropomyosin, OPR, filament, bZIP, G-gamma, M, DUF164; TM=M; 4.14
 420727; H75701; Hs.99886; complement component 4-binding protein, beta; sush; SS=M; 4.14
 433075; NM_002959; ; sortilin 1; Exo, endo, phos, Atrophin-1, BNR, Kelch; TM=M; 4.14
 422783; AA598956; Hs.120439; ethanolamine kinase; Choline, kinase; TM=Y; 4.14
 410726; A1623859; Hs.15936; ESTs; pkinase, pro, isomerase; none; 4.14

- 417903; NM_002342; Hs.1116; lymphotxin beta receptor (TNFR superfamily, member 3); TNFR_c6; TM=M; SS=M; 4.14
- 428307; W27393; Hs.183648; protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1; SAM,SH3,HS1_rep; 4.14
- 442434; AA959787; Hs.129583; ESTs; IRK:none; 4.13
- 5 438361; AA805668; Hs.146217; Homo sapiens cDNA: FLJ23077 fis, clone LNG05840; pkinase,kinase_C:none; 4.13
- 445580; AF167572; Hs.12912; skb1 (S. pombe) homolog; none; SS=M; 4.13
- 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehfand,kazal,erf,ras,7tm_1; TM=M; 4.13
- 400252; ; NM_004651; Homo sapiens ubiquitin specific protease 11 (USP11), mRNA, substrate 1 (PTPNS1), mRNA; UCH-1,UCH-2; TM=M; 4.13
- 446641; AL049229; Hs.15787; Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone DKFZp564O1016); none,pkinase,PBD; 4.13
- 10 400209; ; NM_001668; Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA, VERSION NM_006083.2 Gt; FCH,RhoGAP,SH3; TM=M; 4.13
- 428012; AW629596; Hs.194726; BCL2-associated atlanogene 4; Sm,BAG; SS=M; 4.13
- 411826; AW947946; Hs.26706; CGI-121 protein; none,OSP; 4.13
- 423189; M59371; Hs.171596; EphA2; fn3,pkinase,SAM,EPH_1bd; TM=Y; SS=M; 4.12
- 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; Integrin_B,Glyco_hydro_56; SS=M; 4.12
- 414874; D26351; Hs.77515; inositol 1,4,5-triphosphate receptor, type 3; Ion_trans,MIR,RYDR,ITPR; TM=Y; 4.12
- 15 432047; NM_016247; Hs.272380; Interphotoreceptor matrix proteoglycan 200; EGF,SEA; TM=Y; SS=M; 4.12
- 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 4.12
- 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; zf-C2H2,BTB,K_Ietra,WD40,Syntaxin; 4.12
- 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK-2); pkinase,Activin_rec; TM=M; SS=M; 4.12
- 20 405110; ; C7000189; gij12643960[sp]Q9Y6T7[KDGB_HUMAN DIACYLGLYCEROL KINASE, BETA (DIGLYCERIDE KINASE ; none,none; 4.12
- 414026; AW179058; Hs.99858; ribosomal protein L7a; pkinase,LRR,LRRCT,Ribosomal_L7Aa; none; 4.11
- 443142; AI696513; Hs.108705; protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform; HEAT,Vitellogenin_N,HEAT_PBS; SS=M; 4.11
- 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg; TM=M; 4.11
- 459601; AL044470; Hs.270504; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [Hsapiens]; none,SH3,PGAM,UBA; 4.10
- 25 417300; AI765227; Hs.55610; solute carrier family 30 (zinc transporter), member 1; Cation_efflux; TM=Y; SS=M; 4.10
- 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (from clone DKFZp564N0763); none,spectrin,SH3,PH,CH; 4.10
- 416239; AL038450; Hs.48948; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase; none; 4.10
- 429311; AF080157; Hs.198998; conserved helix-loop-helix ubiquitous kinase; pkinase; none; 4.10
- 30 412148; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); Exo_endo_phos,Altophin-1,BNR,Kelch; TM=M; 4.10
- 418402; AW604405; Hs.324874; hypothetical protein MGC3079; Phosphodiesterase; TM=Y; 4.10
- 434396; AA632270; Hs.162851; Homo sapiens cDNA FLJ14317 fis, clone PLACE3000401; pkinase; none; 4.10
- 454438; AA224053; Hs.172405; cell division cycle 27; SPRY,7tm_3,ANF_receptor; 4.10
- 439578; AW263124; Hs.315111; nuclear receptor co-repressor/HDAC3 complex subunit; WD40; TM=M; 4.10
- 451995; AI827431; Hs.224645; ESTs, Weakly similar to IF16_HUMAN GAMMA-INTERFERON-INDUCIBLE PROTEIN IF1-16 [H.sapiens]; none,PAAD,DAPIN,HIN; 4.10
- 35 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 complex); ITAM; TM=M; SS=M; 4.10
- 442942; AW167087; Hs.131562; ESTs; pkinase; none; 4.09
- 428187; AI687303; Hs.285529; G protein-coupled receptor 49; 7tm_1; none; 4.09
- 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function); Phosphodiesterase; TM=Y; SS=M; 4.09
- 416445; AL043004; Hs.79337; KIA0135 protein; pkinase,PAS; TM=M; 4.08
- 40 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2; pkinase; TM=M; 4.08
- 403608; ; C3001199; gij7494834[br]T15308 hypothetical protein B02862 - Caenorhabditis elegans [J41; 7tm_1,7tm_2,GPS,WIF; TM=Y; SS=M; 4.08
- 427177; AB006537; Hs.173880; interleukin 1 receptor accessory protein; Ig,TIR; TM=Y; SS=M; 4.08
- 401241; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139; SS=M; 4.07
- 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel regulator; WW,HECT,RNA_pol_A; none; 4.07
- 45 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 4.06
- 426006; R49031; Hs.22627; ESTs; pkinase,TBC; 4.06
- 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB; TM=M; 4.06
- 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not available 7496841) [C.elegans]; 7tm_1; none; 4.05
- 50 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD,DAPIN,HIN; SS=M; 4.05
- 413109; AW389845; Hs.110855; ESTs; PHO4; none; 4.05
- 426457; AW894667; Hs.169965; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2; TM=M; 4.05
- 435730; AB020635; Hs.4984; KIA0082B protein; AdoHcyase,TrkA-N_2-HadD_DHL_C; TM=M; 4.04
- 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase); CARD,ICE_p10,ICE_p20; SS=M; 4.04
- 55 444378; R41339; Hs.12569; ESTs; Ig,pkinase,LRR,LRRNT,LRRCT; none; 4.04
- 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; none; TM=Y; SS=M; 4.04
- 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1; none; 4.04
- 413095; AA494359; Hs.30716; potassium voltage-gated channel, Isk-related family, member 3; none,START; 4.04
- 418540; AI821597; Hs.90877; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [Hsapiens]; ank,CAP_GLY,7tm_1; 4.03
- 60 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rm,IRK; SS=M; 4.02
- 448659; AF191838; Hs.21712; TANK-binding kinase 1; pkinase; TM=M; 4.02
- 412935; BE267045; Hs.76084; tubulin-specific chaperone c; none; 4.02
- 414844; AA296874; Hs.77494; deoxyguanosine kinase; dNK; 4.02
- 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; 4.02
- 65 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interacting); SH3,Ig,pkinase,PH,spectrin,RhoGEF; TM=M; 4.02
- 420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind; none; 4.02
- 405102; ; C15001220; gij4469558[gb]AAD21311.1 [AF126008] breast cancer nuclear receptor-binding aux; DAG_PE-bind,PH,RhoGEF,DC1; SS=M; 4.02
- 439964; AI732902; Hs.124652; Homo sapiens cDNA FLJ12376 fis, clone MAMMA1002494; pkinase; none; 4.01
- 429680; AL035754; Hs.2474; toll-like receptor 1; LRR,LRRCT,TIR; TM=M; SS=M; 4.01
- 70 453891; AB037751; Hs.38353; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1035904; none,none; 4.01
- 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 3.99
- 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase,DAG_PE-bind,PH; TM=M; 3.99
- 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none,none; 3.98
- 449517; AW500106; Hs.23643; serine/threonine protein kinase MASK; pkinase; TM=M; 3.98
- 75 404185; ; Target Exon; sugar_in; TM=Y; SS=M; 3.98
- 441226; BE663042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; none; TM=M; 3.98
- 429538; AI916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP,Tropomyosin,spectrin,LBP_BPL_CETP,B56; TM=Y; SS=M; 3.97
- 417386; AL037228; Hs.82043; D123 gene product; NUDIXsecY,E1_dehydro,transket_Pyr; TM=Y; SS=M; 3.97
- 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; MORN,sugar_tr; TM=Y; SS=M; 3.96
- 80 417183; R52089; Hs.172717; ESTs; pkinase,LRRCT,Ig,LRR,LRRNT; none; 3.95
- 439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; none; TM=M; 3.94
- 424490; AJ278016; Hs.55565; ankryrin repeat domain 3; ank,pkinase; TM=M; 3.94
- 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, subfamily J, member 2; IRK; TM=Y; 3.94

- 450746; D82673; Hs.278589; general transcription factor II, ϵ , none; SH3, PX; 3.94
 418516; NM_008218; Hs.85701; phosphoinositide-3-kinase, catalytic, alpha polypeptide; PI3_P14_kinase, PI3K_C2, PI3K_rbd, PI3K_p85B; none; 3.94
 414217; AJ309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fls, clone LNC09846; none; NA; NA; 3.93
 416537; T99086; Hs.144904; nuclear receptor co-repressor 1; myb_DNA-binding, RNA_pol_A; none; 3.93
 450747; A064821; Hs.318535; ESTs, Highly similar to 1818357A EWS gene [H.sapiens]; mm, zf-RanBP, GAS2; 3.93
 444825; AW167613; ; mitogen-activated protein kinase kinase kinase 8; pkinase; TM=M; 3.93
 408354; AJ382803; Hs.159235; ESTs; none; none; 3.93
 453945; NM_005171; Hs.36908; activating transcription factor 1; mm, zf-RanBP, pkinase, GST_C, Ets, SAM_PNT, ABC2_membrane, myosin_head, IQ, Myosin_N, bZIP, C2H2, PHD, BTB, TFIIS, AT_hook, SAM; TM=M; 3.93
 428532; AF157326; Hs.184786; TBP-interacting protein; Armadillo_seg, VHS, HEAT; TM=M; 3.92
 413967; AW204431; Hs.117853; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Armadillo_seg, IBB, PHD, DDT; none; 3.91
 415906; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fls, clone HRC02860; Ephrin; none; 3.91
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none; none; 3.91
 440255; AI932285; Hs.160569; ESTs; none; pkinase; 3.90
 421077; AK000061; Hs.101590; hypothetical protein; ank, pkinase, death, SPRY, SAP, Ribosomal_L24e, SRP54, dDENN, DENN, uDENN; TM=M; 3.90
 433211; H11850; Hs.12808; MARK; pkinase, UBA, KA1; SS=M; 3.90
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3, zf-C3HC4; TM=M; 3.90
 419609; U46415; Hs.270379; gb:HSU46415 Human pancreatic cancer cell line Patu 8988; Homo sapiens cDNA clone xs476, mRNA sequence; PWWP; none; 3.90
 433198; AA992841; Hs.27263; KIAA1458 protein; none; none; 3.89
 407721; Y12735; Hs.38018; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3; pkinase; TM=M; 3.89
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none; TM=M; 3.89
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; none; none; 3.89
 446329; NM_013272; Hs.14805; solute carrier family 21 (organic anion transporter), member 11; kazal, OATP_N, OATP_C; TM=Y; SS=M; 3.89
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M; 3.88
 432074; AA525248; Hs.149723; ESTs; Y_phosphatase; none; 3.88
 435143; R12375; Hs.194600; ESTs; SH3, Jg, pkinase, PH, spectrin, RhoGEF; none; 3.87
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanesa; none; 3.87
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase; TM=M; 3.87
 418073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fls, clone NT2RP2002066, highly similar to Rattus norvegicus transmembrane receptor Unc5H2 mRNA; death, ZU5; SS=M; 3.86
 415457; AW081710; Hs.7369; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; MORN, sugar_br; TM=Y; SS=M; 3.86
 447061; D86984; Hs.17211; dedicator of cyto-kinesis 2; SH3; TM=M; 3.86
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC, PAS; TM=M; 3.86
 451961; NM_003800; Hs.27345; RNA guanylyltransferase and 5'-phosphatase; mRNA_cap_enzyme, DSPc, DNA_ligase, mRNA_cap_C; TM=M; 3.86
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-receptor type 2; Y_phosphatase; TM=Y; 3.86
 446874; AW968304; Hs.56156; ESTs; none; RGS; 3.85
 418630; AJ351311; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; pkinase; none; 3.85
 416140; AJ918035; Hs.301198; roundabout (axon guidance receptor, Drosophila) homolog 1; none; none; 3.85
 425474; Z48054; Hs.158084; peroxisome receptor 1; TPR; TM=M; 3.85
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membrane 20 (yeast) homolog; MAS20, zFA20, VPS9; TM=M; SS=M; 3.85
 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70; TM=M; 3.84
 428782; X12830; Hs.193400; Interleukin 6 receptor; fn3, Ig; TM=Y; SS=M; 3.84
 450684; AA872605; Hs.25333; Interleukin 1 receptor, type II; Ig; TM=Y; SS=M; 3.84
 433376; AJ249361; Hs.74122; caspase 4, apoptosis-related cysteine protease; CARD, ICE_p10, ICE_p20; SS=M; 3.83
 440332; AJ218517; Hs.188051; ESTs; fn3, pkinase, SAM, EPH_rbd; none; 3.83
 445803; AV655264; Hs.4283; ESTs; pkinase, RGS, PH, myosin_head, Myosin_tail; 3.83
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; 3.83
 414991; C17898; ; gb:C17898 Human placenta cDNA (Tfujwara) Homo sapiens cDNA clone GEN-554E10 5', mRNA sequence; Zip; none; 3.83
 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage); fn3; TM=Y; SS=M; 3.82
 419088; AJ538323; Hs.52620; integrin, beta 8; integrin_B; none; 3.82
 411704; AJ499220; Hs.71573; hypothetical protein FLJ10074; pkinase; TM=M; 3.82
 459346; AW510557; Hs.258016; EST; none; TM=M; 3.82
 445330; R52656; Hs.21691; ESTs; 7tm_1; none; 3.82
 451452; BE560065; Hs.26433; dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminophosphotransferase 1 (GlcNAc-1-P transferase); Glycos_transf_4; TM=Y; SS=M; 3.81
 405545; ; ; Target Exon; ABC_tran, SRP54, ABC_membrane; TM=Y; SS=M; 3.81
 448165; NM_005591; Hs.20555; meiotic recombination (S. cerevisiae) 11 homolog B; Metallophos, Ribosomal_L15e; SS=M; 3.81
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; Ig; TM=Y; SS=M; 3.80
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate transporter), member 1; PHO4, LIM; TM=M; 3.80
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg; SS=M; 3.80
 438581; AW977766; Hs.292133; ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase, RIO1; none; 3.79
 439199; R40373; Hs.26299; ESTs; ion_trans; none; 3.78
 450931; N26158; Hs.25648; tumor necrosis factor receptor superfamily, member 5; TNFR_c6; TM=Y; SS=M; 3.78
 417691; AU076610; Hs.82399; low density lipoprotein receptor defect C complementing; none; SS=M; 3.78
 430355; NM_006219; Hs.239818; phosphoinositide-3-kinase, catalytic, beta polypeptide; PI3_P14_kinase, PI3K_C2, PI3K_rbd, PI3K_p85B; TM=M; 3.78
 448119; H38587; Hs.346509; dedicator of cyto-kinesis 1; none; TM=Y; 3.78
 442013; AA506476; Hs.10600; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the splicing factor CC1.3 with a second isoform (CC1.; none; none; 3.77
 425481; AW978162; Hs.18571; ESTs; none; Oxysterol_BP; 3.77
 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA1330 protein [H.sapiens]; RNA_pol_A, Jg, MHCK_EF2_kinase; SS=M; 3.77
 426866; U02330; Hs.172816; neuregulin 1; Peptidase_M49, EGF, Ig, Neuregulin; TM=M; 3.77
 430396; D49742; Hs.241383; hyaluronan-binding protein 2; ank, death, ZU5, EGF, kringla, trypsin, Nebulin, LIM; SS=M; 3.77
 434398; AA121098; Hs.3838; serum-inducible kinase; pkinase, POLO_box; TM=M; 3.77
 415485; AW272990; Hs.18571; ESTs; none; Oxysterol_BP; 3.76
 453225; AA641926; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c; none; 3.76
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase, RIO1; TM=M; 3.76
 424842; AA034127; Hs.153487; signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; SH3, VHS, UIM; TM=M; 3.75
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, P-PLC-Y; TM=M; 3.75
 419952; AK000967; Hs.93872; KIAA1682 protein; none; TM=M; 3.75
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase, UBA, KA1; TM=M; 3.75
 431696; AA259068; Hs.267819; protein phosphatase 1, regulatory (inhibitor) subunit 2; none; SS=M; 3.75

- 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-26H20 on chromosome 20q13.1. Contains part of a gene for a novel protein similar to membrane transport proteins, the 5' end of a novel gene, ESTs, STSs, GSSs and three CpG Islands; pkinase, R01, APH, KOW; TM=M; 3.75
- 405411; ; ENSP00000252213: SODIUM BICARBONATE COTRANSPORTER; none; TM=Y; SS=M; 3.75
- 405602; ; Target Exon; pkinase; SS=M; 3.75
- 429355; AW973253; Hs.292689; ESTs; pkinase, bZIP, Armadillo_seg, none; 3.75
- 430153; AW968128; Hs.326679; ESTs; pkinase, none; 3.74
- 414180; A1863304; Hs.120905; Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391; P13_P14_kinase, P13Ka, P13K_C2, P13K_rbd, P13K_p85B, none; 3.74
- 432235; AA531132; ; gb:ncj47h06.s1 NC1_CGAP_P19 Homo sapiens cDNA clone, mRNA sequence; pkinase, none; 3.74
- 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds; none, spectrin, SH3, PH, CH; 3.74
- 426485; NM_006207; Hs.170040; platelet-derived growth factor receptor-like; Ig; SS=M; 3.74
- 408414; A114688; Hs.17998; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; tn3, Ig; TM=Y; SS=M; 3.73
- 409793; A1825463; Hs.147996; protein kinase, X-linked; pkinase, pkinase_C; TM=M; 3.73
- 412456; T32689; Hs.7859; ESTs; BAG, none; 3.73
- 407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase C-beta 1; C2, PI-PLC-Y, PI-PLC-X; TM=M; 3.73
- 442229; A1885776; Hs.8164; Multibrey nanism; MATH, DENN, GRAM, z1-B_box, dDENN, uDENN; SS=M; 3.73
- 450151; A1088196; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; Ig, pkinase, none; 3.72
- 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M; 3.72
- 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofillin_ADF; SS=M; 3.72
- 403391; ; C3001164; gij1730196[spl]P50573[GAR3_RAT GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT PRE; none; TM=Y; 3.72
- 417527; AA203524; ; gb:z55610.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone 5', mRNA sequence; SH3; SS=M; 3.71
- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase); pkinase; TM=M; 3.71
- 428180; A1129767; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; G-alpha, arf; TM=M; 3.71
- 422127; AW504286; Hs.112049; SET binding factor 1; dDENN, DENN, GRAM, PH; SS=M; 3.70
- 430570; A1417881; Hs.292484; ESTs; 7tm_2, Fz, Fritzzled, none; 3.70
- 452561; A1692181; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; 3.69
- 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm, pkinase; TM=M; 3.69
- 419945; AW290975; Hs.118923; ESTs; SH3, PDZ, Guanylate_kin, transferrin; 3.69
- 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3, PDZ, Guanylate_kin; TM=M; 3.68
- 436534; AA721628; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; Ig; TM=Y; SS=M; 3.68
- 407202; N58172; Hs.109370; ESTs; F5_F8_type_C, pkinase, Ets, none; 3.67
- 420297; A1628272; Hs.88323; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase, TUDOR, none; 3.67
- 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 3.67
- 425304; AA463844; Hs.31339; fibroblast growth factor 11; FGF, Neur_chan_LBD, Neur_chan_membr, none; 3.67
- 418318; U47372; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 3.67
- 419511; AA429750; Hs.75113; general transcription factor IIIA; Glypican, none; 3.66
- 424315; AW614850; Hs.193384; putative 28 kDa protein; none, none; 3.66
- 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; 3.66
- 425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein; none; TM=M; 3.65
- 446983; AA157484; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 3.65
- 434350; AL042940; Hs.93872; KIAA1682 protein; none, none; 3.65
- 457317; AA683016; Hs.12210; hypothetical protein FLJ13732 similar to tensin; SH2; TM=M; 3.65
- 434416; AA805903; Hs.59498; cell division cycle 2-like 5 (cholinesterase-related cell division controller); pkinase, none; 3.65
- 410174; AA306007; Hs.59461; DKFZP434C245 protein; none, DSPc; 3.65
- 423598; BE247600; Hs.155538; ESTs; 7tm_1; TM=Y; SS=M; 3.65
- 440881; BE244115; Hs.7482; KIAA0682 gene product; rrm, Guanylate_kin; TM=M; 3.64
- 454954; AW993013; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; 3.64
- 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none; TM=M; 3.64
- 450587; A1828854; Hs.258538; striatin, calmodulin-binding protein; pkinase, WD40; TM=Y; 3.64
- 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OVARC1001372, highly similar to Homo sapiens liprin-alpha4 mRNA; SAM; SS=M; 3.64
- 425645; AA361027; ; gb:EST70242 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence; HMG_box, DNA_mis_repair, HATPass_c, none; 3.64
- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, Integrin_B; SS=M; 3.63
- 451292; AB037716; Hs.26204; KIAA1295 protein; SH3; TM=M; 3.63
- 412314; AA825247; Hs.250899; heat shock factor binding protein 1; 7tm_1; TM=Y; SS=M; 3.63
- 418303; AA215701; Hs.186541; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; eIF5, eIF2B, W2, pkinase, UBA, KA1; 3.63
- 452716; A1914925; Hs.222240; ESTs; SH2, STAT, STAT_bind, STAT_pro, none; 3.63
- 403859; ; NM_004520; Homo sapiens kinesin heavy chain member 2 (KIF2); mRNA member 3 (KCNQ3); mRNA; kinesin; TM=M; 3.63
- 450377; AB033091; Hs.74313; KIAA1265 protein; Zip; TM=M; SS=M; 3.63
- 417793; AW405434; Hs.82575; small nuclear ribonucleoprotein polypeptide B*; rrm; TM=M; 3.63
- 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD38; TM=Y; SS=M; 3.63
- 429554; NM_012275; Hs.207224; Interleukin 1, delta; IL1; TM=M; 3.63
- 417871; AA521368; Hs.24252; ESTs; IBB, Armadillo_seg, none; 3.62
- 437672; AW748265; Hs.5741; flavohemoglobin b57; heme_1, NAD_binding, lipoxygenase, FAD_binding_6; TM=M; 3.62
- 436698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; lipoxygenase, PLAT, none; 3.62
- 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5_F8_type_C; TM=M; SS=M; 3.61
- 407961; AW672939; Hs.41694; origin recognition complex, subunit 2 (yeast homolog)-like; none, pkinase, pro_isomerase; 3.61
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1; SH2, SH3, pkinase; SS=M; 3.61
- 455608; BE011437; ; gb:CM4-BN0220-080500-170-103 BN0220 Homo sapiens cDNA, mRNA sequence; none, CDK5_activator; 3.61
- 407748; AL079409; Hs.38176; KIAA0608 protein; SCN Circadian Oscillatory Protein (SCOP); PP2C, LRR, PH; TM=M; 3.60
- 421474; U76362; Hs.104637; solute carrier family 1 (glutamate transporter), member 7; SDF; TM=Y; SS=M; 3.60
- 449987; AW079749; Hs.184719; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ABC_tran, ABC_membrane, ion_trans; 3.60
- 403142; ; NM_002706; Homo sapiens protein phosphatase 1B (formerly 2C); magnesium-dependent, beta isoform (PPM1B); mRNA; PP2C; TM=M; 3.60
- 400844; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1); mRNA; EGF, tn3, Idl_recept_L, Idl_recept_L, granulin, BNR; TM=Y; SS=M; 3.59
- 450152; A1138635; Hs.22958; Homo sapiens clone IMAGE:451939, mRNA sequence; Ig, pkinase, none; 3.59
- 429782; NM_005754; Hs.220589; Ras-GTPase-activating protein SH3-domain-binding protein; rrm, NTF2; TM=M; 3.59
- 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; SS=M; 3.59
- 437400; AB011542; Hs.5599; EGF-like domain, multiple 5; TNFR_c6, laminin_EGF; TM=Y; 3.58
- 426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_LB, SH3; 3.58
- 431170; AW971246; Hs.291022; ESTs; LRR, CARD, none; 3.58
- 434542; AA769310; Hs.61260; hypothetical protein FLJ13164; PH, Oxysterol_BP; TM=M; SS=M; 3.58

- 420181; A1380089; Hs.158951; ESTs; none;ig,pkinase,LRR,LRRCT; 3.57
 450572; A1700863; Hs.202494; Homo sapiens cDNA FLJ13245 fs, clone OVARC1000681; Na_sulph_symp;none; 3.57
 433618; AA602539; Hs.345494; ESTs; G-alpha_A_deaminase; 3.57
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; pkinase;none; 3.57
 418512; AW498974; ; diacylglycerol kinase, zeta (104kD); ras;none; 3.57
 451752; AB032997; Hs.26966; KIAA1171 protein; ATP-synt_C,TBC;TM=Y;SS=M; 3.57
 417129; A1381800; Hs.300684; calcitonin gene-related peptide-receptor component protein; none;none; 3.57
 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing); Thf,UBACT,pkinase,UCH-2,UCH-1,rm,zf-C2H2,zf-RanBP,G-patch; 3.57
 412124; H43378; Hs.288550; Homo sapiens cDNA: FLJ23156 fs, clone LNG09609; none;none; 3.56
 435021; AA922192; Hs.54709; ESTs; EPH_Lbd,pkinase,fn3,SAM;none; 3.56
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, alpha type, 4; proteasome;TM=M; 3.56
 437387; A198874; Hs.28847; ADO26 protein; none,7tm_1,WD40; 3.56
 422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha;TM=M; 3.56
 452102; UA2343; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none;TM=Y;SS=M; 3.56
 420112; NM_005109; Hs.95220; oxidative-stress responsive 1; pkinase;TM=M; 3.55
 437639; AA827712; Hs.291880; ESTs; SH3;none; 3.55
 457500; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm,pkinase;TM=M; 3.55
 415660; A1909007; Hs.78563; ubiquitin-conjugating enzyme E2G 1 (homologous to C. elegans UBC7); UQ_con;TM=M; 3.55
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase,PBD;TM=M; 3.55
 426727; AF078847; Hs.191356; general transcription factor IIH, polypeptide 2 (44kD subunit); PHO4,LIM;TM=M; 3.55
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M; 3.55
 408663; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos;TM=M; 3.55
 412350; A1693308; Hs.73826; protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte); Y_phosphatase,Band_41,PDZ;TM=M; 3.55
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 3.55
 427283; A119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin); Sulfatase,Somatomedin_B,Phosphodiesterase;TM=M;SS=Y; 3.55
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17;none; 3.55
 424848; A1263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin;none; 3.54
 402704; ; C1001099;gll5005896[ret]NP_009101.1] testis-specific protein kinase 2 (Homo sapiens) gll4; none;none; 3.54
 444049; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; aa_permeases;TM=Y;SS=M; 3.54
 429687; A1675749; Hs.211608; nucleoporin 153kD; zf-RanBP,Integrin_B;TM=M; 3.53
 413879; AA132951; Hs.212533; Homo sapiens cDNA: FLJ22572 fs, clone HSI02313; none;none; 3.53
 431045; AW968560; Hs.301957; nudix (nucleoside diphosphate linked moiety X)-type motif 5; NUDIX_secY,E1_dehydrog,transal_pyr;TM=Y;SS=M; 3.53
 423855; AA331761; Hs.254859; ESTs; none,pkinase,UQ_con,vwa,FG-GAP,Integrin_A; 3.53
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP;TM=M; 3.52
 410686; A1733735; Hs.114905; IRE1, S. cerevisiae, homolog of; pkinase,Bacterial_PQQ;TM=M;SS=M; 3.52
 449810; AB008681; Hs.23994; activin A receptor, type IIB; pkinase,Activin_recp;TM=Y;SS=M; 3.52
 418755; Y14443; Hs.88219; zinc finger protein 200; zf-C2H2,zf-BED;TM=M; 3.52
 448804; AW512213; Hs.342849; ADP-ribosylation factor-like 5; arf,Ca_channel_B,SH3; 3.52
 438507; AA809052; Hs.182018; ESTs; none;none; 3.52
 456559; A1336273; Hs.102548; glucocorticoid receptor DNA binding factor 1; none,PAS; 3.51
 410054; AL120050; Hs.58220; Homo sapiens cDNA: FLJ23005 fs, clone LNG00398, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP,adenylatekinase; 3.51
 422321; AA906427; Hs.181035; hypothetical protein MGC11296; none;TM=M; 3.51
 445701; AF055581; Hs.113131; lymphocyte adaptor protein; SH2,PH;TM=M; 3.50
 407393; AB038237; ; gb:Homo sapiens mRNA for G protein-coupled receptor C5L2, complete cds.; 7tm_1;TM=Y;SS=M; 3.50
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine protease; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 3.50
 420673; AB008112; Hs.99847; peroxisome biogenesis factor 1; AAA,APS_kinase;TM=M;SS=M; 3.49
 424663; NM_002351; Hs.151544; SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome); SH2;TM=M; 3.49
 429327; AA283981; Hs.199246; prostaglandin E receptor 4 (subtype EP4); 7tm_1;TM=Y;SS=M; 3.49
 400178; ; Eos Control; none,Somatomedin_B; 3.49
 439549; AW937885; Hs.137314; ESTs; SH2;none; 3.49
 436345; AA873008; Hs.121572; ESTs; CARD,BIR,zf-C3HC4,CARD,BIR,zf-C3HC4; 3.49
 427658; H61387; Hs.30868; nogo receptor; LRR,LRRNT,LRRCT;SS=M; 3.48
 402833; ; C1002508;gll6691937[emb]CAB65797.1 (AL096770) bA150A6.2 (novel 7 transmembrane receptor; none;none; 3.48
 442363; A1337304; Hs.23120; PIST; fn3,pkinase,PDZ,DUF139;TM=Y;SS=M; 3.48
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; none;TM=M; 3.47
 417971; Y08991; Hs.83050; phosphoinositide-3-kinase, regulatory subunit 4, p150; pkinase,WD40,HEAT;SS=M; 3.47
 432169; Y00971; Hs.2910; phosphoribosyl pyrophosphate synthetase 2; Pribosyltran; 3.47
 447425; A1963747; Hs.18573; acylphosphatase 1, erythrocyte (common) type; Acylphosphatase;SS=M; 3.47
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 3.46
 401851; ; NM_002401*Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA; pkinase;SS=M; 3.46
 407877; AW016811; Hs.234478; Homo sapiens cDNA: FLJ22648 fs, clone HSI07329; pkinase,pkinase_C;none; 3.45
 432279; N95104; Hs.274260; ATP-binding cassette, sub-family C (CFTR/MRP), member 6; ABC_tran,ABC_membrane;none; 3.45
 437103; AW139408; Hs.152940; ESTs; Choline_kinase;none; 3.45
 420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339, mRNA, complete cds; 7tm_1;TM=Y;SS=M; 3.44
 422209; AF005210; Hs.113222; chemokine (C-C motif) receptor 8; 7tm_1,7tm_2;TM=Y;SS=M; 3.44
 410781; A1375572; Hs.165028; ESTs; pkinase,laminin_Nterm,laminin_EGF_cyclin,F-box,cyclin_C,serpin,ATP-synt_C; 3.44
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPc;TM=M; 3.43
 419855; A1963182; Hs.144139; ESTs; zf-C3HC4,UBA,Cbl_N,Cbl_N2,Cbl_N3,zf-C3HC4,UBA,Cbl_N,Cbl_N2,Cbl_N3; 3.43
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2; Fz,NTR;SS=M; 3.43
 428483; A1908539; Hs.184592; KIAA0344 gene product; none;none; 3.43
 445119; AF035121; Hs.12337; Kinase insert domain receptor (a type III receptor tyrosine kinase); ig,pkinase;TM=Y;SS=M; 3.42
 454468; A1590319; Hs.19122; eukaryotic translation initiation factor 4E-like 3; none,Neur_chan_LBD,Neur_chan_memb,IF4E; 3.42
 410386; W26187; Hs.3327; Homo sapiens cDNA: FLJ22219 fs, clone HRC01637; pkinase,Guanylate_kin,PDZ,SH3,L27;none; 3.42
 422907; A1879263; Hs.77273; Human glucose transporter pseudogene; none;none; 3.42
 449816; A1701457; Hs.38694; ESTs; SET,BAH,PK,PK_C; 3.42
 440074; AA863045; Hs.10669; ESTs; Weakly similar to T00050 hypothetical protein KIAA0400 [H.sapiens]; SH3,ank,tubulin-binding,ArfGap,PH;TM=M;SS=M; 3.42
 425475; W56339; Hs.107057; ESTs; pkinase;none; 3.42
 401242; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 3.41
 429276; AF056085; Hs.198512; G protein-coupled receptor 51; 7tm_3,ANF_receptor,bZIP;TM=Y; 3.41
 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, type I, 107kD; none;none; 3.41
 410908; AA121686; Hs.10592; ESTs; GTP_EFTU,GTP_EFTU_D3,GTP_EFTU_D2;none; 3.41

- 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor type, E; Y_phosphatase,none; 3.40
 447898; AW969638; Hs.112318; 6.2 kd protein; none,none; 3.40
 450402; BE218027; Hs.89969; ESTs; SH3,none; 3.40
 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB,none; 3.40
 408546; W49512; Hs.46348; bradykinin receptor B1; 7tm_1;TM=Y;SS=M; 3.40
 410927; T77635; ; gb:yc91h08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone 5', mRNA sequence; none,none; 3.40
 409646; AW161391; Hs.709; deoxycytidine kinase; dNK;SS=M; 3.39
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ121425 fis, clone COL04162; Sulfate_transp,STAS,HMG_box; 3.39
 449343; A1151418; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); none,none; 3.39
 450511; R07423; Hs.85092; thyroid hormone receptor Interactor 11; Myosin_tail,EGF; 3.39
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M; 3.38
 418428; Y12490; Hs.85092; thyroid hormone receptor Interactor 11; bZIP,kinesin,GTP_cyclohydrol,M;TM=M; 3.37
 422369; AF005216; Hs.115541; Janus kinase 2 (a protein tyrosine kinase); SH2,pkinase;TM=M; 3.37
 456451; A1761180; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none;TM=M; 3.37
 438543; AA810141; Hs.192182; ESTs; SH2,pkinase,none; 3.37
 401943; NM_012434; ; solute carrier family 17 (anion/sugar transporter), member 5; none;TM=M; 3.36
 415276; U88666; Hs.78353; SFRS protein kinase 2; pkinase;TM=M; 3.36
 447881; BE620888; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; pkinase,pkinase; 3.35
 434533; AA639257; Hs.292549; ESTs; SH3,PDZ,Guanylate_kin,none; 3.35
 426339; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence; none,IRK; 3.35
 410678; BE540516; Hs.293732; hypothetical protein MGC3195; Armadillo_seg;TM=M;SS=Y; 3.35
 402807; ; ENSP00000235229:SEMB; Integrin_B,Sema,PS;TM=Y; 3.35
 420189; AW266380; Hs.95821; osteoclast stimulating factor 1; SH3,ank; 3.34
 437389; AL359587; Hs.271586; hypothetical protein DKFZp762M115; secY,E1_dehydrog,transket_pyr,none; 3.34
 453423; NM_002647; Hs.32971; phosphoinositide-3-kinase, class 3; PI3_P14_kinase,PI3Ka,PI3K_C2;TM=M; 3.34
 414270; L20852; Hs.347527; solute carrier family 20 (phosphate transporter), member 2; Enterotoxin_A,PHO4;TM=Y;SS=M; 3.33
 417479; A1057052; ; ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 (H.sapiens); LRR,CARD,none; 3.33
 424946; M64572; Hs.153932; protein tyrosine phosphatase, non-receptor type 3; Band_41,PDZ_Y_phosphatase,none; 3.33
 452681; AF153330; Hs.30246; solute carrier family 19 (thiamine transporter), member 2; Folate_carrier;TM=Y;SS=M; 3.33
 426477; AA379464; ; gb:EST92386 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence; DUF6,MATH,BTB; 3.33
 438283; A1458931; Hs.37282; ESTs; none,transmembrane4; 3.33
 421327; AA837295; Hs.188802; ESTs; none,IMP4_Y_phosphatase; 3.33
 432481; AW451645; Hs.151504; Homo sapiens cDNA FLJ11973 fis, clone HEMB81001221; laminin_G,Collagen,COLFI,CorA,TPSN,none; 3.33
 452682; AA458193; Hs.9071; progesterone membrane binding protein; homeobox,none; 3.32
 428997; AF065391; Hs.194718; zinc finger protein 265; zf-RanBP;TM=M; 3.32
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 3.31
 443601; A1078554; Hs.15682; ESTs; ank,pkinase,death,Ribosomal_S14; 3.31
 430597; AF062006; Hs.285529; G protein-coupled receptor 49; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 3.31
 418912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (GEF) 4; SH3,PH,RhoGEF;TM=M; 3.31
 400380; NM_018485; Hs.283079; G protein-coupled receptor CSL2; 7tm_1;TM=Y;SS=M; 3.31
 415983; A136798; Hs.117078; Homo sapiens cDNA: FLJ23028 fis, clone LNC01852, highly similar to HSU08023 Human cellular proto-oncogene (c-met) mRNA; fn3,lg,pkinase;TM=Y;SS=M; 3.31
 441054; AA913591; Hs.126480; ESTs; none,7tm_1; 3.31
 418342; BE002723; ; lepton receptor; ICE_p20,DED,ICE_p10,ICE_p20,DED; 3.31
 446128; AW836779; Hs.113029; ribosomal protein S25; none,7tm_1; 3.31
 425086; AW957571; Hs.12319; Homo sapiens cDNA FLJ12774 fis, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11); none,Guanylate_kin,PDZ,SH3; 3.31
 425725; NM_012243; Hs.158322; solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3; DUF6;TM=Y;SS=M; 3.30
 422608; AW160844; Hs.118695; potassium voltage-gated channel, subfamily G, member 1; ion_trans,K_letra;TM=Y; 3.30
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M; 3.30
 433656; AW974941; Hs.292385; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase (H.sapiens); pkinase,ABC1,none; 3.30
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic) inhibitor alpha; PKI;SS=M; 3.30
 402603; ; ENSP00000251206:KIAA0778 PROTEIN (FRAGMENT); none;TM=Y; 3.30
 418801; AA228366; Hs.115122; ESTs; Integrin_A,FG-GAP,none; 3.30
 400275; ; NM_006513:Homo sapiens seryl-tRNA synthetase (SARS), mRNA. (SAM68), mRNA.; tRNA-synt_2b,Seryl_tRNA_N;TM=M; 3.29
 440286; U29589; Hs.7138; cholinergic receptor, muscarinic 3; 7tm_1;TM=Y; 3.29
 409101; NM_004297; Hs.50812; guanine nucleotide binding protein (G protein), alpha 14; G-alpha,none; 3.29
 432738; AA788898; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.29
 408738; NM_014785; Hs.47313; KIAA0258 gene product; none;TM=M; 3.29
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955; Aa_trans,none; 3.29
 405328; ; NM_005391:Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3), mRNA; HATPase_c;SS=M; 3.28
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit 6; none,none; 3.28
 408756; AA524743; Hs.44883; ESTs; Armadillo_seg,IBB,DEAD,helicase_C,Sec63,DDT,PHD,bromodomain;TM=M; 3.28
 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15; mito_car;TM=M; 3.28
 417805; U38545; Hs.82587; phospholipase D1, phosphatidylcholine-specific; PH,PLDc,PX;TM=M; 3.28
 410254; BE004131; Hs.318510; Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15; etfhand,none; 3.28
 443968; AA287702; Hs.10031; KIAA0955 protein; CARD;TM=M;SS=M; 3.28
 438899; AF085833; Hs.135624; ESTs; none,PI3_P14_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 3.27
 415663; AW296841; Hs.313332; ESTs; UQ_con,Neur_chan_LBD,Neur_chan_memb; 3.27
 414087; W19712; ; gb:zb36d03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 3.27
 442833; AA328153; Hs.88201; ESTs, Weakly similar to A Chain A, Crystal Structure Of The Human Acyl Protein Thioesterase 1 At 1.5 A Resolution (H.sapiens); abhydrolase_2;TM=M; 3.27
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 3.26
 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis repressor with CARD domain); CARD;TM=M; 3.26
 458943; AW249181; Hs.19954; ESTs, Weakly similar to T19873 hypothetical protein C41C4.2 - Caenorhabditis elegans [C.elegans]; none,pkinase,RGS; 3.26
 411974; AW880414; Hs.84264; acidic protein rich in leucines; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,asp; 3.26
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate cotransporter, member 4; HCO3_cotransp;TM=Y; 3.26
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 3.25
 442643; U82756; Hs.3991; PRP4/STK4WD splicing factor; WD40;SS=M; 3.25
 417525; R93355; Hs.192991; ESTs, Weakly similar to ALUB_HUMAN III ALU CLASS B WARNING ENTRY III (H.sapiens); SH3,lg,pkinase,PH,spectrin,RhoGEF;SS=M; 3.25
 412283; BE069084; ; gb:QV3-BT0379-140100-058-g12 BT0379 Homo sapiens cDNA, mRNA sequence; ion_trans,RYDR,JTPR,MIR,none; 3.25
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 3.25
 400352; AF227133; ; taste receptor, type 2, member 7; none;TM=Y;SS=M; 3.25

- 402974; ; Target Exon; Y_phosphatase, GnRH, hormone5, hormone4; 3.25
 407644; D16815; Hs.37288; nuclear receptor subfamily 1, group D, member 2; hormone_rec, zf-C4; TM=M; SS=M; 3.25
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; helicase_C; SS=M; 3.25
 438022; AW517524; Hs.135201; NOD2 protein; LRR_CARD_GTP_CDC_Viral_helicase1; TM=M; 3.24
 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M; 3.24
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; EGF_sushi, trypsin, CUB, ABC_tran, ABC_membrane; SS=M; 3.24
 427319; AW631495; Hs.27135; B-cell receptor-associated protein BAP29; filament; TM=Y; SS=M; 3.24
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RRN3;
 aa_pemases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BOLA, RUN; TM=M; 3.24
 411887; AW182924; Hs.128790; ESTs; pkinase; TM=M; 3.24
 430180; AA331406; Hs.75456; A kinase (PRKA) anchor protein 10; RGS; SS=M; 3.24
 410267; AW978005; Hs.12600; N-ethylmaleimide-sensitive factor attachment protein, beta; none; NTF2; 3.23
 410240; AL157424; Hs.61289; synaptotagmin 2; Exo_endo_phos, Syja_N, nm, Gram-ve_porins; TM=M; 3.23
 434510; AF143885; Hs.18190; EST; SH3, FCH, none; 3.22
 422592; BE081857; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none; PI-PLC-X, PH, PI-PLC-Y, C2; 3.22
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none; none; 3.22
 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; 3.22
 409245; AA361037; Hs.288036; IRNA isopentenylpyrophosphate transferase; Armadillo_seg; TM=M; 3.22
 458946; AA009716; Hs.42311; ESTs; none; DSPc_Y_phosphatase; 3.22
 409048; H59990; Hs.37699; ESTs; Armadillo_seg, IBB, none; 3.22
 420357; U94333; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 3.22
 426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin, trdn_4; SS=M; 3.21
 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activating protein) 1; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 3.21
 438333; R39382; Hs.25283; cyclin-dependent kinase 8; pkinase, none; 3.20
 414202; BE275653; Hs.270379; transmembrane 6 superfamily member 1; 7tm_5, none; 3.20
 429651; D79248; Hs.279870; ESTs; Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; MglE, none; 3.20
 400987; ; C11000939.gli11464933[ref]NP_065260.1 gene for odorant receptor MOR83 [Mus musculus] gli1; none; TM=Y; SS=M; 3.20
 413760; Z25101; Hs.25127; Homo sapiens mRNA for KIAA1725 protein, partial cds; none, ank, ArfGap; 3.20
 408468; AI909712; Hs.93837; phosphatidylinositol transfer protein, membrane-associated; PX, PH, PLDc, PH, PLDc, PX; 3.20
 409463; AI458165; Hs.17296; hypothetical protein MGC2376; K_tetra; TM=M; 3.20
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 3.19
 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbonate cotransporter, member 7; HCO3_cotransp; TM=Y; SS=M; 3.19
 407753; AL045918; Hs.293419; ESTs; Ephrin, none; 3.19
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 3.19
 454128; AL031259; Hs.41639; programmed cell death 2; zf-MYND; TM=M; 3.19
 421202; AF193339; Hs.102506; eukaryotic translation initiation factor 2-alpha kinase 3; pkinase; TM=Y; SS=M; 3.19
 446360; N42553; Hs.267914; homolog of mouse transient receptor potential-phospholipase C-interacting kinase CHAK; hypothetical protein FLJ20117;
 lon_trans, MHCK_EF2_kinase; TM=M; 3.18
 458882; R34993; Hs.226666; ESTs; Moderately similar to I54374 gene NF2 protein [H.sapiens]; CRAL_TRIO, PKI; 3.18
 424124; AA335609; Hs.7589; ESTs; Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; pkinase, TBC; 3.18
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated protein, 240 kDa subunit; none; TM=M; 3.18
 426399; AA652588; Hs.301348; Homo sapiens cDNA FLJ13271 fis, clone OVARC1001000; SH3, HS_1_rep, none; 3.18
 425836; AW955696; Hs.90960; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 3.18
 403335; ; NM_021815; Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA; SSF; TM=Y; SS=M; 3.17
 428788; AF082283; Hs.193616; B-cell CLL/lymphoma 10; CARD; TM=M; 3.17
 429558; AI391454; Hs.20725; nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein; none; SS=M; 3.17
 440248; AA878138; Hs.153136; ESTs; SH2, none; 3.17
 423708; U95218; Hs.131924; G protein-coupled receptor 65; 7tm_1; TM=Y; SS=M; 3.17
 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 3.17
 446163; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270; none; NA; NA; 3.17
 456773; AI038192; Hs.129764; EGF-like repeats and discoidin I-like domains 3; nm, SH3, myosin_head, IQ, MyTH4, EGF, F5_F8_type_C, Band_41; TM=M; 3.17
 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone HRC12631; pkinase, none; 3.16
 435972; W95088; Hs.114198; ESTs; pkinase, OPR, none; 3.16
 441401; AI824338; Hs.126891; ESTs; Tissue_fac; TM=M; SS=M; 3.16
 410497; AI157648; Hs.157078; Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033; none, none; 3.16
 401113; Z25530; ; solute carrier family 22 (organic cation transporter), member 1-like; none; SS=M; 3.16
 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS; SS=M; 3.15
 453880; AI803166; Hs.28462; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; HSP70, none; 3.15
 435391; AA704588; Hs.58934; ESTs; PIP5K, none; 3.15
 428065; AI534046; Hs.157313; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 3.15
 452688; AA721140; Hs.49930; ESTs; Weakly similar to putative p150 [H.sapiens]; SH3, none; 3.15
 426839; M74782; Hs.172689; Interleukin 3 receptor, alpha (low affinity); none; TM=M; SS=M; 3.15
 421247; BE391727; Hs.102910; general transcription factor IIH, polypeptide 4 (52kD subunit); none; TM=M; 3.14
 440249; AI248590; Hs.249175; ESTs; TatD_DNase, pkinase, death, none; 3.14
 409618; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; 3.13
 446135; AW130288; Hs.170318; hypothetical protein FLJ10147; hormone_rec, zf-C4; SS=M; 3.13
 400440; X83957; Hs.83870; nebulin; SH3, Nebulin; 3.12
 409099; AK000725; Hs.50579; hypothetical protein FLJ20718; Armadillo_seg; TM=M; 3.12
 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none; SS=M; 3.12
 428179; AI127772; Hs.279695; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; pkinase, PX, pkinase_C; SS=M; 3.12
 422824; NM_012108; Hs.121128; BCR downstream signaling 1; SH2, PH; TM=M; 3.11
 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14E12, mRNA sequence; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 3.11
 435411; AW444619; Hs.138211; ESTs; none, pkinase; 3.11
 424852; AI222779; Hs.144848; ESTs; adenylate kinase, SH2, pkinase, none; 3.11
 441970; AW959918; Hs.155160; ESTs; nm, zf-C2H2; 3.11
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran, ABC_membrane; TM=Y; 3.11
 413285; BE078405; ; gb:QV2-BT0617-080300-071-g03 BT0617 Homo sapiens cDNA, mRNA sequence; GCV_T; SS=M; 3.10
 429458; BE161832; Hs.292689; ESTs; pkinase, bZIP, Armadillo_seg, none; 3.10
 401185; ; NM_021825; Homo sapiens vanilloid receptor-related osmotically activated channel; OTRPC4 protein (OTRPC4), mRNA; ank, lon_trans; TM=Y; 3.10
 404537; Z25884; ; chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant); none; TM=Y; 3.10
 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone HEP03834; voltage_CLC, CBS, none; 3.09
 450792; AA400323; Hs.183041; ESTs; none, ABC_tran; 3.09

- 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP, 7tm_1; 3.09
 444040; AF204231; Hs.182982; golgin-57; SH3,C2,PH,RhoGEF,efhand;TM=M; 3.09
 416990; AF124145; Hs.80731; autocrine motility factor receptor; zf-C3HC4,CUE;TM=Y; 3.09
 442215; A1703172; Hs.129005; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; none,none; 3.09
 424187; AA338561; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK,none; 3.09
 426623; AA382826; Hs.132793; ESTs; none;TM=M; 3.08
 419577; L36531; Hs.91296; Integrin, alpha 8; Integrin_A,FG-GAP;TM=Y; 3.08
 426618; AL036456; Hs.171374; smg GDS-ASSOCIATED PROTEIN; Armadillo_seg;TM=M; 3.08
 445133; AW157646; Hs.153506; ESTs; efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,Flid,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CHAI/P3;TM=M; 3.08
 423681; AB023215; Hs.131525; Homo sapiens mRNA; cDNA DKFZp434E199 (from clone DKFZp434E199); partial cds; TTL;TM=M; 3.08
 428730; AA625947; Hs.25750; ESTs; HECT,none; 3.08
 427976; AW977808; Hs.80545; mitogen-activated protein kinase 8 interacting protein 2; Ribosomal_L37e,pkinase; 3.08
 412448; L12964; Hs.73895; tumor necrosis factor receptor superfamily, member 9; TNFR_c6;TM=Y;SS=M; 3.08
 416814; AW192307; Hs.80042; dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransferase; Alg6_Alg8,7tm_1;TM=Y;SS=M; 3.08
 427395; AW298741; Hs.78861; ESTs, Moderately similar to 138022 hypothetical protein [H.sapiens]; none,aldedh,aaknase; 3.08
 436267; AW450938; Hs.180115; ESTs; none,PFK; 3.07
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic acid transporters), member 6; sugar_tr;TM=Y;SS=M; 3.07
 439238; U47305; Hs.46668; ESTs; 7tm_1;TM=Y;SS=M; 3.07
 458760; AI498631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.07
 424236; AW058114; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M; 3.06
 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway substrate 8; SH3,TonB_boxC;TM=M; 3.06
 423878; AJ907090; Hs.52891; hypothetical protein PRO1853; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.06
 419270; NM_005232; Hs.89639; EphA1; tn3,pkinase,SAM,EPH_lbd;TM=M;SS=M; 3.06
 450407; NM_000810; Hs.24969; gamma-aminobutyric acid (GABA) A receptor, alpha 5; Neur_chan_LBD,Neur_chan_memb;TM=Y; 3.06
 456249; AI208144; Hs.82508; HRIHFB2206 protein; none;SS=M; 3.06
 441560; F13386; Hs.7888; Homo sapiens clone 23736 mRNA sequence; pkinase,Recep_L_domain,Furin-like,YLP,none; 3.05
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 3.05
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); pyr_redox;TM=M; 3.05
 425390; AJ092634; Hs.156114; protein tyrosine phosphatase, non-receptor type substrate 1; lg;TM=Y;SS=M; 3.04
 409705; M37762; Hs.58023; brain-derived neurotrophic factor; NGF;SS=M; 3.04
 413962; AA331563; Hs.24678; sphingosine-1-phosphatase; PAP2;TM=Y; 3.04
 426578; R23027; ; gb:yh27e07.r1 Soares placenta Nb2HP Homo sapiens cDNA clone 5', mRNA sequence; pkinase,none; 3.04
 438005; BE151746; ; gb:PM1-HT0305-061299-003-a06 HT0305 Homo sapiens cDNA, mRNA sequence; pkinase,UBA,KAI,none; 3.04
 438316; AA789249; Hs.80042; gb:aj27g08.s1 Soares testis_NHT Homo sapiens cDNA clone 1391582 3', mRNA sequence; none,none; 3.04
 452850; H23230; Hs.22481; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; CBS,voltage_CLC,none; 3.03
 405266; ; ; Target Exon; arl,G-alpha;SS=M; 3.03
 402615; ; ; C1003844:gi6912550[ref]NP_036483.1| olfactory receptor, family 10, subfamily J, member 1; none;TM=Y;SS=M; 3.03
 422803; W28669; Hs.139041; ESTs; transmembrane4,none; 3.02
 439325; AF086139; Hs.150423; cyclin-dependent kinase 9 (CDC2-related kinase); pkinase,Mur_ligase,Mur_ligase_C; 3.02
 416389; AA180072; Hs.149846; Integrin, beta 5; Integrin_B,none; 3.02
 418838; AI655499; Hs.161712; ESTs; pkinase,Activin_recpt,PDZ,ZU5,death; 3.02
 438956; AW748336; Hs.110613; KIAA0421 protein; none;TM=M; 3.02
 422676; D28481; Hs.1570; histamine receptor H1; 7tm_1;TM=Y;SS=M; 3.02
 450267; AW505538; Hs.243620; ESTs; pkinase,none; 3.01
 400566; ; ; Target Exon; none;TM=Y; 3.01
 407816; AW500857; Hs.40137; anaphase-promoting complex 1; meiotic checkpoint regulator; PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN,none; 3.01
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase); Y_phosphatase,Band_41,PDZ;SS=M; 3.01
 41001417; ; gb:PM1-HT0305-061299-003-a06 HT0305 Homo sapiens cDNA, mRNA sequence; pkinase,UBA,KAI,none; 3.00
 403212; ; NM_019595:Homo sapiens intersectin 2 (ITSN2), mRNA. (CHRNA9), mRNA; SH3,efhand,C2,PH,RhoGEF;TM=M; 3.00
 410141; R07775; Hs.287657; Homo sapiens cDNA: FLJ21291 fs, clone COL01963; F5_F8_type_C,pkinase,Ets,none; 3.00
 421059; AI654133; Hs.30212; thyroid receptor interacting protein 15; none,none; 3.00
 452335; AW188944; Hs.61272; ESTs; none,IRK; 2.99
 437644; AA748575; Hs.136748; lectin-like NK cell receptor; lectin_c;TM=Y;SS=M; 2.99
 435876; AW612586; Hs.160271; G protein-coupled receptor 48; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 2.99
 429177; AA447527; Hs.207429; ESTs; 7tm_1,none; 2.99
 449289; BE466067; Hs.225660; ESTs; 3Beta_HSD,pkinase; 2.99
 454701; AW854930; ; gb:PM0-CT0263-201099-003-f06 CT0263 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prol,none; 2.99
 409995; AW960597; Hs.129206; ESTs; pkinase,none; 2.98
 446860; AV660685; Hs.282953; ESTs; none,PP2C; 2.98
 438684; AA830105; Hs.194976; SH2 domain-containing phosphatase anchor protein 1; lg;TM=Y;SS=M; 2.98
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M; 2.98
 403290; ; ; C100010111:gi14758212[ref]NP_004411.1| dual specificity phosphatase 6 [Homo sapiens] gi1601; none;TM=M; 2.97
 433556; W58321; Hs.111460; calcium/calmodulin-dependent protein kinase (CaM kinase) II delta; pkinase,none; 2.97
 421990; T31811; Hs.110480; DC12 protein; GKAP,DUF159;TM=M; 2.97
 428315; AA688152; Hs.98505; ESTs; pkinase,none; 2.97
 411140; AW819463; ; gb:RC5-ST0293-061299-031-C07 ST0293 Homo sapiens cDNA, mRNA sequence; Choline_kinase,Cam_acyltransf,Sulfatase,Cam_acyltransf; 2.97
 453998; H47802; Hs.7557; FK506-binding protein 5; none,none; 2.97
 401342; ; ; Target Exon; none,none; 2.97
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); dNK,none; 2.96
 410976; R36207; Hs.25092; hypothetical protein MGC10744; none;TM=M;SS=M; 2.96
 431074; BE072772; Hs.153279; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; none,serpin; 2.95
 443829; A087954; Hs.23348; S-phase kinase-associated protein 2 (p45); F-box,none; 2.95
 400356; AF227137; ; taste receptor, type 2, member 13; none;TM=Y;SS=M; 2.95
 422559; AW247696; Hs.155839; hypothetical protein MGC12934; adh_zinc,PGK,Semialdehyde_dh;SS=M; 2.95
 423482; BE280172; Hs.129228; galactokinase 2; GHMP_kinases;TM=M; 2.95
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.95
 414581; AA256213; Hs.72010; ESTs; none,Cam_acyltransf,Choline_kinase,SCO1-SenC,Glycos_transf_3,Glycos_trans_3N; 2.95
 453058; AW611229; Hs.288684; Homo sapiens cDNA FLJ11750 fs, clone HEMBA1005568; SH2,SH3,C2,PH,RasGAP,none; 2.95
 430556; AW967807; Hs.13797; ESTs; HECT,none; 2.94
 400471; ; ; Target Exon; none;TM=M; 2.94
 419459; AW291128; Hs.278422; DKFZP586G1122 protein; Metallophos,7tm_1; 2.94
 407013; U35637; ; gb:Human nebulin mRNA, partial cds; SH3,Nebulin; 2.94
 421476; AW953805; Hs.21887; ESTs; Ptw1,PAZ,Ptw; 2.94

- 426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank.pkinase,UPF0073,SS=M; 2.94
 405588; ; NM_000299; Homo sapiens plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) (PKP1), mRNA; Armadillo_seg; TM=M; 2.94
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none, none; 2.94
 416737; AF154335; Hs.79591; LIM domain protein; LIM.PDZ; TM=M; 2.93
 428522; R10184; Hs.191987; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none,ArfGap,PH,TNFR_c6; 2.93
 447818; W79940; Hs.21906; Homo sapiens clone 24670 mRNA sequence; none, pkinase; 2.93
 432925; AA878324; ; ESTs; none, none; 2.93
 443670; AW178935; Hs.238707; ESTs; RmaAD, DENN, dDENN, uDENN; TM=M; 2.93
 447555; AJ391662; Hs.160963; Homo sapiens, clone MGC:12318, mRNA, complete cds; none; TM=M; 2.93
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; none; TM=M; 2.93
 417670; R07785; ; gb:Y15c06.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5' similar to contains Alu repetitive element; contains MSR1 repetitive element ;, mRNA sequence; XYPPX,ABC,membrane,ABC,tran; 2.93
 424148; BE242274; Hs.1741; integrin, beta 7; integrin_B,EGF,metalithio,PSI; TM=Y,SS=M; 2.92
 439090; H65724; Hs.347158; gb:Y76a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5', mRNA sequence; pkinase, none; 2.92
 408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemin; TM=M; 2.92
 428796; AU076734; Hs.193665; solute carrier family 28 (sodium-coupled nucleoside transporter), member 2; Nucleoside_tra2,BPD_transp_2; TM=Y; 2.92
 415272; AA164215; Hs.203186; ESTs; none,Exo_endo_phos,BNR,Atrophin-1,B56,pkinase,Ig,TPR; 2.92
 424775; AB014540; Hs.153026; SWAP-70 protein; ethand,PH,Neuregulin; TM=M; 2.92
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL; TM=M; SS=M; 2.92
 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg; TM=M; 2.91
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1; Somatomedin_B,Endonuclease,Phosphodiesterase; TM=Y; SS=M; 2.91
 400398; AF137396; Hs.283878; ubiquitin 3; 7tm_1,Abi; TM=Y; SS=M; 2.91
 435592; AJ830490; Hs.1456; glycerol kinase; FGGY,FGGY_C; TM=M; 2.90
 400539; ; Target Exon; none; TM=M; 2.90
 403743; ; C1002604; gl|B39366[ref]NP_058989.1 kinase interacting with leukemia-associated gene (st; none; TM=M; 2.90
 418913; BE046745; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Y_phosphatase,IMP4,none; 2.90
 428169; AJ928984; Hs.182793; golgi phosphoprotein 2; photoRC,UPF0118; TM=Y; 2.90
 403912; ; C5000394; gl|12737280[ref]XP_006682.2 keratin 18 (Homo sapiens)||6633; none; TM=M; 2.89
 431868; BE246400; Hs.285176; acetyl-Coenzyme A transporter; none; TM=Y; 2.89
 421558; AB011125; Hs.105749; KIAA0553 protein; none; TM=M; 2.89
 444100; AA383343; Hs.22116; CDC14 (cell division cycle 14, S. cerevisiae) homolog B; Y_phosphatase,DSPC; TM=M; 2.89
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled, 2; 7tm_1,SH2; TM=Y; SS=M; 2.89
 431512; BE270734; Hs.2795; lactate dehydrogenase A; Idh,Idh_C,SH3,pkinase,UBA; TM=M; 2.89
 446601; AJ312783; Hs.155772; Homo sapiens thymic stromal co-transporter mRNA, complete cds; sugar_tr; TM=Y; 2.89
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK; TM=M; 2.88
 449459; BE546846; Hs.195048; ESTs; ank,ras,PH,ArfGap,HCO3_cotransp; 2.88
 405099; ; Target Exon; C2,PI-PLC-Y,PI-PLC-X; TM=M; 2.88
 445890; AF055019; Hs.21906; Homo sapiens clone 24670 mRNA sequence; pkinase,pkinase; 2.88
 401445; ; NM_021161; Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA; ion_trans; TM=Y; SS=M; 2.87
 405480; ; Target Exon; none, none; 2.87
 400189; ; Eos Control; LRR,PPTA; TM=M; 2.87
 450125; AA005418; Hs.158186; ESTs; CIDE-N,7tm_1,none; 2.87
 432056; AB040973; Hs.272385; G protein-coupled receptor 72; 7tm_1; TM=Y; SS=M; 2.86
 423619; T48891; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2; TM=Y; SS=M; 2.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; xan_ur_permease,RA; 2.86
 420035; F26725; Hs.187908; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; HATPase_c,MOZ,SAS,zf-C2H2; 2.86
 425480; AB023198; Hs.158135; KIAA0981 protein; PIP5K; SS=M; 2.86
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a putative CpG; none; TM=M; 2.86
 444595; AL121094; Hs.83572; hypothetical protein MGC14433; Y_phosphatase,SH2,Y_phosphatase,SH2; 2.85
 411331; AW837178; ; gb:CV1-LT0037-070300-100-d11 LT0037 Homo sapiens cDNA, mRNA sequence; SH2,none; 2.85
 410763; AF279145; Hs.8968; hypothetical protein FLJ121776; none, none; 2.85
 440617; AA894880; Hs.181181; ESTs; none, none; 2.85
 454071; AJ041793; Hs.42502; ESTs; 7tm_1,none; 2.85
 411040; AF007393; Hs.177574; protein-kinase, Interferon-Inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor); HLH; TM=M; 2.85
 402183; ; NM_004491; Homo sapiens glucocorticoid receptor DNA binding factor 1 (GRF1), mRNA; none; SS=M; 2.85
 428753; AW939252; Hs.192927; hypothetical protein FLJ20251; none; TM=M; 2.84
 417070; T19077; Hs.172004; titin; fn3,Ig,SGXXSG,pkinase; TM=M; 2.84
 458456; AJ122709; Hs.153609; ESTs; bZIP,Armadillo_seg,rm,NTF2,none; 2.84
 421226; AL096748; Hs.102708; DKFZP434A043 protein; Armadillo_seg,Integrin_B,PSI,TIG; TM=M; SS=M; 2.84
 436733; BE327477; Hs.166941; ESTs; 7tm_3,oxidored_q5_N,Presenilin,PWI; 2.84
 427161; AJ024559; Hs.97508; a disintegrin and metalloproteinase domain 6; Ig; TM=Y; SS=M; 2.84
 419462; AF071076; Hs.112255; nucleoporin 98kD; DEAD,helicase_C,Nucleoporin_FG,homeobox; SS=M; 2.83
 413658; AA055369; Hs.75456; A kinase (PRKA) anchor protein 10; none, none; 2.83
 400749; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF,fn3,Ig,ldl_recept_a,ldl_recept_b,granulin,BNR; TM=Y; SS=M; 2.83
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; TB2_DP1_HVA22; TM=Y; SS=M; 2.83
 413243; AA769266; Hs.193657; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.83
 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]; ion_trans,IQ,none; 2.82
 447993; AW139525; Hs.170362; ESTs; none, none; 2.82
 423061; AJ290473; Hs.44807; ESTs; integrin_B,Sema,PSI,TIG,none; 2.82
 440619; AW408586; Hs.91052; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; abhydrolase_2,none; 2.82
 423497; U92642; Hs.129701; G protein-coupled receptor 45; 7tm_1; TM=Y; SS=M; 2.81
 446126; AW085909; Hs.10177; pleckstrin homology domain interacting protein; none, none; 2.81
 452488; N74921; Hs.184389; ESTs; none; TM=M; 2.80
 449515; AV653378; Hs.302012; ESTs; ion_trans; TM=Y; SS=M; 2.79
 443881; R64512; Hs.237146; hypothetical protein FLJ12752; none, none; 2.79
 449638; AJ656608; Hs.281328; ESTs, Weakly similar to T00378 KIAA0641 protein [H.sapiens]; pkinase,hormone3; TM=Y; SS=M; 2.78
 424348; AB020523; Hs.266258; endonuclease G-like 1; Endonuclease; TM=M; SS=M; 2.78
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT; TM=M; 2.78
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; MIF,sugar_tr,none; 2.78

- 450010; AW293801; Hs.255052; ESTs; ARID,7tm_1; 2.78
 452813; U54727; Hs.191445; ESTs; pkinase,Activin_recpt,none; 2.78
 418177; N44967; ; ESTs; pkinase,none; 2.78
 408014; AA723782; Hs.41749; protein kinase, cGMP-dependent, type II; cNMP_binding,pkinase;SS=M; 2.77
 448362; AA841767; Hs.21015; hypothetical protein DKFZp564L0864 similar to HIAT1; sugar_tr;TM=Y;SS=M; 2.77
 423994; X01057; Hs.1724; Interleukin 2 receptor, alpha; sushi;TM=Y;SS=M; 2.77
 427342; AL110150; Hs.176580; Homo sapiens mRNA; cDNA DKFZp586D0724 (from clone DKFZp586D0724); none;NA;NA; 2.76
 447574; AF162668; Hs.18895; tousel-like kinase 1; pkinase;TM=M; 2.76
 442681; AJ809182; Hs.130907; ESTs; transketolase,E1_dehydrog,transket_pyr,transketolase_C,pkinase; 2.75
 433637; AW024214; Hs.102307; ESTs; Na_sulph_symp,aa_permeases;TM=Y;SS=M; 2.75
 458997; AW937420; Hs.69662; ESTs; SH3,RhoGAP,FCH;TM=M; 2.75
 432284; AA532807; Hs.105822; ESTs; pkinase,none; 2.74
 406139; ; Target Exon; Ig,Tub;TM=Y;SS=M; 2.74
 439518; W76326; ; gb:zd60d04.r1 Scores_fetal_heart_NbHH19W Homo sapiens cDNA clone 5' similar to contains Alu repetitive element, mRNA sequence; Armadillo_seg,none; 2.74
 428536; AJ143139; Hs.2288; vishin-like 1; ehband;SS=M; 2.73
 400211; ; NM_003899; Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. VERSION NM_003897.1 GI; SH3,PH,RhoGEF,Terpeno_synt;TM=M; 2.73
 402129; ; Target Exon; SH2,Peptidase_C9;TM=M; 2.73
 424238; AA337401; Hs.137635; ESTs; none;TM=M;SS=M; 2.73
 433834; AA620742; Hs.130786; ESTs; SPX,EXS;TM=Y; 2.73
 409339; AB020686; Hs.54037; ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function); Sulfatase,Phosphodiester;TM=M;SS=M; 2.73
 408163; AW779842; Hs.258217; ESTs; 7tm_1,zf-B_box,zf-C3HC4,7tm_1,zf-B_box,zf-C3HC4; 2.73
 422358; AL133030; Hs.115429; Homo sapiens mRNA for KIAA1666 protein, partial cds; SH3;TM=M; 2.73
 426409; AA594207; ; gb:nn29e01.s1 NCL_CGAP_Gas1 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,Fibrillarin,none; 2.72
 400645; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor,none; 2.72
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fs, clone HEP11919; adenylatekinase,none; 2.71
 442572; AJ001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 2.71
 409317; U20165; Hs.53250; bone morphogenetic protein receptor, type II (BMPR2); pkinase,Activin_recpt;TM=M;SS=M; 2.71
 403201; ; Target Exon; none; 2.71
 459357; AW848421; ; gb:IL3-CT0214-150200-075-B11 CT0214 Homo sapiens cDNA, mRNA sequence; ABC_tran,ABC_membrane,ion_trans; 2.70
 439935; S75105; Hs.8358; glutamate receptor, ionotropic, kainate 2; ANF_receptor,lig_chan,none; 2.70
 414924; C06267; Hs.44247; ESTs; none,none; 2.69
 421008; BE259378; Hs.103147; hypothetical protein FLJ21347; DUF255; 2.69
 449951; AA004982; Hs.120904; ESTs; DED,Calsequestrin; 2.69
 411226; AW833022; ; gb:RC3-TT0005-191099-012-d04 TT0005 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.68
 417625; U59305; Hs.44708; Ser-Thr protein kinase related to the myotonic dystrophy protein kinase; pkinase,bZIP,G-gamma,K-box,pkinase_C;SS=M; 2.68
 408051; AJ623351; Hs.172148; ESTs; PH,RhoGAP,none; 2.68
 412521; AW753481; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 2.68
 413922; AJ535895; Hs.221024; ESTs; ion_trans,RYDR,ITPR,MIR,UDPGT; 2.68
 432188; AJ362952; Hs.2928; solute carrier family 7 (cationic amino acid transporter, y system), member 1; aa_permeases;TM=Y;SS=M; 2.67
 415516; F11411; ; gb:HSC2WF081 normalized infant brain cDNA Homo sapiens cDNA clone c-2w08, mRNA sequence; ion_trans,none; 2.67
 419749; X73608; Hs.93029; sparcosteonectin, cwcv and kazal-like domains proteoglycan (testican); kazal,thyroglobulin_1;SS=M; 2.66
 416095; AW014327; Hs.221951; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Ig,zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3,none; 2.66
 403609; ; C3001199;gi7494834|pir|T15308 hypothetical protein B0286.2 - Caenorhabditis elegans|41; 7tm_1,7tm_2,GPS,WIF;TM=Y;SS=M; 2.66
 458213; AL047521; Hs.12210; hypothetical protein FLJ13732 similar to tensin; pkinase,none; 2.66
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.66
 435410; AL135057; Hs.117182; ESTs; none,pkinase,RBD,DAG_PE-bind; 2.66
 437838; AJ307229; Hs.184304; ESTs; CARD,ICE_p20,ICE_p10,HIT,voltage_CLC,CBS,HCCA_Isomerase; 2.66
 430293; AJ416988; Hs.238272; inositol 1,4,5-triphosphate receptor, type 2; ion_trans,RYDR,ITPR,MIR,none; 2.65
 433090; AJ720050; ; Immunization-upregulated protein; none;SS=M; 2.65
 432103; T15803; Hs.272458; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); Metallophos;TM=M; 2.65
 435852; H72303; Hs.36011; ESTs; pkinase,none; 2.64
 433327; AJ674779; Hs.126744; ESTs; none,7tm_1; 2.64
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13555 fs, clone PLACE1011503; none,FMO-like; 2.64
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface receptor; none;TM=M;SS=M; 2.63
 446963; AJ862668; Hs.176333; ESTs; OMPDecase,Pribosyltran,pkinase,RhoGEF,PH; 2.63
 444821; AA053684; Hs.12040; STE20-like kinase; pkinase;TM=M; 2.63
 436206; AK001451; ; CD2-associated protein; none,none; 2.63
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic receptor; death,Kunitz_BPTI;TM=Y;SS=M; 2.63
 439039; AJ656707; Hs.48713; ESTs; pkinase,none; 2.63
 449656; AA002008; Hs.188533; ESTs; PIP5K,none; 2.63
 429341; X73874; Hs.2393; phosphorylase kinase, alpha 1 (muscle); none;TM=M; 2.62
 445174; AV652850; Hs.172004; titin; tn3,Ig,SGXSG,none; 2.62
 424950; AA602917; Hs.156974; ESTs; none,CDP-OH_P_transf; 2.62
 438141; AW946871; ; gb:RC2-ET0022-080500-012-d02 ET0022 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prot,none; 2.61
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC16169, mRNA, complete cds; pkinase,TBC,Rhodanese;TM=M; 2.61
 409264; NM_014937; Hs.52463; KIAA0966 protein; Syja_N;TM=M; 2.60
 458438; AI141520; Hs.151464; ESTs, Weakly similar to ALUC_HUMAN !!!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]; pkinase,none; 2.60
 400719; ; NM_004055; Homo sapiens calpain 5 (CAPN5), mRNA. VERSION NM_004335.2 GI; C2,Peptidase_C2,Capain_III;TM=M; 2.60
 427318; AF186081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 2.59
 426088; T94907; Hs.188572; ESTs; PH,Ets,CH,spectrin,Ca_channel_B,none; 2.59
 430105; X70297; Hs.2540; cholinergic receptor, nicotinic, alpha polypeptide 7; Neur_chan_LBD,Neur_chan_memb,pkinase;TM=Y;SS=M; 2.58
 411495; AP000693; Hs.70359; KIAA0136 protein; HATPase_c,bZIP;TM=M; 2.58
 438167; R28363; Hs.24286; ESTs; none;TM=Y;SS=M; 2.58
 418749; N75147; Hs.22488; ESTs; none,zf-C2H2,KRAB,pkinase; 2.58
 454289; AL137554; Hs.49927; protein kinase NYD-SP15; dCMP_cyt_deam;TM=M; 2.58
 443605; H06865; Hs.134131; ESTs; ehband,ion_trans,none; 2.57
 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 2.57
 403088; ; NM_003319; Homo sapiens titin (TTN), mRNA. mRNA; tn3,Ig,SGXSG;TM=M; 2.57
 409190; AU076536; Hs.50984; sarcoma amplified sequence; transmembrane4;TM=Y;SS=M; 2.57
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fs, clone HRC04468; Ig;TM=Y;SS=M; 2.56
 403328; ; Target Exon; Glyco_hydro_35;TM=M; 2.56

- 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS; 2.56
 428695; A1355647; Hs.189999; purinergic receptor (family A group 5); 7tm_1; TM=Y; SS=M; 2.54
 419285; D31887; Hs.89868; KIAA0062 protein; Zip; TM=Y; SS=M; 2.54
 415740; N80486; Hs.39911; Homo sapiens mRNA for FLJ00089 protein, partial cds; CBM_21; TM=M; 2.53
 403305; NM_006825; ; transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; pkinase; TM=Y; SS=M; 2.53
 443804; AL135352; Hs.255883; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Peptidase_M18,Peptidase_M18,Y_phosphatase; 2.53
 450425; H06607; Hs.6099; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,none; 2.51
 401702; ; NM_001171; Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA; ABC_tran,ABC_membrane; TM=Y; SS=M; 2.50
 439463; W69304; ; gb:zd4601.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5', mRNA sequence; fn3,Y_phosphatase,none; 2.50
 425975; AB011082; Hs.165559; organic cationic transporter-like 4; sugar_tr; TM=Y; 2.50
 443259; AW090601; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1,none; 2.50
 400777; ; NM_007325; Homo sapiens glutamate receptor, ionotropic, AMPA 3 (GRIA3), transcript variant flip, mRNA; lig_chan,SBP_bac_3,ANF_receptor; TM=M; SS=Y; 2.49
 426044; AA502490; Hs.170290; ESTs; none,none; 2.48
 454564; AW807573; ; gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapiens cDNA, mRNA sequence; pkinase,none; 2.48
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; KH-domain,TUDOR; TM=M; SS=M; 2.47
 426481; AW963941; ; gb:EST376014 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence; Y_phosphatase,Band_41,DSPC,none; 2.46
 426005; AA377499; ; gb:EST90341 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence; tubulin,FKBP,COX6B,7tm_1,tubulin_C; SS=M; 2.46
 424879; AA348013; Hs.273385; ESTs; arf-G-alpha,none; 2.46
 415156; X84908; Hs.78060; phosphorylase kinase, beta; none; TM=M; 2.46
 416508; R39769; ; ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; SH3,PDZ,Guanylate_kin,ZU5,none; 2.46
 408087; AW150645; ; gb:cg54107.x1 NCL_CGAP_U14 Homo sapiens cDNA clone 3', mRNA sequence; XYPPX,ABC_membrane,ABC_tran; 2.46
 433434; AA588429; ; gb:nc022b03.s1 NCL_CGAP_Pr22 Homo sapiens cDNA clone 3', mRNA sequence; pkinase,DNA_mis_repair,HATPase_c; 2.45
 446768; AV660305; Hs.110286; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 2.45
 437158; AW090198; ; KIAA1150 protein; none; NA; NA; 2.45
 430177; AW969233; Hs.302746; MSTP028 protein; K_tetra,none; 2.45
 422270; AF114494; Hs.114062; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member alpha; none; TM=Y; 2.45
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Y_phosphatase,Adaptin_N,Y_phosphatase; 2.44
 446569; AW248031; Hs.155839; hypothetical protein MGC12934; adh_zinc,PGK,Semialdehyde_dh; SS=M; 2.44
 411902; AW875344; ; gb:RC1-PT0009-220300-013-06 PT0009 Homo sapiens cDNA, mRNA sequence; none,pkinase,anic; 2.43
 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, type 1A (BMPRIA) (ALK-3); Activin_rec,pkinase; TM=Y; SS=M; 2.43
 446338; AJ289121; Hs.206978; ESTs; none,SH3; 2.42
 426221; AB007881; Hs.110613; KIAA0421 protein; none,Ribosomal_S8; 2.42
 446786; A1652497; Hs.110103; RNA polymerase I transcription factor RRN3; none,none; 2.41
 428360; H10291; Hs.30974; ESTs; pkinase,PBD,none; 2.40
 428379; X06026; Hs.2259; CD3G antigen, gamma polypeptide (TIT3 complex); ITAM; TM=Y; SS=M; 2.40
 432488; AA551010; Hs.216640; ESTs; Na_sulph_symp,none; 2.40
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, yeast, homolog)-like; none,Ribosomal_S13,Galactosyl_T,Zip,adh_shor,zf-C3HC4; 2.40
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT; TM=Y; SS=M; 2.40
 428283; A1439096; Hs.323079; Homo sapiens mRNA; cDNA DKFZp564P116 (from clone DKFZp564P116); Y_phosphatase,fn3,Ig,none; 2.39
 432460; H12912; Hs.274691; adenylate kinase 3; adenylatekinase,none; 2.38
 429549; A1333013; Hs.250505; retinoic acid receptor, alpha; none,zf-C3HC4,BRCT,Ig_chan; 2.38
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; Phosphodiester,Somatomedin_B,Endonuclease,none; 2.36
 417473; M55268; Hs.82201; casein kinase 2, alpha prime polypeptide; pkinase,ABC1; TM=M; 2.35
 453186; AK001708; Hs.32271; hypothetical protein FLJ10846; TK,DUF300; TM=Y; SS=M; 2.33
 447276; AL049795; Hs.17987; hypothetical protein MGC1203; none; TM=M; 2.33
 445310; AJ242490; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 2.31
 432942; AF083955; Hs.279852; G protein-coupled receptor; 7tm_1,globin; TM=Y; SS=M; 2.30
 434693; AW976001; Hs.337603; ESTs; none,none; 2.26
 452034; F12234; Hs.75893; ankyrin 3, node of Ranvier (ankyrin G); ZU5,death,none; 2.25
 423732; AF058056; Hs.132183; solute carrier family 16 (monocarboxylic acid transporters), member 7; sugar_tr; TM=Y; SS=M; 2.25
 404958; ; C1003210; gi|6912582|ref|NP_036524.1| poflin [Homo sapiens] gi|6009487|dbj|BAA84922.1| (AB; none,PI3_P4_kinase,PI3K_C2,PI3K_rbd,PX,PI3Ka,C2; 2.24
 452183; NM_006594; Hs.28298; adaptor-related protein complex 4, beta 1 subunit; Adaptin_N,Y_phosphatase; 2.23
 420529; D25259; Hs.319844; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase,DAG_PE-bind,RBD,ras,DC1,GFP; TM=M; 2.21
 408808; BE074219; Hs.17230; hypothetical protein FLJ22087; Armadillo_seg; TM=M; SS=M; 2.21
 451932; AA360954; Hs.27268; Homo sapiens cDNA: FLJ21933 fis, clone HEP04337; SH3,PH,RhoGEF; TM=M; 2.21
 432008; AW298791; Hs.193170; hypothetical protein FLJ21687; LIM,Synaptophysin,Ion_trans,KOW; 2.20
 455840; BE145897; ; gb:MR0-HT0208-221299-204-b07 HT0208 Homo sapiens cDNA, mRNA sequence; PI3_P4_kinase,PI3Ka,PI3_P4_kinase,PI3Ka; 2.19
 429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor type, R; Y_phosphatase; TM=Y; SS=M; 2.19
 430975; AA490055; ; gb:ab05b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 3', mRNA sequence; adenylatekinase,Thymidylate_kin; TM=M; 2.17
 407174; T79938; Hs.77062; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5; Ig,none; 2.16
 450921; AA098790; Hs.146245; ESTs, Moderately similar to T17242 hypothetical protein DKFZp568B1417.1 [H.sapiens]; none; NA; NA; 2.15
 427209; H06509; Hs.92423; KIAA1566 protein; pkinase; TM=M; 2.14
 401917; AL050149; ; RAN binding protein 3; Oreln,SH2,STAT,STAT_bind,STAT_prot,Ion_trans,PAC,PAS,none; 2.12
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase,none; 2.07
 439520; W76548; Hs.336621; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Ion_trans,none; 2.06
 410439; R35943; Hs.63758; transferrin receptor 2; PA; TM=Y; 2.05
 448698; A1564769; Hs.173070; EST, Weakly similar to ZN42_HUMAN ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1) [H.sapiens]; none,zf-C2H2; 2.04
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,Ion_trans,none; 2.04
 453496; AA442103; Hs.33084; solute carrier family 2 (facilitated glucose/fructose transporter), member 5; sugar_tr; TM=Y; SS=M; 2.02
 443952; A149106; Hs.143530; ESTs; pkinase,none; 2.02
 437589; AA761322; Hs.269662; ESTs; SH2,SH3,C2,PH,RasGAP,none; 2.02
 422637; AA399024; Hs.118838; myoglobin; globin; TM=M; 2.01
 450253; AL133047; Hs.24715; Homo sapiens mRNA; cDNA DKFZp434D0215 (from clone DKFZp434D0215); partial cds; SH3; TM=M; 1.97
 401984; ; C17000146; gi|2143629|pir|A57168 Ca2+-calmodulin-dependent protein kinase (EC 2.7.1.123) I; pkinase; 1.96
 453464; A1884911; Hs.32989; receptor (calcitonin) activity modifying protein 1; none; TM=Y; 1.95
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown protein; none; NA; NA; 1.94
 411450; H49619; Hs.127301; ESTs; pkinase,none; 1.82
 406303; ; C16000922; gi|7499103|pir|T20903 hypothetical protein F14F4.3b - Caenorhabditis elegans gi; ABC_tran,GTP_EFTU,PRK,ABC_membrane; TM=Y; 1.80
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor type, M; fn3,Ig,Y_phosphatase,MAAM; TM=Y; SS=M; 1.74

425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (soluble); PEPC; TM=M; 1.65
 425958; AW163271; Hs.301839; intracellular antigen detected by monoclonal antibody K1-1; Intracellular hyaluronan-binding protein; Y_phosphatase, DSPc; TM=M; 1.63
 432563; NM_013261; Hs.198468; peroxisome proliferative activated receptor, gamma, coactivator 1; nm; TM=M; 1.51

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TABLE 49B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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Pkey CAT Number Accession

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438091 22448_1 AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646053 AV651985 AV646184
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 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552
 BF999056 R63430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353
 BF155184 N98343 N79072 H01812 T55581

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414883 8371_2 AF274943 BG494894 AI19075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360
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451320 12225_2 AK057826 AJ311982 AA224195 AI701458 AA890570 AW966562 AW071907 AI671352 AI375892 T03517 AI214088 R88265 AI084316 BF223720
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400205 2538_1 NM_006265 D38551 X98294 BM477931 BM461568 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355
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400210 133_1 BC014030 NM_004068 BC004996 AK057883 D63475 BM468205 BG386792 BG750447 BG575842 BG479084 BG741027 AU118129 BE901043
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 AA375562 AA700011 AA926883 W37310 AL566236 BF677809 BG760021 AW361433 BE828605 BE268449 BF805977 BG292452 BF981071
 BF217108 BF928698 R33993 AW882841 AI857453 AW078733 AI433035 AI018103 R90927 AA804720 AA551734 R33835 H19741 R78754
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20	412283 1163164_1 409745 MH1944_5	AW936035 AW935951 AW935789 AW935881 AW936018 AW935892 BE069084 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
25	413285 12794_9 426578 358276_1 438005 694209_2 454701 352355_1 411140 1071177_1 407013 2073_7 432925 225876_1 417670 2139687_1	BE078405 BE078404 BE168534 AV742719 R23027 R63874 AA381749 BG542693 D63271 T94955 AA774994 BF697879 BG984482 AW854930 AW854941 AW814115 AW814431 AW814190 BF325887 BF325890 BF985536 AW819463 AW819514 AW819617 AW819618 AW819609 U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376 AA878324 AI619686 AI014377 T85948 R07785 T86972
30	400189 2140_1	Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589886 AI244419 AA749261 AA535435 AW206689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG828155 BF093014 AW837178 T77002 F13038
35	411331 1076355_1 418177 6503_2	AK056654 AJ420421 AI127111 AA705921 AA749298 AA776967 AI343768 AW070583 AA766587 AA804876 AA460658 AA394137 W72279 AW071467 AI343843 AA393817 AW769379 AA861873 AA715043 AW512448 AI452856 AI819873 T17354 AW779778 BF477620 AI783605 AI624523 AA261906 AA514931 BI964124 AW576481 AI864544 AA490863 AA860972 BI963076 AI632879 AA291985 AA255873 BI966876 BI963833 Z38970 BI495302 BI495301 AI784395 AU185472 AA652150 AA652026 D20449 BI088167 BI260636 BE869946 AI935271 BI792882 AI762915 AI809275 AI813351 BF447139 AI052069 AI057127 AA398950 AA291984 AA292934 AA262543 BF760287 R64455 R72980 H90786 BE698016 AW959314 BI031449 AL574617 AW76284 AA393770 BM455617 BI602104 BI793150 N36710 H59529 BI005937 BI600748 BF085914 BF085907 BF835429 BF835210 BF085926 AA226136 BF836829 BF836608 BM007373 AI669807 BF085930 W25119 BI252884 BI001270 BE549079 BF238403 R56934
40	439518 23842_1 400211 3532_1	AF086341 W76326 W72300 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 AJ032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE248232 D17055 AW013876 AW014877 T09464 T08407 AA830248 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904266 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448533 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16748 AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806296 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG988685 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
45		
50	426409 320121_1 459357 1086411_1 411226 1073516_1 415518 1875286_1 433090 7504_2 436206 31207_1	AW964027 AA377709 AW848421 T71427 T62567 AW833022 AW833054 H20760 R15237 Z43915 BF372479 F11411 AB038318 BC008888 BE905346 BE301941 AA705936 AW014954 BE378742 AI720050 BE395327 BG951204 AK001451 AU151098 AW515640 AW439618 AI671555 AW304963 AA565885 AI829434 AW590882 AI889234 AW117522 AA847824 AI636224 AA883540 AA169387 AW771571 AI130803 BF438773 AA088710 AI972638 AI762358 AI473907 AI925905 AA502277 BG943806 BG218468 AA194853 AU128875 AA306025 BG986896 AA778849 AW946871 AW946782 AW946955 AF086283 W69200 W69304 AW807573 AW807572 AW963941 AA379825 AW963944 AA379564
55		
60	438141 1173217_1 439463 23351_1 454564 1061820_1 426481 1229053_1 426005 MH790_19	NM_054014 X52220 BC005147 BI551326 AI393601 AW592611 AA608921 AA731598 W96331 AW590007 AI076813 AI022644 AA158365 AI699321 AI146747 AW296894 H85337 AA017692 AA354519 AA018512 D20081 R02704 AA825671 AA017651 AL135600 R02585 AA018849 BG749616 BF689840 R85326 AA677955 AA702354 AI076645 AI057359 H53178 W86484 H53074 BG988909 AW962456 AA367326 AA377499 R39769 T53143 H60012 AW150645 AW811024 AW811148 AW811068 BF812525 AW504832 AI972567 AA588429 AI299694 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393806 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AA68349 I19588 AW090199 AW043993 R39847 AW875344 AW875287 AW875285 AW875286 BF361295 AW875402 AW875400 BE145816 BE145897 BF349721 BE145885 AK057266 BI767614 BI828586 AW069362 BI829572 AI826091 BI819382 AL040402
65	416508 1974161_1 408097 633588_1 433434 194862_1 437158 59575_1	
70		
75		
80	411902 1141058_1 455840 1518844_1 430975 56593_2	

TABLE 49C

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
10	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	401027	7230983	Minus	70407-70554,71060-71160
	400991	8096825	Plus	159197-159320
	406137	9166422	Minus	30487-31058
15	404083	9944029	Minus	16650-17082
	404440	7528051	Plus	80430-81581
	400792	7382433	Plus	134339-134593
	404289	2769644	Plus	15049-15286,30287-30457
20	401083	3242744	Plus	33192-33360
	402211	7689783	Minus	67414-68229
	402705	8782736	Plus	89961-90114,90773-90895,91131-91261
	402233	7690102	Plus	90281-91477
25	405370	2078469	Minus	38980-39111
	400846	9188605	Plus	39310-39474
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	401345	9926424	Plus	148042-148392
30	400843	9188605	Plus	5883-5970,7653-7784,8892-9023,9673-9807,
	406364	9256114	Minus	50715-50833
	405490	7705240	Plus	20683-20850
	400755	8119083	Minus	120084-120889
35	404276	9885189	Plus	127624-127856
	402915	7406502	Minus	140-276
	405616	5649378	Minus	2782-3308
	400847	9188605	Plus	44643-44835
40	402328	4464283	Minus	13758-13922,14558-14752
	405369	2078469	Minus	34183-34357,35686-35751
	400845	9188605	Plus	34428-34612
	403716	7239669	Plus	86899-87122
45	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	404140	9843520	Plus	37761-38147
	405516	9454624	Plus	112707-112876,113676-113854
	405110	8096888	Minus	118940-119100
50	403608	8308266	Minus	121321-121476
	401241	4827300	Minus	30503-30844,31056-31248
	405102	8076881	Minus	120922-121296
	404185	4572584	Minus	129171-129327
55	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405411	3451356	Minus	17503-17778,18021-18290
	405602	4753260	Plus	44647-44778
	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,8797
60	403869	7280046	Minus	34379-34583
	404942	7382153	Plus	92095-92252
	403142	9444521	Plus	89286-90131
	400844	9188605	Plus	24746-24872,25035-25204
65	402704	8782736	Plus	37368-37493
	402833	8918545	Plus	26987-27778
	401851	7770425	Minus	148443-148684,147794-147971,148351-14848
	401242	4827300	Minus	32616-32863
70	401943	4914397	Plus	65925-66371
	402807	6456148	Minus	101542-101660,103476-103656
	402603	9909396	Minus	141663-141852
	405328	3253114	Plus	21399-21583
75	402974	9563349	Plus	124035-124321
	400987	8086488	Minus	22052-22185
	403335	8568884	Plus	112307-112524,114074-114703
	401113	9966541	Minus	19419-19959
80	401185	9825304	Minus	177393-177691
	404537	8247909	Minus	188775-189573
	405268	4156171	Minus	63337-63552
	402615	9926801	Plus	131390-132157
	400566	9884730	Plus	64486-64714
	403212	7630897	Minus	156037-156210
	403290	8083176	Plus	19288-20076
	401342	9908882	Plus	3096-3242
	400471	9931670	Minus	105629-105760
	405588	5002511	Plus	46180-46366
	400539	7574902	Plus	8559-8721
	403743	7652003	Minus	136463-136646
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	405099	8074292	Minus	114365-114514,128635-128831
	401445	8218584	Minus	93700-93886
	405480	2766593	Plus	33325-33659
	402183	7658390	Minus	100618-104298
	400749	7331445	Minus	9162-9293
	406139	9166768	Minus	72397-72602

5	402129	7704953	Minus	166156-166365
	400645	8117693	Minus	58471-58716
	403201	9958297	Minus	109782-109934
	403609	8308266	Minus	125974-126320
	400719	8118911	Minus	44579-44656,45294-45487,46449-46641
	403088	8954241	Plus	169894-170193,170504-170806
	403328	8469086	Minus	120428-120703
	403305	8099945	Plus	114632-114805
10	401702	1871197	Minus	68182-68325
	400777	8131653	Plus	70745-71121
	404956	7387343	Plus	55883-56203
	401917	9502466	Plus	25054-25229
	401984	4454511	Plus	103825-104024
15	406303	8575868	Plus	173622-173786

20 Table 50A lists about 414 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 85th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

25 Table 51A lists about 518 genes up-regulated in seminomatous testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" seminomatous testicular cancer level was set to the 85th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 Table 52A lists about 673 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal testicular adult tissues was greater than or equal to 2. The "average" testicular cancer level was set to the 75th percentile amongst testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

35 Table 53A lists about 735 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 3. The "average" testicular cancer level was set to the 95th percentile amongst testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 Table 54A lists about 476 testis-specific genes downregulated in testicular cancer (non-seminomatous and seminomatous). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio (R1) of normal testis to normal adult tissues was greater than or equal to 3. R1 was calculated as the mean number of interquartile range values over the median normal adult body tissue expression among normal testicular samples. The ratio (R2) of "average" normal testis to "average" testicular cancer among these genes was greater than or equal to 2. The "average" normal testis level was set to the 50th percentile amongst normal testis. The "average" normal testicular cancer level was set to the 95th percentile amongst testicular cancer samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

50 Table 55A lists about 586 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 95th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

55 Table 56A lists about 812 genes up-regulated in seminomatous testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" seminomatous testicular cancer level was set to the 50th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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TABLE 50A:
Pkey: Unique Eos probe set identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues

Pkey	ExAccn	Unigene	Unigene Title	R1
432666	AW204069		ESTs, Weakly similar to unnamed protein	74.60
432730	AI066520	Hs.131358	ESTs	50.55
450581	AF081513	Hs.25195	TGF-beta 4	47.85
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	44.05
423458	AI204212		ESTs	36.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	30.60
448981	AI968719	Hs.195387	ESTs	26.40
407710	AW022727	Hs.23616	ESTs	24.00
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.35
451106	BE382701	Hs.25960	N-MYC oncogene	18.85
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi]	18.40
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	18.25

	424578	AK001973	Hs.150890	hypothetical protein	17.86
	418756	AA252264	Hs.226949	ESTs	17.20
	404996			Target Exon	16.15
5	447534	AW953935	Hs.288655	ESTs	15.80
	456847	AI360456	Hs.37776	ESTs	15.00
	446979	AI654443	Hs.197683	ESTs	14.80
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome ragl	14.75
	452838	U55011	Hs.30743	preferentially expressed antigen in mela	14.70
10	449322	AI638616	Hs.196566	ESTs	14.35
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	12.95
	433330	AW207084	Hs.132818	hypothetical protein MGC14801	12.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi	12.55
15	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.43
	406547			Target Exon	12.35
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	12.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	11.65
	408908	BE296227	Hs.250822	serine/threonine kinase 15	11.55
20	437099	N77783	Hs.48659	ESTs, Highly similar to S14458 laminin a	11.05
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (10.08
	426866	U02330	Hs.172816	neuregulin 1	10.05
	446791	AI632278	Hs.195922	ESTs	9.85
	433159	AB035898	Hs.150587	kinesin-like protein 2	8.95
25	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.95
	427521	AW973352		ESTs	8.92
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	8.90
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.52
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
30	408465	AW196940	Hs.253277	ESTs	8.47
	444971	AI651116	Hs.148659	ESTs	8.35
	413318	AU076607	Hs.75285	Inter-alpha (globulin) Inhibitor, H2 pol	8.35
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	8.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.95
35	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75
	412265	AA101325	Hs.86164	hypothetical protein FLJ12457	7.65
	407340	AA810168	Hs.284289	villigo-associated protein VIT-1	7.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	7.36
	422958	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	7.25
40	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	7.22
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.13
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.13
	412537	AL031778		nuclear transcription factor Y, alpha	7.08
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	7.05
	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.88
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453392	U23752	Hs.32964	SRV (sex determining region Y)-box 11	6.75
	437052	AA861697	Hs.120591	ESTs	6.75
50	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.72
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.71
	457465	AW301344	Hs.122908	DNA replication factor	6.62
	442832	AW206560	Hs.253569	ESTs	6.54
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	6.30
55	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	6.30
	448588	AI970276	Hs.166906	KIAA1676	6.12
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	6.09
	415857	AA868115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	5.95
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	5.85
60	443068	AI188710		ESTs	5.85
	438450	AI050868	Hs.65853	nodal, mouse, homolog	5.81
	441287	AW293132	Hs.131373	ESTs	5.80
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	5.76
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
65	436902	AW247145	Hs.192729	ESTs	5.70
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
	432407	AA221036	Hs.13273	gb:zr03f12r1 Stratagene NT2 neuronal pr	5.56
	436812	AW298067		gb:U1-H-BWO-ajp-g-09-0-UI.s1 NCI_CGAP_Su	5.55
70	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.51
	431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransferase 3 be	5.51
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.45
	435663	AI023707	Hs.134273	ESTs	5.40
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.40
75	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.21
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	5.15
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.15
	430272	X04896	Hs.237658	apolipoprotein A-II	5.12
80	427961	AW293185	Hs.143134	ESTs	5.05
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.05
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN [III	5.00
	418477	AW022983		gb:U146h12.y1 Morton Fetal Cochlea Homo	5.00
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95

5	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.94
	443537	D13305	Hs.203	cholecystokinin B receptor	4.92
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	4.90
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	4.80
10	449592	AI655494	Hs.195718	ESTs	4.75
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stralagene HeLa cell s3 93	4.73
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.68
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.60
15	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-I	4.48
	402145			Target Exon	4.48
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	4.47
20	453289	AI188161	Hs.144627	ESTs	4.45
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	4.40
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	4.32
	426427	M86699	Hs.169840	TTK protein Kinase	4.30
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.20
25	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.18
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (4.15
	416209	AA238775	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.10
	438188	AA779975	Hs.128859	ESTs	4.10
	435514	AW592804		ESTs	4.10
30	442333	AI650877	Hs.129302	ESTs	4.05
	413627	BE182082	Hs.246973	Intron of Bicaudal D homolog 1	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	448038	AW016073	Hs.232026	ESTs, Weakly similar to RO52_HUMAN 52 KD	4.00
	458814	AJ498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.95
35	419423	D26488	Hs.90315	KIAA0007 protein	3.95
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	3.95
	441553	AA281219	Hs.121296	ESTs	3.95
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.91
	409757	NM_001898	Hs.123114	cystatin SN	3.89
40	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.88
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	3.85
	403780			C4001759:gl 133250 sp P19474 RO52_HUMAN	3.84
	421917	AB028943	Hs.109445	KIAA1020 protein	3.84
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.84
45	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	3.82
	410193	AJ132592	Hs.59757	zinc finger protein 281	3.80
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.80
	415829	AW450198	Hs.163742	ESTs	3.78
	440953	AJ683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.77
50	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.70
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.68
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.66
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	3.65
	420900	AL045633	Hs.44269	ESTs	3.65
55	426572	AB037783	Hs.170523	hypothetical protein FLJ11183	3.65
	426496	D31765	Hs.170114	KIAA0061 protein	3.60
	452461	N78223	Hs.108106	transcription factor	3.60
	418379	AA218940	Hs.137516	fidgin-like 1	3.50
	442573	H93365	Hs.7567	branched chain aminotransferase 1, cytos	3.48
60	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.45
	419384	AA490865	Hs.39429	ESTs	3.44
	453932	AW006303	Hs.328296	ESTs, Weakly similar to (define not ava	3.43
	446293	AJ420213	Hs.149722	LIM domain transcription factor LIM-1 (h	3.41
	422094	AF129535	Hs.272027	F-box only protein 5	3.40
65	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.40
	423198	M81933	Hs.1634	cell division cycle 25A	3.39
	424153	AA451737	Hs.141496	MAGE-like 2	3.38
	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.37
	443715	AI583187	Hs.9700	cyclin E1	3.34
70	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.34
	449571	AW016812	Hs.200266	ESTs	3.34
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31
	452807	AA028933	Hs.162434	ESTs	3.31
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	3.30
75	421650	AA781795	Hs.122587	ESTs	3.30
	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, elp	3.28
	438494	AA908678	Hs.130183	ESTs	3.23
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.22
	433764	AW753676	Hs.39582	zinc finger protein RINZF (NM_023929)	3.20
80	427642	R40761	Hs.9834	ESTs	3.20
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.18
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.18
	442618	R56222	Hs.26514	ESTs	3.17
	415799	AA653718	Hs.225841	DKFZP434D193 protein	3.17
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.15
	450431	AW136797	Hs.266041	ESTs	3.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.12

	430835	AI240006	Hs.192326	ESTs	3.12
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.10
	417791	AW965339	Hs.111471	ESTs	3.10
5	434609	R76593		gb:vi60c11.1 Soares placenta Nb2HP Homo	3.05
	430253	AK001514	Hs.235844	hypothetical protein FLJ10652	3.04
	411975	AI916058	Hs.144583	ESTs	3.01
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fls, clone NT	2.99
10	440207	AI371978	Hs.128325	ESTs	2.98
	435726	BE535787	Hs.113170	ESTs	2.97
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.97
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	2.95
	435373	AW665338	Hs.117689	ESTs	2.93
15	452571	W31518	Hs.34665	ESTs	2.93
	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	2.91
	414972	BE263782	Hs.77695	KIAA0008 gene product	2.90
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.90
	420092	AA814043	Hs.88045	ESTs	2.89
20	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.89
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.87
	422746	NM_004484	Hs.119651	glypican 3	2.87
	446258	AI283476	Hs.263478	ESTs	2.86
	444371	BE540274	Hs.239	forkhead box M1	2.86
25	409517	X90780		troponin I, cardiac	2.85
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	2.84
	443169	AI038687	Hs.133338	ESTs	2.84
	447519	U46258	Hs.339665	ESTs	2.84
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.84
30	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.83
	416201	AA467752	Hs.195161	ESTs	2.83
	412140	AA219591	Hs.73625	RAB6 interacting, kinesin-like (rabklins	2.83
	457191	AI376228		Friend leukemia virus integration 1	2.82
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.81
35	413646	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	2.80
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	2.75
	427719	AI393122	Hs.134726	ESTs	2.75
	451684	AF216751	Hs.26813	CDA14	2.75
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	2.74
40	442032	AW016786		ESTs	2.73
	437123	AL049285	Hs.302053	Homo sapiens mRNA; cDNA DKFZp564M193 (fr	2.72
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	2.72
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.71
	438180	AA808189	Hs.272151	ESTs	2.70
45	453900	AW003582	Hs.228414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.70
	423765	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.69
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	2.69
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	2.68
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.67
50	445413	AA151342	Hs.12677	CGI-147 protein	2.66
	448769	N66037	Hs.38173	ESTs	2.66
	411022	AW936378		gb:QV4-DT0021-301299-071-f05 DT0021 Homo	2.65
	423600	AI633559	Hs.310359	ESTs	2.65
55	447175	AI385208	Hs.293606	ESTs	2.65
	414151	AW976468	Hs.257245	ESTs	2.65
	448877	AI583696	Hs.253313	ESTs	2.62
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.61
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	2.61
	449665	AI655391	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.61
60	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.60
	429228	AI553633		ESTs	2.60
	410929	H47233	Hs.30643	ESTs	2.59
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.58
	446142	AI754693	Hs.145968	ESTs	2.58
65	445093	AI207197		ESTs	2.58
	413686	AI469213	Hs.71404	ESTs	2.55
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.55
	420218	AW958037		ribosomal protein L4	2.55
70	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	2.55
	414312	AA155694	Hs.191060	ESTs	2.55
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthet	2.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.52
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.51
	435096	AA664977		gb:nu73b07.s1 NCI_CGAP_Alv1 Homo sapiens	2.50
75	422468	AA355210		gb:EST63589 Jurkat T-cells V Homo sapien	2.50
	449576	AW014631	Hs.225068	ESTs	2.50
	415684	D59356		sorbitol dehydrogenase	2.50
	452226	AA024898	Hs.157103	ESTs	2.50
	421451	AA291377	Hs.50831	ESTs	2.50
80	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.50
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.49
	453941	U39817	Hs.36820	Bloom syndrome	2.49
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.49
	449655	AI021987	Hs.59970	ESTs	2.49

	430521	NM_016383	Hs.242183	HOM-TES-65 tumor antigen	2.49
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	2.48
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.48
5	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	2.47
	452404	AW450675	Hs.212709	ESTs	2.46
	444823	BE262989	Hs.12045	putative protein	2.46
	427675	AW138190	Hs.180248	zinc finger protein 124 (HZF-16)	2.45
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like 2 (bright	2.45
10	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.45
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.45
	447350	AI375572		v-erb-a avian erythroblastic leukemia vi	2.45
	428728	NM_016625	Hs.191381	hypothetical protein	2.43
15	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.43
	410276	AJ554545		angiopoietin-2	2.42
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.42
	419029	AA233397	Hs.326290	hypothetical protein FLJ12581	2.42
	437908	AJ082424		ESTs	2.41
20	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.41
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	2.40
	425212	AW962253	Hs.171618	ESTs	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.38
	425601	AW629485	Hs.140720	GSK-3 binding protein FRAT2	2.38
25	449576	AW380579	Hs.209657	ESTs	2.38
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.37
	453227	AW135862	Hs.243991	ESTs	2.37
	417833	AW003251	Hs.86264	hypothetical protein FLJ14549	2.36
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.36
30	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.35
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	2.35
	410060	NM_001448	Hs.58367	glypican 4	2.35
	449138	AW294215	Hs.195631	ESTs	2.35
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.35
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	2.35
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.34
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.34
	407818	AL021938	Hs.40154	jumonji (mouse) homolog	2.34
	417777	AJ823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	2.33
40	401704			NM_021195*:Homo sapiens claudin 6 (CLDN6	2.33
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	2.32
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.32
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.31
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.30
45	432865	AJ753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.30
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	2.30
	448755	AW503807	Hs.21907	histone acetyltransferase	2.30
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	2.29
50	441031	AJ110684	Hs.7645	fibrinogen, B beta polypeptide	2.29
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.28
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	2.27
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.26
	401220			branched chain aminotransferase 1, cytos	2.26
55	453985	N44545	Hs.251865	ESTs	2.25
	414890	BE281095	Hs.77573	uridine phosphorylase	2.25
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.25
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	2.25
	424765	AA428211		hypothetical protein FLJ14033 similar to	2.25
60	419278	AU076799	Hs.1247	apolipoprotein A-IV	2.24
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.24
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	2.23
	417273	AK002209	Hs.81831	Homo sapiens cDNA FLJ11347 fis, clone PL	2.23
	449722	BE280074	Hs.23960	cyclin B1	2.22
65	443184	AJ638728	Hs.131973	ESTs	2.22
	416391	AJ878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.21
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.21
	435045	BE297155	Hs.143698	ESTs	2.21
	414883	AA926960		CDC28 protein kinase 1	2.21
70	446323	AJ288274	Hs.345792	ESTs	2.20
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.20
	448757	AJ366784	Hs.48820	TATA box binding protein (TBP)-associat	2.20
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	2.20
	418973	AA233056	Hs.191518	ESTs	2.20
75	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.20
	434334	AA912477	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.20
	443748	AW208447		gb:U1-H-B11-atg-g-02-0-U1.s1 NCI_CGAP_Su	2.20
	415989	AJ267700		ESTs	2.20
80	400195			NM_007057*:Homo sapiens ZW10 interactor	2.20
	428878	AA436884	Hs.48926	ESTs	2.20
	431805	NM_014053	Hs.270594	FLVCR protein	2.19
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.19
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	2.18
	417389	BE260964	Hs.82045	midkine (neurtin growth-promoting factor	2.18

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	2.18
	413992	W26276	Hs.104557	RNA, U2 small nuclear	2.18
	412722	A1343300	Hs.15091	ESTs	2.18
	409089	NM_014781	Hs.50421	KIAA0203 gene product	2.17
	430809	A1791150	Hs.262009	ESTs, Moderately similar to I38022 hypo	2.17
	406542			C19000728::g 1258555Z sp Q9Y2Q1 Z257_HU	2.17
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.17
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothe	2.17
10	425580	L11144	Hs.1907	galanin	2.16
	439398	AA284267	Hs.221504	ESTs	2.16
	452833	BE559681	Hs.30736	KIAA0124 protein	2.15
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	2.15
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	2.15
15	449410	AA001356	Hs.18159	ESTs	2.15
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypothe	2.15
	427953	AA417944	Hs.44331	ESTs	2.15
	422281	M36803	Hs.346935	hemopexin	2.15
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.14
20	444960	AJ611317	Hs.341531	ESTs	2.14
	415890	H08225	Hs.268712	ESTs	2.14
	402099			ENSP000000217725*:Laminin alpha-1 chain p	2.14
	427779	AA906997	Hs.180780	TERA protein	2.14
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien	2.14
25	422170	A1791949	Hs.112432	anti-Mullerian hormone	2.14
	414161	AA136106	Hs.184852	KIAA1553 protein	2.14
	437623	D63880	Hs.5719	chromosome condensation-related SMC-esso	2.13
	449810	AB006681	Hs.23994	activin A receptor, type IIB	2.11
	450663	H43540	Hs.25292	ribonuclease HI, large subunit	2.11
30	419525	T79257	Hs.1259	asialoglycoprotein receptor 2	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.10
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.10
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.10
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (tr	2.09
35	418552	AF198254	Hs.86088	IGF-II mRNA-binding protein 1	2.09
	408291	AB023191	Hs.44131	KIAA0974 protein	2.09
	425474	Z48054	Hs.158084	peroxisome receptor 1	2.09
	453028	AB006532	Hs.31442	RacQ protein-like 4	2.09
	447831	AI433293	Hs.164115	ESTs	2.08
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.08
	429166	AB033096	Hs.197668	KIAA1270 protein	2.08
	432446	AA542845	Hs.294088	GAJ protein	2.08
	417865	AW087903	Hs.82772	collagen, type XI, alpha 1	2.07
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.07
45	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.07
	449569	AI656634	Hs.195389	ESTs	2.07
	429999	AI761902	Hs.99597	ESTs	2.06
	420552	AK000492	Hs.98806	hypothetical protein	2.06
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	2.05
50	406137			NM_000179*:Homo sapiens mufS (E. coli) h	2.05
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.05
	450375	AA009647		a disintegrin and metalloproteinase doma	2.05
	409066	AA062980	Hs.66960	ESTs	2.05
	425700	AF076292	Hs.159251	forkhead box H1	2.05
55	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fls, clone HE	2.05
	409093	BE243834	Hs.50441	CGI-04 protein	2.05
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.04
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434f143	2.04
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.04
60	429840	AA459699	Hs.99496	ESTs	2.03
	409717	AW452871	Hs.56043	CGI-115 protein	2.02
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.02
	448275	BE514434	Hs.20830	kinesin-like 2	2.02
	432731	R31178	Hs.287820	fibronectin 1	2.02
65	405157			NM_003213*:Homo sapiens TEA domain famil	2.02
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.01
	423739	AA398155	Hs.97600	ESTs	2.01
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	2.00
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	2.00
70	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.00
	407259	L02256		gb:Human Fab fragment binding syncytial	2.00

TABLE 50B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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80	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991848 AA864939
	423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
			BG215094 BG198867 BG196332 BG208220 BG212418

5	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
	427521	513212_1	AJ352469 BE061601 BI062752 AW818206 BF887722
	427486	684159_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AJ341422 AI206248 AI206165
	412537	14066_1	AA548736 AA768578 AU539081 AW025957 AA736837 N79575 AW594357 AA480892
10	418378	1227421_1	BF510715 BE673055 BE464111 AW590520 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
	422689	874209_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114
	435514	132288_1	AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364
	439780	49082_1	BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793
15	434609	14739_1	AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
	454679	174325_1	AV752763 AI032142 N30308 N22181 H95390 AW675632
	434414	35978_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
			BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
20	409517	4537_1	AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
	406687	0_0	AA218925 AW962081 AA354237
	457191	1389182_1	AW954733 AA315006 AW856665
	410704	1054673_1	AA683356 AW592804 AI150287
25	410704	1054673_1	AL109688 R23665 R26578
	413646	1525656_1	AF147390 R76593 R76594
	442032	15407_1	AW813110 BF771370 BF771371 AW813113 AW003381
	411022	106866_1	AF134164 BF809407 AA218567 BF842853 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
30	429228	215430_1	AA055556 BF773400 BF998669 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
	445093	175963_1	AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
	420218	191547_1	BF854337
	435096	125215_1	NM_000363 X54163 M64247 AI265781 AI706060 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070
35	422468	216674_1	C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255
	415684	18695_18	T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339
	447350	2267324_1	M31126
	437908	13268_11	AI216469 AI354789 AA446136 H24336 AA446443 AI376228 R48940
40	418866	245947_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
	424765	6857_1	BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
	414883	8371_2	AW840571
	400195	16894_2	BE155042 BE155040 BE154987 BE155012
45	400195	16894_2	BF223060 BF222818 AI950472 AW016788 AI207136 AI969730 BF222890 AI633857 AI968711 AA974235 AI352637
	450375	16559_3	AW936378 AW936544 AW813513
			BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE114620
			AW969605 AI553633
50	443748	669881_1	AI207197 BF773544 AW196462
	415989	10194_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
	400195	16894_2	AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
	450375	16559_3	H30075 AA684977 AW975278
55	400195	16894_2	AW962701 AA310998 AW962699
			BF666746 D59356 BG678312 N56640 AA166861
			AI375572 AM80404 BF430912 T06882
			AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
60			AI740586 AA771806 BE500996 AW204531 AI082424 AI033879 BF093176 AA771764 D38676
			T65754 AA229658 AA229857
			AK021881 AU145974 AU145787 C16964 AA428211 AU119698 AA993264 BF999192 AW903017 AA346559 AU119446 AW581679 AA991677
			AW898165 AW386878 AW890957 Z18340
65			AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI826996 AA527373 AW972459 AI831360
			AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871
			AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278897
			AA459292 AI94230 BF507531 AI492600 AA962596 AW613002 AA233140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407
70			AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
			BM467830 AI084433 AW206447 AI400976 AI248530 R16553
			BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172058 BE940298 BF909208 BF909980 BF095153
			BG285837 AI720344 BF541715 AA355086 AA172236
75			BM477554 BM423967 BC020979 AF067656 NM_007057 BI869291 BG468263 BG760599 BI261788 AA855060 BE257094 BF212452 BE888249
			BI259219 AW409765 BE089556 AL564377 BI258884 AW440401 AL578460 AL578434 AL556136 BG036804 AL531381 AW371767 BG610641
			BF102552 BE294929 BF792282 BG121657 BG502285 BG777493 AL564510 AW770358 AA573448 AA564001 AA969560 AW078946 AW750065
			AL573860 AA143778 H99221 AA969210 AW103401 AW750073
80			BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410
			H59605 BE157601 AA113758

TABLE 50C

Pkey:

Ref:

Strand:

NL_position:

Unique number corresponding to an Eos probaset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
406547	7711513	Minus	172780-174358
402145	8018280	Plus	113086-114800
403780	8076989	Plus	93160-93409
403432	9719611	Minus	68204-68392
401704	3097841	Plus	24712-25374
403433	9719611	Minus	72225-72437
401220	9929324	Minus	48079-48279
406542	7711499	Plus	117335-118473
402099	8117697	Plus	121553-121742,123265-123423
406137	9166422	Minus	30487-31068

405157 9966228 Plus 156363-156502,157573-157746

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TABLE 51A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of seminomatous testicular cancer compared to normal adult tissues

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	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	56.62
	432666	AW204089		ESTs, Weakly similar to unnamed protein	49.00
	432730	AI066520	Hs.131358	ESTs	37.64
	426534	U58096	Hs.2051	testis specific protein, Y-linked	37.60
20	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	32.70
	420367	AA259090	Hs.257028	ESTs	29.98
	420347	AI033539	Hs.97124	Human DNA sequence from clone RP1-309H15	26.50
	437052	AA861697	Hs.120591	ESTs	26.42
	407710	AW022727	Hs.23616	ESTs	23.85
25	420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	23.12
	424578	AK001973	Hs.150890	hypothetical protein	22.27
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	22.06
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	20.46
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	18.44
30	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	15.92
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	15.44
	423458	AI204212		ESTs	15.28
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	15.26
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	14.84
35	427687	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	12.98
	426427	M86699	Hs.169840	TTK protein kinase	12.44
	420401	AK001907	Hs.97464	hypothetical protein	12.40
	406937	U14622		gb:Human transketolase-like protein gene	11.60
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	11.55
40	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	11.52
	418477	AW022983		gb:xd46h12.y1 Morton Fetal Cochlea Homo	10.94
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	10.78
	436812	AW298067		gb:UH-H-BWO-gjp-g-09-0-UI.s1 NCL CGAP_Su	10.54
	437789	AI561344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	10.40
45	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	10.32
	421241	X91817	Hs.102866	transketolase-like 1	10.14
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi]	10.02
	418134	AA397769	Hs.86617	ESTs	9.76
	433159	AB035898	Hs.150587	kinesin-like protein 2	9.56
50	433975	AA971953	Hs.122055	ESTs	9.36
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	9.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	9.22
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	9.16
	436899	AA764852		ESTs	8.76
55	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.76
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	8.64
	408908	BE296227	Hs.250822	serine/threonine kinase 15	8.50
	413627	BE182082	Hs.246973	Intron of Bicaudal D homolog 1	8.42
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	8.30
60	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.14
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	8.14
	406547			Target Exon	8.02
	424153	AA451737	Hs.141496	MAGE-like 2	7.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.64
65	437421	AA917062		ESTs	7.53
	409731	AA125985	Hs.58145	thymosin, beta, identified in neuroblast	7.50
	419423	D26488	Hs.80315	KIAA0007 protein	7.38
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.38
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.32
70	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (7.29
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	7.25
	435206	AI432364	Hs.160594	ESTs	7.20
	414972	BE263782	Hs.77695	KIAA0008 gene product	7.12
	407340	AA810168	Hs.284289	vitellogenesis-associated protein VIT-1	7.10
75	426518	Z43039	Hs.170198	KIAA0009 gene product	7.10
	436513	AJ278110	Hs.125507	DEAD-box protein	7.04
	427521	AW973352		ESTs	6.98
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.92
	422232	D43945	Hs.113274	transcription factor EC	6.90
80	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	6.83
	431041	AA490967	Hs.197855	KIAA0704 protein	6.76
	427335	AA448542	Hs.251677	G antigen 7B	6.58
	422797	AB033064	Hs.236463	KIAA1238 protein	6.55
	418379	AA218940	Hs.137516	fidgetin-like 1	6.46

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	6.45
	433764	AW753676	Hs.39982	zinc finger protein RUNZF (NM_023929)	6.44
	422665	AJ011812	Hs.119018	transcription factor NRF	6.38
	433701	AW445023	Hs.15155	ESTs	6.34
	436909	AA907120		ESTs	6.28
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	6.27
	429228	AJ553633		ESTs	6.26
	419384	AA490866	Hs.39429	ESTs	6.23
10	435514	AW592804		ESTs	6.08
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	5.90
	430835	AI240006	Hs.192326	ESTs	5.89
	438188	AA779975	Hs.128859	ESTs	5.88
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	5.80
15	408758	NM_003656	Hs.47504	exonuclease 1	5.78
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	5.70
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.67
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	5.64
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	5.58
20	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothi	5.58
	419556	U29615	Hs.91093	chitinase 1 (chitinobiosidase)	5.55
	438494	AA908678	Hs.130183	ESTs	5.52
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	5.52
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.48
25	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	5.45
	413623	AA825721	Hs.246973	Intron of Bicaudal D homolog 1	5.36
	402145			Target Exon	5.30
	414136	AA812434		SMC2 (structural maintenance of chromoso	5.28
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	5.22
30	428949	AA442153	Hs.104744	hypothetical protein DKFP434J0617	5.16
	408460	AA054726	Hs.285574	ESTs	5.14
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.12
	420900	AL045633	Hs.44269	ESTs	5.08
	426496	D31765	Hs.170114	KIAA0061 protein	5.01
35	407122	H20276	Hs.31742	ESTs	5.00
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.95
	402199			Target Exon	4.90
	409103	AF251237	Hs.112208	XAGE-1 protein	4.90
	416859	H43437	Hs.80305	hypothetical protein MGC14258	4.84
40	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	4.82
	410929	H47233	Hs.30643	ESTs	4.73
	417886	AA214584		ESTs	4.73
	426223	AW977812	Hs.130391	ESTs	4.72
	409421	AA199883	Hs.67624	ESTs	4.72
45	428249	AA130914	Hs.183291	zinc finger protein 268	4.71
	429999	AI761902	Hs.99597	ESTs	4.68
	431721	AB032996	Hs.268044	KIAA1170 protein	4.68
	408321	AW405882	Hs.44205	coristatin	4.67
	419197	N48921	Hs.27441	KIAA1615 protein	4.66
50	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	4.64
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	4.64
	427119	AW880562	Hs.272525	ESTs	4.64
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.64
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.64
55	409066	AA062980	Hs.66960	ESTs	4.62
	416201	AA467752	Hs.195161	ESTs	4.53
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.52
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.50
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	4.46
60	415799	AA653718	Hs.225841	DKFP434D193 protein	4.46
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.34
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	4.32
	418971	AA360392	Hs.87113	ESTs	4.30
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (4.29
65	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.21
	415717	AA167270	Hs.130435	ESTs	4.18
	423198	M81933	Hs.1634	cell division cycle 25A	4.12
	433849	BE465884	Hs.280728	ESTs	4.12
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.11
70	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.07
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFP434B0425 (f	4.07
	414725	AA769791		ring finger protein 21, interferon-respo	4.05
	408291	AB023191	Hs.44131	KIAA0974 protein	4.05
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFP564B083 (fr	4.04
75	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.04
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.03
	421917	AB028943	Hs.109445	KIAA1020 protein	4.02
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	4.02
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.01
80	436360	AI962796	Hs.156100	ESTs	4.00
	438624	AA889055	Hs.123468	ESTs	3.99
	434609	R76593		gb:yl60c11.1.r1 Soares placenta Nb2HP Homo	3.92
	411945	AL033527	Hs.92137	L-myo-2 protein(MYCL2)	3.90
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.90

	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.90
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.88
	438456	AA913381	Hs.20594	ESTs	3.88
5	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B)	3.87
	412537	AL031778		nuclear transcription factor Y, alpha	3.86
	418651	NM_001949	Hs.1189	E2F transcription factor 3	3.85
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	3.83
	422094	AF129535	Hs.272027	F-box only protein 5	3.82
10	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.80
	416350	AF188625	Hs.189507	phospholipase A2, group IID	3.78
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.76
	401435			C140003977:gl[7499898]pir[733295] hypoth	3.76
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	3.74
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.70
15	409089	NM_014781	Hs.50421	KIAA0203 gene product	3.70
	426067	AW664691	Hs.97053	ESTs	3.67
	415684	D69356		sorbitol dehydrogenase	3.66
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.62
20	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	3.62
	427761	AA412205	Hs.140996	ESTs	3.61
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	3.60
	418216	AA662240	Hs.283099	AF15q14 protein	3.59
	438180	AA808189	Hs.272151	ESTs	3.58
25	424281	AA766243		gb:aa13b11.s1 NCI_CGAP_GC81 Homo sapiens	3.56
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.55
	428878	AA436884	Hs.48926	ESTs	3.54
	438885	AJ886558	Hs.184987	ESTs	3.53
	416445	AL043004	Hs.79337	KIAA0135 protein	3.52
30	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.51
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.49
	427298	AA400495		ESTs	3.48
	420218	AW958037		ribosomal protein L4	3.40
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.40
35	410420	AA224053	Hs.172405	cell division cycle 27	3.40
	432809	AA565509	Hs.131703	ESTs	3.36
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.34
	421373	AA808229	Hs.46677	ESTs	3.34
40	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.31
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	3.30
	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.30
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.26
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.22
	432407	AA221038	Hs.13273	gb:zn03f12.r1 Stratagene NT2 neuronal pr	3.21
45	434288	AW189075	Hs.116265	fibrillin3	3.20
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.19
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.17
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.17
	420161	AJ683069	Hs.120817	ESTs	3.17
50	414618	AJ204800	Hs.96978	hypothetical protein MGC10764	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.14
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.14
	423419	R55336	Hs.23539	ESTs	3.13
	410275	U85658	Hs.61786	transcription factor AP-2 gamma (activat	3.12
55	408092	NM_007057	Hs.42650	ZW10 Interactor	3.12
	423685	BE350494	Hs.49763	uveal autoantigen with coiled coil domai	3.12
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.12
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.12
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.11
60	420552	AK000492	Hs.98806	hypothetical protein	3.11
	402408			NM_030920:Homo sapiens hypothetical pro	3.10
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.10
	415829	AW450198	Hs.163742	ESTs	3.09
	423739	AA398155	Hs.97600	ESTs	3.07
65	418459	R85436	Hs.268814	ESTs	3.07
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.07
	437257	AJ283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	3.06
	429830	AJ537278	Hs.225841	DKFZP434D193 protein	3.06
	420524	AB010575	Hs.98547	amiloride-sensitive cation channel 3, te	3.06
70	433023	AW864793		thrombospondin 1	3.04
	421633	AF121860	Hs.108260	sorting nexin 10	3.04
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.04
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	3.03
	414598	AJ094221	Hs.135150	lung type-I cell membrane-associated gly	3.03
75	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (3.03
	425312	AA354940	Hs.145958	ESTs	3.02
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.01
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.01
	432446	AA542845	Hs.294088	GAJ protein	3.01
80	424513	BE385884	Hs.149894	mitochondrial translational initiation f	3.00
	436902	AW247145	Hs.192729	ESTs	3.00
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.00
	430056	X97548	Hs.228059	KRAB-associated protein 1	2.98
	427617	D42063	Hs.199179	RAN binding protein 2	2.98

	406367		NM_022357: Homo sapiens putative metalop	2.97
	418866	T65754	gb:yc11c07.s1 Stratagene lung (937210) H	2.97
	435918	AF263538	Hs.86232 growth differentiation factor 3	2.97
	436511	AA721252	Hs.291502 ESTs	2.96
5	402680		Target Exon	2.96
	414161	AA136186	Hs.184852 KIAA1553 protein	2.95
	427239	BE270447	ubiquitin carrier protein	2.95
	433683	AI817723	Hs.22678 hypothetical protein FLJ21832	2.94
10	417576	AA339449	Hs.82285 phosphoribosylglycinamide formyltransfer	2.94
	402299		Target Exon	2.92
	420697	AA827705	Hs.26605 ESTs	2.90
	427719	AI393122	Hs.134726 ESTs	2.90
	419131	AA406293	Hs.109526 ESTs	2.89
	410048	W76467	Hs.343874 proline oxidase homolog	2.89
15	427314	AB033024	Hs.175475 KIAA1198 protein	2.89
	424315	AW614850	Hs.193384 putative 28 kDa protein	2.88
	430335	D80007	Hs.239499 KIAA0185 protein	2.87
	410361	BE391804	Hs.62661 guanylate binding protein 1, interferon-	2.87
20	413686	AI469213	Hs.71404 ESTs	2.87
	429183	AB014604	Hs.187955 KIAA0704 protein	2.88
	430292	AK000634	Hs.238270 hypothetical protein FLJ20627	2.86
	422726	U11690	Hs.1572 faciogenital dysplasia (Aarskog-Scott sy	2.86
	437834	AA769294	gb:nc36g03.s1 NCI_CGAP_GCB1 Homo sapiens	2.86
25	435159	AA668879	Hs.116649 ESTs	2.84
	428361	NM_015905	Hs.183858 transcriptional intermediary factor 1	2.84
	430388	AA356923	Hs.240770 nuclear cap binding protein subunit 2, 2	2.84
	434070	AF116652	Hs.270087 hypothetical protein PRO0813	2.83
	429323	NM_001649	Hs.2391 apical protein, Xenopus laevis-like	2.83
30	433247	AB040948	Hs.142856 KIAA1515 protein	2.82
	415884	H22966	Hs.13471 ESTs	2.82
	427668	AA298760	Hs.180191 hypothetical protein FLJ14904	2.82
	437162	AW005505	Hs.5464 thyroid hormone receptor coactivating pr	2.81
	401091		decay accelerating factor for complement	2.81
35	425601	AW629485	Hs.140720 GSK-3 binding protein FRAT2	2.79
	428597	AK000147	Hs.295909 hypothetical protein FLJ10700	2.79
	417705	AW134952	Hs.175220 hypothetical protein FLJ14541	2.79
	438243	AI581311	ESTs	2.78
	418203	X54942	Hs.83758 CDC28 protein kinase 2	2.78
40	410704	BE076754	gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.77
	429063	AW363845	Hs.322903 ESTs, Weakly similar to A46010 X-linked	2.76
	427147	AA398587	Hs.97414 ESTs	2.76
	430552	AA176374	Hs.243886 nuclear autoantigenic sperm protein (his	2.76
	437660	W31708	Hs.55304 ESTs	2.74
45	425237	U07695	Hs.155227 EphB4	2.72
	419335	AW960146	Hs.284137 hypothetical protein FLJ12888	2.72
	426386	AA748850	Hs.125830 bladder cancer overexpressed protein	2.70
	423123	NM_012247	Hs.124027 SELENOPHOSPHATE SYNTHETASE ; Human selen	2.70
	430958	AW972830	gb:EST384925 MAGE resequences, MAGL Homo	2.70
50	420596	NM_002692	Hs.99185 polymerase (DNA directed), epsilon 2	2.68
	419741	NM_007019	Hs.93002 ubiquitin carrier protein E2-C	2.68
	401464		histone deacetylase 5	2.68
	411856	H67899	Hs.4190 Homo sapiens cDNA: FLJ23269 fis, clone C	2.68
	411365	M76477	Hs.289082 GM2 ganglioside activator protein	2.68
55	419029	AA233397	Hs.326290 hypothetical protein FLJ12581	2.67
	421654	AW163267	Hs.106469 suppressor of var1 (S.cerevisiae) 3-like	2.66
	421535	AB002359	Hs.105478 phosphoribosylformylglycinamide syntha	2.66
	423453	AW450737	Hs.128791 CGT-09 protein	2.66
	412673	AL042957	Hs.31845 ESTs	2.65
60	410006	AW732308	Hs.57783 eukaryotic translation initiation factor	2.65
	434159	AW135214	Hs.191828 ESTs	2.65
	427260	AA663848	gb:aa70b06.s1 Stratagene schizo brain S1	2.64
	439053	BE244588	Hs.6456 chaperonin containing TCP1, subunit 2 (b	2.64
	414706	AW340125	Hs.76989 KIAA0097 gene product	2.64
65	433979	AA620999	gb:ag03a08.s1 Soares_testis_NHT Homo sap	2.64
	403969		ENSP00000034663: Zinc finger protein 131	2.64
	420582	BE047878	Hs.99093 Homo sapiens chromosome 19, cosmid R2837	2.64
	418355	L42563	Hs.1165 ATPase, H7 transporting, nongastric, alp	2.63
	411127	AA668995	Hs.218329 hypothetical protein	2.62
70	437205	AL110232	Hs.279243 Homo sapiens mRNA; cDNA DKFZp564D2071 (f	2.62
	412123	BE251328	Hs.73291 hypothetical protein FLJ10881	2.61
	436481	AA379697	Hs.5199 HSPC150 protein similar to ubiquitin-con	2.60
	408446	AW450669	Hs.45068 hypothetical protein DKFZp434i143	2.59
	437033	AW248364	Hs.5409 RNA polymerase I subunit	2.58
75	418592	X99226	Hs.284153 Fanconi anemia, complementation group A	2.58
	415585	R59946	Hs.184852 KIAA1553 protein	2.57
	424800	AL035588	Hs.153203 MyoD family inhibitor	2.57
	426470	AA528794	Hs.126844 ESTs	2.57
	426919	AL041228	ELAV (embryonic lethal, abnormal vision,	2.56
80	421209	AJ010230	Hs.102576 ret finger protein-like 1 antisense	2.56
	437496	AA452378	Hs.146668 Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.56
	401837		NM_025109: Homo sapiens hypothetical prot	2.56
	428743	AL080060	Hs.301549 Homo sapiens mRNA; cDNA DKFZp564H172 (fr	2.56
	422809	AK001379	Hs.121028 hypothetical protein FLJ10549	2.55

	418648	AW979223	Hs.292478	ESTs	2.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.54
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.54
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	2.54
5	428728	NM_016625	Hs.191381	hypothetical protein	2.53
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	2.52
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	2.52
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.52
10	422406	AF025441	Hs.116208	Opa-Interacting protein 5	2.52
	433228	F28212	Hs.14953	KIAA1491 protein	2.51
	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44508 C02F5.6 p	2.51
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.50
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.50
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.48
15	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14235 fis, clone NT	2.48
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.47
	435726	BE535787	Hs.113170	ESTs	2.47
	404068			Target Exon	2.46
20	403137			NM_005381*:Homo sapiens nucleolin (NCL),	2.46
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppressor	2.46
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.46
	429652	AA766810	Hs.259290	ESTs	2.45
	416204	AW972270	Hs.195161	ESTs	2.45
25	414713	BE465243	Hs.12664	ESTs	2.44
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.44
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.44
	435244	N77221	Hs.187824	ESTs	2.44
	402679			NM_000478:Homo sapiens alkaline phosphat	2.43
30	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.42
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.41
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisqu	2.41
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.41
	423232	BE244625	Hs.125742	leucine-rich neuronal protein	2.40
35	427578	AI591305	Hs.169084	ESTs, Highly similar to TUL3_HUMAN TUBBY	2.40
	409934	R91601	Hs.190466	hypothetical protein FLJ22584	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	2.39
	438869	AF076009		gb:Homo sapiens full length insert cDNA	2.38
40	434981	AW182577	Hs.293077	ESTs	2.38
	417911	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (2.38
	409210	AA251812	Hs.51120	cathelicidin antimicrobial peptide	2.37
	424425	AB031480	Hs.146824	SPR1 protein	2.37
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	2.37
45	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	2.37
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.37
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	2.36
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (52k	2.36
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	2.36
50	410968	AA199907	Hs.67397	homeo box A1	2.36
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	2.36
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	2.36
	412389	AW947655		gb:RC0-MT0003-140300-031-b07 MT0003 Homo	2.35
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.35
55	403780			C4001759:gil133250[sp]P19474[RO52_HUMAN	2.34
	437681	AJ207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	2.34
	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	2.34
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	2.34
60	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	2.34
	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	2.33
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.33
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.32
	418821	AA436002	Hs.183161	ESTs	2.32
	437437	AA226859		hypothetical protein DKFZp762L0311	2.32
65	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.31
	425848	BE242709	Hs.159637	valyl-tRNA synthetase 2	2.30
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.30
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	2.30
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	2.29
70	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	2.29
	427728	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	2.29
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.28
	412721	AW183165	Hs.95600	ESTs	2.28
	404071			C12000514*:gil7302471[gb]AAF57556.1[AE	2.27
75	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.26
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.26
	424935	AI655010	Hs.120363	hypothetical protein MGC15634	2.28
	415791	H09366	Hs.78853	uracil-DNA glycosylase	2.26
	431667	AA812573	Hs.245787	ESTs	2.26
	424169	AA336399	Hs.153797	ESTs	2.25
80	436540	BE397032	Hs.14468	hypothetical protein MGC14226	2.25
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	2.24
	403242			Target Exon	2.24
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.24

	421002	AF116030	Hs.100932	transcription factor 17	2.24
	438833	BE612940	Hs.88252	ESTs	2.24
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	2.23
5	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	2.23
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.23
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	2.23
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.23
	435251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.23
10	418826	AK000375	Hs.88820	HDCMC28P protein	2.23
	428612	AA770001		ESTs	2.22
	433220	AI076192	Hs.131933	ESTs	2.22
	422225	BE245652	Hs.118281	zinc finger protein 266	2.22
	437549	AA759149	Hs.128757	gbrah70e03.s1 Soares_testis_NHT Homo sap	2.22
15	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.22
	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.22
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.21
	420062	AW411096	Hs.94785	TGF(beta)-induced transcription factor 2	2.21
	432820	AI554057	Hs.152477	ESTs	2.21
20	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.21
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.20
	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_U14 Homo sapiens	2.20
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	2.20
	423875	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	2.20
25	433698	H24201	Hs.247423	adducin 2 (beta)	2.19
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	2.19
	435541	AA687361	Hs.221318	ESTs	2.19
	412019	AA485890	Hs.69330	Homo sapiens cDNA FLJ13835 fis, clone TH	2.19
	418753	BE217818	Hs.87016	hypothetical protein FLJ22938	2.19
30	435461	AI075846	Hs.133996	ESTs	2.19
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	2.18
	421098	AI697901	Hs.192425	ESTs	2.18
	400587			C10000649*:gll7296574[gb]AAF51857.1] (AE	2.18
	407832	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.18
35	427159	U80735	Hs.173854	PAX transcription activation domain inte	2.17
	405770			NM_002362:Homo sapiens melanoma antigen,	2.17
	412722	AI343300	Hs.15091	ESTs	2.16
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.16
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.16
40	417420	T85150	Hs.268814	ESTs	2.16
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	2.16
	412851	AI826502	Hs.97269	ESTs	2.16
	414702	L22005	Hs.76932	cell division cycle 34	2.16
	409670	AI368109		KIAA1856 protein	2.16
45	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.15
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.15
	434750	BE019254	Hs.4112	t-complex 1	2.15
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.15
	418574	N28754		M-phase phosphoprotein 9	2.15
50	409019	AW385412		myosin regulatory light chain 2, smooth	2.15
	416608	R11499	Hs.189716	ESTs	2.14
	436027	AI864063	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.14
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	2.13
	422805	AA436989	Hs.121017	H2A histone family, member A	2.13
55	410284	U50939	Hs.61828	amyloid beta precursor protein-binding p	2.13
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.12
	430935	AW072916		zinc finger protein 131 (clone pMZ-10)	2.12
	433252	AB040957	Hs.151343	KIAA1624 protein	2.12
	416819	U77735	Hs.80205	plm-2 oncogene	2.12
60	437218	AL117497	Hs.58185	ESTs, Weakly similar to T42727 prolifera	2.12
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	2.12
	433947	AA927996	Hs.112876	ESTs, Weakly similar to AF129535 1 F-box	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.11
	435703	AW630133	Hs.83313	GK003 protein	2.11
65	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.11
	422192	AA305159	Hs.113019	fts485	2.11
	407861	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	2.10
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.10
	414151	AW976468	Hs.257245	ESTs	2.10
70	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.10
	424196	AL133660	Hs.142926	Homo sapiens beta cysteine string protei	2.10
	408831	AF090114	Hs.48433	endocrine regulator	2.10
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	2.09
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	2.09
75	409637	AA323948	Hs.55407	Homo sapiens mRNA: cDNA DKFZp434K0621 (f	2.09
	403532			NM_024638:Homo sapiens hypothetical prot	2.09
	432141	BE410964	Hs.272736	nuclear receptor binding protein	2.08
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.08
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.08
80	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	2.08
	418755	Y14443	Hs.88219	zinc finger protein 200	2.08
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.07
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.07
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protel	2.07

5	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.07
	417230	U40998	Hs.81728	unc119 (C.elegans) homolog	2.07
	425966	NM_001761	Hs.1973	cyclin F	2.07
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine receptor	2.06
	407162	N63855	Hs.142634	zinc finger protein	2.06
	422382	D79888	Hs.115778	KIAA0166 gene product	2.06
	402677		NM_000478	Homo sapiens alkaline phosphatase	2.06
	433017	Y15067	Hs.279914	zinc finger protein 232	2.05
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	2.05
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.05
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.05
	402678			Target Exon	2.05
	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.05
	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	2.04
15	427447	T65414	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT	2.04
	433219	AB040916	Hs.24106	KIAA1483 protein	2.04
	431126	AF085243	Hs.283619	zinc finger protein 236	2.04
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	2.04
	419669	AJ007041	Hs.92236	KIAA0304 gene product	2.04
20	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.03
	426242	AL096727	Hs.168249	Homo sapiens mRNA; cDNA DKFZp434B104 (fr	2.02
	432185	AA221032	Hs.272838	hypothetical protein FLJ10494	2.02
	437108	AA434054	Hs.80624	hypothetical protein MGC2550	2.02
	408636	BE294925	Hs.46680	CGI-12 protein	2.02
25	420005	AW271106	Hs.133294	ESTs	2.02
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.02
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.02
	425358	AL079658	Hs.338207	FK506 binding protein 12-rapamycin assoc	2.01
30	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.01
	438450	AI050866	Hs.65853	nodal, mouse, homolog	2.00
	431629	AJ077025	Hs.265827	interferon, alpha-inducible protein (clo	2.00
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial (DNA dire	2.00
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.00
35	414251	AL042306	Hs.97689	VASA protein	2.00

TABLE 51B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

40	Pkey	CAT Number	Accession
45	432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
	423458	30480_1	BC018070 BG702493 AI204212 AA60929 AA93606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
			BG215094 BG198867 BG196332 BG208220 BG212418
	418477	4172_1	BC022538 AI990847 BF478249 BG217966 BG212702 BG182057 AW589883 BF000085 AA93969 BG479023 BG220014 BG679466 BE907092
			AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA84705 AI910424
50	436812	659779_1	AW978773 AW280867 AA810101 AW194180 AA731645 AI690673
	436899	1000797_1	AA764852 AA736937
	437421	978554_1	AA917062 AA757369 AW592218
	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
			AI352469 BE061601 BI062752 AW818206 BF887722
55	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059501 AI961162 AI341422 AI206248 AI206165
			AA548738 AA768578 AI539081 AW025957 AA738837 N79575 AW594357 AA480892
	436909	596835_1	AW102570 AA907150 AA907120 AA737188 AI248890 AW977353
	429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620
			AW969605 AI553833
60	435514	132288_1	AA683356 AW592804 AI150287
	422689	874209_1	AW954733 AA315006 AW856665
	421974	864120_1	AA301270 AA301379 AA301366
	414136	30243_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920
			AI566634 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AI154486
65			AW605017 AW450072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812
	417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
	418235	886897_1	BE072634 BE072653 AA830615 AA214736 AA331718
	414725	19377_1	NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936
			AI650276 AI654206 BE503226 AI651327 AW873562 AW21269 AW271565 AI873518 AI207150 AI338826 AI650258 AI626362 AA227117 AI207149
70			AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112
			BI054316
	434609	14739_1	AF147390 R76593 R76594
	408065	101881_1	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
	412537	14066_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114
75			AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N65509 AA736741 AA382555 AW075811 AV759188 BI259384
			BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793
			AA382556 AW235763 AA927051 AI852075 BE886691 BE619282
	415684	18695_18	BF666746 D59356 BG678312 N56640 AA166861
	433641	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080233 AL535594
80			AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680633 AW614951
			N29986 N25695 H69001 U87598 BE673974 AI797496 AI701526 AA703395 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611
			AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833
			AA207155 BI004758 AA206262 AI365204 H77608 AW590511
	424281	892055_1	AA338252 AA338213

427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
420218	191547_1	AW958037 R42557 AJ337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
418049	12052_4	AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
433023	3970_8	AJ314547 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234
418866	245947_1	AV731417 R42406 H04996 T98498 R12489 R12577 R42405
427239	20459_2	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148
		AJ968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
		T65754 AA229658 AA229857
		AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
		AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
		AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
		AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420
		AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
		AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
		BF187773 BF718645 AW074868 BE857822
		BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296
		AA769294 AW749297 AW749295 AW749292 BE002573
		AI581311 AA781682 AA781678
		AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
		BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
		AW840571
		AW972830 AA489820 AA527647 AA570362
		AA401424 AA400100 AA663848
		N50454 AA620999 T16375
		BI917595 AI203314 AL041228 AV727959 D61361 D82004 BI753157 AA961066 AI990307 BF439651 AI453076 AI376075 AI014836 AI018308
		AW183530 AA393346 AA935601 AA628633 AI150282 AI028574 AI217182 AA431478 AW087473 AW900295 H50055 AL041229 BI917726
		AF075009 R63109 R63068
		AW947655 AW984020
		NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355
		AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750
		BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769
		BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE099924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628
		AA143164 AW748953 BG498922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL045011 BF590668 AI017447
		AA579936 AI367597 AA695622 BE280597 AI124620 AI082548 AW274985 AA577870 AI056767 BE551689 AA287642 H94499 AJ752427 AI652365
		AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761
		BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858
		AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818
		AA852821 AW576342 AA827107 AA173317 AW180014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896
		AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25857 BG952995 BF801437 AI172077 AU155890
		AU149783 AI720804 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427
		BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI905607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471
		BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085595 BF847252 BG024608 BE540261 BG531236
		AL579993 BG108733 BG483503 BG571032 BG492605
		AA427363 AW962128 AA355353
		BC009352 BC014630 AU131857 AL527140 AU131768 BI769362 BI753220 AU129886 AU128771 AA314135 AU126819 AI333799 AA479336
		AA258503 AL597351 AI359619 BG697218 BI254283 AI743846 AA236444 AA397533 AA247450 AI051464 AI224533 AU153442 AU151001
		AU152621 AU151829 AU153069 AW269958 AU154195 AI862754 AI589780 AW273839 AI338155 AI126632 BE046048 AA976930 AI289304
		AI625961 AI222288 AI280054 AA973329 AI524262 AI242371 AA296517 AI567865 AI590681 AJ346616 AW247913 AI422051 AI475352 AI689531
		AW469308 AW198034 AA936939 AU151059 AU148134 AA486419 AU151953 AI830968 BI493265 BI493264 AU149861 BE268763 AV763495
		AW962827 BM480300 AA228669 AL529368 BM451957 AU132714 BI871319 AA380739 BI911351 BF795906 BE548853 AW579751
		AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852
		BF173139 BE010038
		BE218720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AJ440295 H52800 BE218790 AI681575
		AW300064 AW262133 H21568 AI363015 AI884914 H85948
		AA770001 AA431112 AA432126
		AI625045 AW504152 AI469086 AA905873 AW504662 AW136114 AI927270 BE041754 AI648386 AA662655 AA400052 AI143501 AI744934
		AI400147 AI381657 AA676551 AA974367 AW117437 AI570383 AI242456 AI274581 AA678138 R49939 AI393926 AA345854 AW605850 AI869780
		AW391171 R77044
		AW955043 AI990326 AA776406 AI016250 AW451882 AA843878 BF916900 AW945895 AI979339 N23129 W70051 AA322672 N23137
		BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA496668 AW968806 AW085196
		AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773843 AA490285
		BC017923 AA789302 AW466994 BF513878 AI819842 AI184913 AW469044 AI220572 AW072916 AI280239 AI473811 AW841126 D60937
		AA489195 N59350 AA693435 BG531204 AA484243 AW514092
		U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708

TABLE 51C

Phy:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
NL_position:	Indicates nucleotide positions of predicted exons.		

75	Phy	Ref	Strand	NL_position
	406547	7711513	Minus	172780-174358
	402145	8018280	Plus	113086-114800
	402199	8576116	Minus	84187-84744
	401435	8217934	Minus	54508-55233
	402408	9796239	Minus	110326-110491
	406367	9256126	Minus	58313-58489
	402680	8113438	Plus	137634-137768, 139702-139893, 140475-14059
	402298	6693370	Plus	23367-25175
	401091	9958240	Plus	94760-94898

	401464	6682291	Minus	170688-170834
	403969	8569909	Plus	31237-31375,32405-32506
	401837	7630990	Minus	120993-121095,121660-121729
	404068	3168621	Minus	18123-18766
5	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402679	8113438	Plus	132079-132216
	403780	8076989	Plus	93160-93409
	404071	7210053	Minus	167354-167859,168810-168920,169000-16910
	403242	7637817	Minus	11297-12511
10	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	400587	9887626	Plus	25435-25588,25668-25747
	405770	2735037	Plus	61057-62075
	403532	8076842	Minus	81750-81901
	406137	9166422	Minus	30487-31058
15	402677	8113438	Plus	22135-22309,23063-23238
	402678	8113438	Plus	37395-37514,37866-37981

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TABLE 52A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of testicular cancer (non-seminomatous and Seminomatous) compared to normal adult testicular tissues

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	414438	AI879277	Hs.76136	thioredoxin	51.77
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	49.93
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	49.20
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	44.46
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.70
35	406658	AI920965	Hs.77961	major histocompatibility complex, class	39.64
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	38.70
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	38.25
	413053	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	37.50
	430542	AI557486	Hs.119122	ribosomal protein L13a	37.22
40	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	35.98
	432730	AI066520	Hs.131358	ESTs	35.25
	444582	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	31.69
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	31.33
	417088	M54915	Hs.81170	p1m-1 oncogene	31.20
45	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	29.93
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	29.35
	426295	AW367283		zinc finger protein 6 (CMPX1)	29.32
	406856	AW515336	Hs.29797	ribosomal protein L10	28.93
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	27.99
50	440207	AI371978	Hs.128326	ESTs	27.75
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	28.95
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.90
	420367	AA259090	Hs.257028	ESTs	26.50
	429978	AA249027		ribosomal protein S6	26.43
55	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	26.36
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	26.23
	412636	NM_004415		desmoplakin (DPI, DPII)	26.15
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	25.25
	446899	NM_005397	Hs.16426	podocalyxin-like	25.25
60	442562	BE379584		dolichyl-diphosphooligosaccharide-prote	25.15
	406658	M16714	Hs.89643	major histocompatibility complex, class	25.13
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	24.78
	423961	D13666	Hs.138348	periostin (OSF-2os)	24.48
	425543	R23313	Hs.334895	ribosomal protein L10a	24.38
65	420676	AI434780	Hs.4248	vav 2 oncogene	24.18
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	23.96
	440859	NM_014297	Hs.7486	protein expressed in thyroid	23.80
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	23.56
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	23.22
70	446827	AI973016	Hs.15725	hypothetical protein SBBI48	22.93
	449571	AW016812	Hs.200266	ESTs	22.83
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	22.81
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	22.68
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	22.45
75	422714	AB018335	Hs.119387	KIAA0792 gene product	22.45
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	22.30
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.69
	406648	AA563730	Hs.277477	major histocompatibility complex, class	21.58
	448588	AI970276	Hs.156905	KIAA1676	21.23
80	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	21.19
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.70
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	20.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	20.57

5	420754	W79431	Hs.346911	ribosomal protein L22	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	20.15
	424800	AL035588	Hs.153203	MyoD family inhibitor	20.10
	412915	AW087727	Hs.74823	NM_004541: Homo sapiens NADH dehydrogenas	20.01
	452322	BE566343	Hs.26988	glutaredoxin (thioltransferase)	19.89
	410143	AA188169		KIAA1191 protein	19.41
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	19.08
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.03
10	425535	AB007937	Hs.158287	KIAA0468 gene product	18.78
	411573	AB029000	Hs.70823	KIAA1077 protein	18.63
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.53
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	18.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	18.50
	426083	AV962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	18.50
15	429183	AB014604	Hs.197955	KIAA0704 protein	18.48
	450000	AJ952797	Hs.10888	hypothetical protein FLJ21709	18.44
	450377	AB033091		KIAA1265 protein	18.40
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.15
20	440528	BE313555	Hs.7252	KIAA1224 protein	18.05
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	17.98
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	17.80
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	17.75
	428782	X12830	Hs.193400	interleukin 6 receptor	17.48
25	415221	W07418	Hs.78225	annexin A1	17.47
	429614	AJ371172	Hs.211539	hypothetical protein MGC4248	17.40
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	17.30
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	17.14
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	17.13
30	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	17.10
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	17.03
	425966	W67330		hypothetical protein AL110115	16.98
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	16.98
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	16.98
35	427521	AW973352		ESTs	16.93
	421181	NM_005574	Hs.184585	UIM domain only 2 (thrombin-like 1)	16.93
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	16.53
	449338	H73444	Hs.394	adenomedullin	16.36
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	16.23
40	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	16.21
	430332	R51790	Hs.239483	Human clone Z3933 mRNA sequence	16.15
	427691	AW194426	Hs.20726	ESTs	16.13
	406786	AW161678	Hs.111334	ferritin, light polypeptide	16.11
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.10
45	451106	BE382701	Hs.25960	N-MYC oncogene	16.09
	408380	AF123050	Hs.44532	diubiquitin	16.00
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	15.93
	456236	AF045229	Hs.82280	regulator of G-protein signaling 10	15.70
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	15.69
50	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	15.64
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	15.55
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	15.55
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	15.53
	410185	BE294068	Hs.737	immediate early protein	15.49
55	422105	AI929700	Hs.111680	endosulfine alpha	15.23
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	15.23
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	15.05
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	15.02
	426552	BE297660	Hs.170328	moesin	14.96
60	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.88
	436860	H12751	Hs.5327	PRO1914 protein	14.85
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	14.84
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	14.78
	412623	R28898	Hs.74170	metallothionein 1E (functional)	14.70
65	408989	AW361666	Hs.49500	KIAA0746 protein	14.53
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	14.48
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	14.31
	410325	AB023154	Hs.62264	KIAA0937 protein	14.23
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	14.20
70	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase II	14.19
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	14.18
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.13
	447211	AL161961	Hs.17767	KIAA1554 protein	14.08
	417426	NM_002291	Hs.82124	laminin, beta 1	14.08
75	414420	AA043424	Hs.76095	immediate early response 3	14.04
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.02
	454413	AI653672	Hs.40092	PNAS-123	13.93
	452651	AI218918	Hs.30209	KIAA0854 protein	13.86
	450581	AF081513	Hs.25195	TGF-beta 4	13.85
80	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.78
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.63
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.59
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.57
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	13.53

	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	13.43
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	13.41
	447534	AW553935	Hs.288655	ESTs	13.33
5	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.31
	428065	AI634046	Hs.157313	ESTs	13.30
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	13.28
	436398	H87136	Hs.5174	ribosomal protein S17	13.18
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	12.93
10	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-link	12.90
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	12.90
	408437	AW957744	Hs.278469	lactin-like protein rich protein	12.90
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	12.89
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.83
15	405743	AA911558	Hs.279860	tumor protein, translationally-controlled	12.79
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	12.78
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	12.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ty	12.73
	430630	AW269920	Hs.2621	cystatin A (stafin A)	12.68
20	409208	Y00093		Integrin, alpha X (antigen CD11C (p150),	12.65
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	12.50
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	12.48
	437374	AL359571	Hs.44054	nihelin (GSK3B interacting protein)	12.43
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.43
25	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	12.41
	412247	AF022375	Hs.73793	vascular endothelial growth factor	12.41
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	12.40
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	12.38
	432409	AA806538	Hs.130732	KIAA1575 protein	12.33
30	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.33
	419384	AA490866	Hs.39429	ESTs	12.33
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.32
	432805	X94630	Hs.3107	CD97 antigen	12.32
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	12.25
35	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB88_HUMAN RAS-R	12.13
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	12.12
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	12.03
	402145			Target Exon	12.01
	407179	AA206465		thymosin, beta 4, X chromosome	12.00
40	433208	AW002834	Hs.24095	ESTs	11.95
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.90
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	11.83
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	11.75
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	11.75
45	427761	AA412205	Hs.140996	ESTs	11.68
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	11.58
	436075	BE090176	Hs.179902	transporter-like protein	11.50
	440774	AI420611	Hs.153934	ESTs	11.35
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	11.25
50	419223	X60111	Hs.1244	CD9 antigen (p24)	11.08
	424528	AI073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	11.08
	444658	AI277924	Hs.145199	ESTs	10.98
	420943	AI718702	Hs.279930	major histocompatibility complex, class	10.96
	450294	H42587	Hs.238730	hypothetical protein MGC10823	10.92
55	413688	AI469213	Hs.71404	ESTs	10.83
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	10.78
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	10.75
	407252	AA659037	Hs.163780	ESTs	10.75
	445929	AI089660	Hs.323401	dpy-30-like protein	10.70
60	451864	N20370	Hs.69547	ESTs	10.69
	429307	AU076592	Hs.198951	Jun B proto-oncogene	10.64
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	10.63
	447519	U46258	Hs.339665	ESTs	10.63
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	10.59
65	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	10.55
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	10.54
	437103	AW139408	Hs.152940	ESTs	10.50
	449961	AW265634	Hs.133100	ESTs	10.50
	441244	BE612935	Hs.184052	PP1201 protein	10.49
70	450139	AK001838		serum/glucocorticoid regulated kinase	10.48
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	10.48
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rholekin, clone	10.47
	446682	AW205632	Hs.211198	ESTs	10.43
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.43
75	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	10.40
	424950	AA602917	Hs.156974	ESTs	10.40
	434442	AA737415		ESTs	10.33
	438089	W05391		nuclear receptor subfamily 1, group I, m	10.33
	432559	AW452948	Hs.257631	ESTs	10.30
80	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (etlin)	10.30
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	10.28
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	10.27
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	10.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	10.23

	445245	AB032973	Hs.12461	LCHN protein	10.18
	446488	AB037782	Hs.15119	KIAA1361 protein	10.15
	410611	AW954134	Hs.20924	KIAA1628 protein	10.15
5	425875	AJ077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	10.14
	416926	H03109	Hs.263395	HTD18 protein	10.07
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	10.05
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	10.04
	411975	AJ916058	Hs.144583	ESTs	10.03
10	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	10.00
	409784	AW971350	Hs.63388	ESTs	9.95
	444795	AJ193356	Hs.160316	ESTs	9.93
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.90
	400440	X83967	Hs.83870	nebulin	9.90
15	414829	AA321568	Hs.77436	pleckstrin	9.88
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.88
	426827	AW067805	Hs.172665	methylentetrahydrofolate dehydrogenase	9.85
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	9.83
	446795	AJ797713	Hs.156471	ESTs	9.78
20	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	9.67
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	9.65
	419904	AA974411	Hs.18672	ESTs	9.63
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	9.63
	414405	AJ362533		KIAA0306 protein	9.58
25	418840	AJ821614	Hs.185831	ESTs	9.53
	453716	AA037675	Hs.152675	ESTs	9.50
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	9.50
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.45
	408360	AJ806090	Hs.44344	hypothetical protein FLJ20534	9.45
30	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	9.43
	434423	NM_006769	Hs.3844	LIM domain only 4	9.43
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	9.43
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	9.42
	410397	AF217517	Hs.63042	DKFZp564J157 protein	9.37
35	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	9.37
	434524	AA635931	Hs.249716	ESTs	9.36
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.35
	414774	X02419	Hs.77274	plasminogen activator, urokinase	9.32
	411960	R77776	Hs.18103	ESTs	9.30
40	428818	AJ131291	Hs.102308	potassium inwardly-rectifying channel, s	9.28
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.28
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.27
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	9.27
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothet	9.25
45	427968	AJ857607	Hs.181301	calthepsin S	9.23
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	9.23
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	9.23
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.18
	417315	AJ080042	Hs.180450	ribosomal protein S24	9.18
50	421098	AJ697901	Hs.192425	ESTs	9.18
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.18
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	9.17
	425246	AJ085561	Hs.155321	serum response factor (c-fos serum respo	9.17
55	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.15
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	9.14
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.13
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	9.12
	420099	D80011	Hs.95140	KIAA0189 gene product	9.10
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	9.08
60	441436	AW137772	Hs.185980	ESTs	9.08
	448019	AW947164	Hs.195841	ESTs, Moderately similar to I38022 hypot	9.08
	437888	BE264111	Hs.31314	retinoblastoma-binding protein 7	9.08
	430566	AW987807	Hs.13797	ESTs	9.07
	450147	AW373713	Hs.148324	CGI-145 protein	9.06
65	442806	AW294522	Hs.149991	ESTs	9.05
	431187	AW971146	Hs.293187	ESTs	9.05
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	9.03
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	9.03
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	9.02
70	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	9.00
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.99
	432314	AA533447	Hs.312989	ESTs	8.98
	414591	AJ888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.95
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	8.94
75	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	8.93
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.90
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	8.90
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.89
	417228	AL134324	Hs.7312	ESTs	8.88
80	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	8.88
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	8.88
	438980	AW502384		gb:UH-HF-BR0p-aka-f-12-0-ULr1 NIH_MGC_5	8.85
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	8.85
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	8.85

	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	8.83
	445612	N94126	Hs.12569	hypothetical protein	8.80
	427254	AL121523	Hs.97774	ESTs	8.80
5	428970	BE276891	Hs.194691	retinoic acid induced 3	8.80
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	8.79
	430162	AW450843	Hs.346348	ESTs	8.75
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.73
	446659	AI335361	Hs.226376	ESTs	8.73
	447198	D61523	Hs.283435	ESTs	8.73
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-decay accelerating factor for complement	8.70
	401091			ESTs	8.68
	442832	AW206560	Hs.253569	ESTs	8.68
	442495	AI184717		ESTs	8.63
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	8.63
15	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	8.61
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	8.59
	425580	L11144	Hs.1907	galanin	8.55
	449656	AA002008	Hs.188633	ESTs	8.55
	412093	BE242691	Hs.14947	ESTs	8.54
20	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.54
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.53
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	8.51
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.45
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	8.45
25	425284	AF155568		NS1-associated protein 1	8.45
	441623	AA315805		desmoglein 2	8.43
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	8.42
	441021	AW578716	Hs.7644	H1 histone family, member 2	8.40
30	446630	AW384793	Hs.15740	Homo sapiens mRNA: cDNA DKFp434E033 (fr	8.40
	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associated	8.35
	433655	AL036559	Hs.3463	ribosomal protein S23	8.33
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.32
	446976	BE246446	Hs.16695	ubiquitin-activating enzyme E1-like	8.31
35	437697	AA731491	Hs.334477	hypothetical protein MGC14879	8.30
	414662	AL036058	Hs.76807	major histocompatibility complex, class	8.30
	414601	AV660804	Hs.301417	AHNAK nucleoprotein (desmoyokin)	8.29
	406699	L05505	Hs.182979	ribosomal protein L12	8.28
	443884	N20617	Hs.194397	leptin receptor	8.28
40	442821	BE391929	Hs.8752	transmembrane protein 4	8.26
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	8.24
	436968	AW161481	Hs.111577	integral membrane protein 3	8.23
	440327	R12581	Hs.191146	ESTs	8.23
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.22
45	435684	NM_001290	Hs.4980	LIM domain binding 2	8.16
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	8.15
	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	8.14
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown (H.s	8.13
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	8.10
50	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	8.09
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	8.08
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	8.07
	423523	AW29828	Hs.193580	ESTs	8.03
	426759	AI590401	Hs.21213	ESTs	8.03
55	426780	BE242284	Hs.172199	adenylate cyclase 7	8.03
	426215	AW963419	Hs.155223	stannocalcin 2	8.03
	435748	AA699756	Hs.117335	ESTs	8.00
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	8.00
	447500	AI381900	Hs.159212	ESTs	8.00
60	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	8.00
	426728	NM_016625	Hs.191361	hypothetical protein	8.00
	434511	R26982	Hs.18108	ESTs	7.99
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	7.98
	424875	AI187945	Hs.199310	ESTs	7.95
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	7.95
65	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7.93
	425277	NM_001241	Hs.155478	cyclin T2	7.91
	451831	NM_001874	Hs.460	activating transcription factor 3	7.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	7.90
70	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	7.90
	429999	AI761902	Hs.99597	ESTs	7.90
	445493	AI915771		metallothionein 1E (functional)	7.89
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.88
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	7.88
75	453485	BE620712	Hs.33026	hypothetical protein PP2447	7.87
	434159	AW135214	Hs.191828	ESTs	7.85
	432666	AW204069		ESTs, Weakly similar to unnamed protein	7.83
	430915	AA488953		gb:aa55e05.r1 NCL CGAP_GCB1 Homo sapiens	7.83
	425913	AA365799		SEC22, vesicle trafficking protein (S. c	7.80
80	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	7.80
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	7.79
	435905	AW997484	Hs.5003	KIAA0456 protein	7.78
	406663	U24683		immunoglobulin heavy constant mu	7.78
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.78

	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	7.75
	438962	BE046594		gb:hm41c11.x1 NCL CGAP_RDF2 Homo sapiens	7.75
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.73
5	422900	AA641201	Hs.222051	ESTs	7.73
	432598	AI341227	Hs.157106	ESTs	7.72
	449322	AI638616	Hs.196566	ESTs	7.71
	416987	D86957	Hs.80712	KIAA0202 protein	7.67
	410800	BE280421	Hs.94499	ESTs	7.67
10	416801	X98834	Hs.79971	sal (Drosophila)-like 2	7.67
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.65
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.65
	401466			vesicle-associated membrane protein 4	7.65
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	7.64
15	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.63
	457250	AA811987	Hs.125779	ESTs	7.63
	412949	AI471639	Hs.71913	ESTs	7.63
	406819	AA908472		gb:og82a10.s1 NCL CGAP_Ov8 Homo sapiens	7.62
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.62
20	414799	AI752416	Hs.77326	Insulin-like growth factor binding prote	7.61
	435937	AA830893	Hs.119769	ESTs	7.60
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.60
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.60
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	7.56
25	418134	AA397769	Hs.86617	ESTs	7.55
	451812	X81889	Hs.152151	plekophilin 4	7.55
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.54
	429083	Y09397	Hs.227817	BCL2-related protein A1	7.54
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	7.52
30	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.52
	407784	AW139585	Hs.12708	ESTs	7.52
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	7.50
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	7.50
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	7.48
35	446013	AI360167	Hs.152774	ESTs	7.48
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.48
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.45
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.45
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	7.44
40	447082	T85314	Hs.54629	thioredoxin-like	7.43
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	7.43
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.43
	439971	W32474	Hs.301748	RAP2A, member of RAS oncogene family	7.43
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	7.43
45	436394	AA531187	Hs.126705	ESTs	7.39
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	7.39
	446258	AI283476	Hs.263478	ESTs	7.38
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	7.37
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.36
50	435541	AA687361	Hs.221318	ESTs	7.35
	453932	AW005303	Hs.329296	ESTs, Weakly similar to (define not ava	7.35
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.35
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.35
	418336	BE179882		glutathione peroxidase 3 (plasma)	7.35
55	448877	AI583696	Hs.253313	ESTs	7.35
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.35
	444838	AV651680	Hs.208558	ESTs	7.33
	422693	BE300073	Hs.278860	tumor protein, translationally-controlled	7.31
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.30
60	441878	AI801869	Hs.127982	ESTs	7.29
	406542			C19000728~g 12585552 sp Q9Y2Q1 Z257_HU	7.28
	408418	AW963897	Hs.44743	KIAA1435 protein	7.28
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor l	7.26
	442492	AA528469	Hs.234518	ribosomal protein L23	7.25
65	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	7.25
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	7.25
	426501	AW043782	Hs.293616	ESTs	7.25
	411251	R19774	Hs.22635	HHGP protein	7.25
	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.25
	418117	AI922013	Hs.83496	linker for activation of T cells	7.24
70	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	7.24
	434817	AA082118	Hs.102737	gollioth protein	7.23
	419970	AW612022		ESTs	7.23
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	7.23
75	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	7.23
	433891	AA613792		gb:mo97h03.s1 NCL CGAP_Pr2 Homo sapiens	7.21
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	7.21
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	7.20
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.20
80	441224	AI076964	Hs.7753	calumenin	7.18
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.18
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	7.15
	447341	AF106941	Hs.18142	arrestin, beta 2	7.15
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	7.14

	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	7.14
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.13
	421633	AF121860	Hs.106260	sorting nexin 10	7.10
5	410668	BE379794	Hs.159651	hypothetical protein	7.09
	435812	AA700439	Hs.188490	ESTs	7.08
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	7.08
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	7.08
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	7.06
10	408505	AF025374	Hs.46465	T-cell, immune regulator 1	7.06
	416401	N80139	Hs.268916	ESTs	7.05
	415799	AA653718	Hs.225841	DKFZP434D193 protein	7.05
	415995	NM_004573		phospholipase C, beta 2	7.05
	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.05
15	417535	AA203569	Hs.191482	ESTs	7.04
	449567	AI990790	Hs.188614	ESTs	7.03
	429355	AW973253	Hs.292689	ESTs	7.03
	442460	NM_014135	Hs.8345	PRO0841 protein	7.03
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541.1 clone 4	7.03
20	430280	AA361258	Hs.237868	Interleukin 7 receptor	7.03
	426124	AI268389	Hs.250697	phosphatidylinositol glycan, class F	7.02
	442685	AB033017	Hs.8594	KIAA1191 protein	7.01
	433735	AA608955	Hs.109653	ESTs	7.00
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.98
25	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.96
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.95
	409956	AW103384	Hs.727	inhibin, beta A (activin A, activin AB a	6.95
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.93
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	6.93
30	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.93
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothetical	6.93
	451838	AW005866	Hs.193969	ESTs	6.91
	436812	AW288067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCI_CGAP_Su	6.90
	443749	R38828	Hs.143463	ESTs	6.90
35	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.90
	427919	AA173942	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	6.90
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.90
	435655	AW105663	Hs.6947	HSPC069 protein	6.90
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	6.85
40	418259	AA215404		ESTs	6.85
	407244	M10014		fibrinogen, gamma polypeptide	6.85
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	6.83
	441321	H17182	Hs.7771	B-cell associated protein	6.80
	433162	AI025842		ESTs	6.80
45	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.80
	434372	AA631373		gb:np86c01.s1 NCI_CGAP_Thy1 Homo sapiens	6.80
	456629	AW891965		histone deacetylase 3	6.78
	430283	BE391688		RAB7, member RAS oncogene family	6.77
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	6.76
50	406858	AI865720	Hs.29797	ribosomal protein L10	6.75
	429582	AI569068	Hs.22247	ESTs	6.75
	401113			solute carrier family 22 (organic cation	6.75
	449576	AW014631	Hs.225068	ESTs	6.75
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	6.72
55	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.72
	430451	AA836472	Hs.297939	cathepsin B	6.72
	410503	AW975746	Hs.188662	KIAA1702 protein	6.70
	415682	AI347128	Hs.191870	ESTs	6.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi)	6.70
60	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.70
	457073	AA233210	Hs.179943	ribosomal protein L11	6.69
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	6.68
	436137	AI056769	Hs.133512	ESTs	6.68
	425787	AA363867	Hs.155029	ESTs	6.67
65	437802	AI475995	Hs.122910	ESTs	6.65
	432636	AA340864	Hs.278562	claudin 7	6.65
	407340	AA810168	Hs.284289	villiggo-associated protein VIT-1	6.65
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	6.65
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein Interac	6.63
70	441355	AI822034	Hs.137097	ESTs	6.63
	430958	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.63
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.63
	447232	AW499834	Hs.327	Interleukin 10 receptor, alpha	6.62
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	6.60
75	449217	AA278536	Hs.23262	ribonuclease, RNase A family, kb	6.60
	449057	AB037784	Hs.22941	KIAA1363 protein	6.60
	446979	AI654443	Hs.197683	ESTs	6.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	6.60
	424868	AI568170	Hs.96885	ESTs	6.59
80	409485	S80990	Hs.252136	ficofin (collagen/fibrinogen domain-cont	6.58
	451603	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	6.58
	426158	NM_001982	Hs.199067	v-erb-b2avian erythroblastic leukemia v	6.58
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	6.57
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.56

	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	6.56
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.55
	418459	R85436	Hs.268814	ESTs	6.55
5	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ110417 fis, clone NT	6.55
	406745	AW511970	Hs.279860	tumor protein, translationally-controlled	6.55
	446173	BE565849	Hs.14158	copine III	6.53
	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	6.53
	423825	NM_004402	Hs.133089	DNA fragmentation factor, 40 kD, beta po	6.53
10	443441	AW291196	Hs.92195	ESTs	6.51
	428403	AI393048	Hs.326159	leucine rich repeat (in FLJ) interactin	6.50
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	6.50
	450219	AI826999	Hs.224624	ESTs	6.50
	408896	AI610447	Hs.48778	niban protein	6.50
15	442618	R56222	Hs.26514	ESTs	6.49
	422773	AB028962	Hs.301552	KIAA1039 protein	6.48
	413653	BE247585	Hs.75462	BTG family, member 2	6.48
	418905	BE539674		actinin, alpha 4	6.48
	405086			NM_006662: Homo sapiens Snf2-related CBP	6.45
20	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.45
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.45
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	6.45
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	6.43
	426496	D31765	Hs.170114	KIAA0061 protein	6.43
25	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	6.42
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	6.41
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypol	6.40
	435918	AF263538	Hs.86232	growth differentiation factor 3	6.38
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.38
30	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.38
	436716	AI433540		gb:U69g05.x1 NCL CGAP_Kid11 Homo sapien	6.38
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	6.38
	413326	H88621	Hs.19762	ESTs, Weakly similar to KIAA1140 protein	6.38
	441970	AW959918	Hs.73737	ESTs	6.38
35	430835	AI240006	Hs.192326	ESTs	6.38
	414890	BE281095	Hs.77573	uridine phosphorylase	6.37
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.37
	414768	AW376989	Hs.259855	elongation factor-2 kinase	6.36
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	6.36
40	407198	H91679		gb:vv04e07.s1 Soares fetal liver spleen	6.35
	432586	AA568548		ESTs	6.35
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	6.35
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	6.35
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.35
45	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.35
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosyl	6.35
	437296	AA350994	Hs.20281	KIAA1700	6.35
	427747	AW411425	Hs.180655	serine/threonine kinase 12	6.33
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	6.33
50	410387	AI277387	Hs.47094	ESTs	6.33
	413677	AW503116	Hs.301819	zinc finger protein 146	6.31
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	6.31
	443634	H73972	Hs.134460	ESTs	6.30
	409453	AI885516	Hs.85612	ESTs	6.29
55	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	6.29
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.29
	410532	T53088	Hs.155376	hemoglobin, beta	6.28
	428453	AB011110	Hs.184367	GTPase activating protein-like	6.27
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	6.26
60	458965	AA010319	Hs.60389	ESTs	6.25
	419926	AW900992	Hs.93795	DKFZP586D2223 protein	6.25
	426797	AW836258	Hs.342849	ADP-ribosylation factor-like 5	6.25
	412528	AI123478	Hs.32112	ESTs	6.25
	410079	U94362	Hs.58589	glycogenin 2	6.25
65	427477	AW973119	Hs.178391	ribosomal protein L44	6.24
	416297	AA157834	Hs.79172	solute carrier family 25 (mitochondrial	6.24
	435961	BE293127	Hs.283722	GTT1 protein	6.23
	424090	X99699	Hs.139262	XIAP associated factor-1	6.23
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.23
70	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	6.23
	409731	AA125985	Hs.58145	thymosin, beta, identified in neuroblast	6.23
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	6.22
	428773	BE256238	Hs.193163	bridging integrator 1	6.20
	436372	AW972301	Hs.310286	ESTs	6.19
75	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	6.18
	406685	M18728		gb:Human nonspecific crossreacting anti	6.18
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	6.17
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	6.16
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	6.15
80	406806	AW088535		ribosomal protein, large, P0	6.15
	420151	AA255931	Hs.186704	ESTs	6.14
	413441	AI929374	Hs.75367	Sro-like-adaptor	6.13
	449317	AW293413	Hs.132906	19A24 protein	6.13
	421568	W85858	Hs.99804	ESTs	6.13

5	435919	AI052189	Hs.114104	ESTs	6.13
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFpZ586F1822 (f	6.13
	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	6.13
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucn 2 p	6.13
	406857	AA613726	Hs.29797	ribosomal protein L10	6.11
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	6.11
	425095	AW014160	Hs.182585	KIAA1276 protein	6.10
	435756	AI418466	Hs.33665	ESTs	6.10
10	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	6.10
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	6.10
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	6.10
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	6.08
	447832	AI433357		ESTs	6.08
	434421	AI915927	Hs.34771	ESTs	6.08
15	437438	AL359620	Hs.14217	hypothetical protein DKFpZ62P2111	6.08
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	6.08
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	6.07
	433339	AF019226	Hs.8036	glioblastoma overexpressed	6.06
20	435511	AA683336	Hs.189046	ESTs	6.06
	423458	AI204212		ESTs	6.06
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.06
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.06
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathl	6.06
25	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	6.05
	432925	AA878324	Hs.264750	ESTs	6.05
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	6.05
	449810	AB008681	Hs.23994	activin A receptor, type IIB	6.04
	406797	AI432224		ribosomal protein L6	6.04
30	450157	AW961576	Hs.60178	ESTs	6.03
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.03
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-in	6.03
	453331	AI240665		ESTs	6.03
	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	6.02
35	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	6.01
	409945	AW015935	Hs.122642	ESTs	6.00
	419641	BE170543	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	6.00
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.00
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	6.00

TABLE 52B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

45	Pkey	CAT Number	Accession
50	438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646384 AV687497 BF155183 AV646370 AW787876 AI906821 X56196 BE833835 AA528440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146384 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF382762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA63522 BI003244 AI299180 AW04186 BE174210 BF939091 BF434180 AW579001 T65662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI216830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI795964 AA917471 AI400531 AA668626 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI918336 AI350590 BF198106 AI433377 AI300638 AI672828 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627 BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW195655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963196 C06195 AI678018 M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW888475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF893352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995815 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873879 AW178000 BE082526 BF476868 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE699470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE075957 BE705966 BE705968 AW848723

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 BE177661 H06215 BE144709 BE144829
 BE005398 AA628822 AA594155
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 AA947566
 AA662701 AA633929 AA737415
 BM475665 BE644917 AW770789 AW952971 N84863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440
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5		AW771624 AA663041 AJ991576 AI160622 AA771763 BE089784 BE089788 AJ22942 AW418516 AA329211 AI095736 BE550294 AA738345
		BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634
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10		AW371849 BE153241 BC017410 AJ337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023984 AI458424
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		AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522
		BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595
		BI094458 BE706702 BG496559 BF248373 BG494800
445493	423456_1	AV711317 AI809938 AI808768 AI240593 AJ915771
432666	144_7	AA558585 AA565499 AI350576 AW204069 AA991648 AA854939
430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
425913	4123_2	AV703649 AW959818 AI582119 AI523459 AI874473 AW663543 AA825476 AI353231 BF742805 AA426156 AI253626 AA846477 AI024230
		BF221780 AI493027 AW006841 AA814699 H99650 AI088977 AA442691 AI783528 BF207915 AI752847 AA782635 AI978980 AA788634 BG119454
		BF678528 AI627829 BG993975 AV701283
20		AI207343 BF813684 BF928775 AA828585
		AA075144
		AA908472
		R36075 R36167 AI366546
		AW969583 BI772505 BE179578 AJ493714 AJ937718 AA663709 BI868925 AW138743 AJ911314 BE645538 BG911947 AI380325 AI265803 W56175
		AI658779 AI675997 AW565991 AI459263 AJ202121 Z38874 AA570115 AW301008 AA216257 BF062662 BI772789 H05969 BF085523 BI001277
25		U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708
		AK055270 BE348291 AI190289 AW612022 AI269508 AI266578 AI269675 AWZ71406 BE879851 BF574163 BI497126 AW903775 BI917368
		AW150900 BF244813 H79201
		AW182329 AA613792 T05304 AW858385
30		MS9578 NM_004573 AI530754 AI439623 AW374413 BF898880 AW630959 BF875526 AW402206 BF818690 BF893068 AW504110 AW408049
		BG002913 AI530753 AI524084 AW769231 AA649702 AA293723 AI095051 AI953375 AI982938 BM146050 AW575804 AA962489 AI655426
		BM146046 T28538 BE241936 T89023 BI910963 AI416986 AI767111 AI422290 AW468260 BE676853 AI656771 AI961755 F04875 AA682826
		AA737606 BM194382 AA912021 AW183098 BE676682 AI962227 AI591366 AA621765 AA293724 R51642 F10194 BI909727 BF892632 AW950600
		AW950138 BG258587 BF892649 AI800647 BF892710 AA353176 BF894726 AA465038 BI040869 BI837749 BE244320 H18054 T74300 AW797026
		AK926790 F32814 AW751282 AI933994 AA578823 T78372 BF899896 BF882808 BF974969
35		BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858
		AJ302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694
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		BM310925 AA426110 BM310629 BF434286 AW015091 BF475995 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969
		BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563
40		AA459408 AA459633 AA418444 W23507 BG940150 AI934445 AW054729 AJ221929 AI868744 AA215405 AA766713 AA621546 BF928317
		BE464132 AI990909 AWZ71459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 RG9057 BF766886 BE769254
		W05240
		AJ742311 AI025842 AA578843
45		BG622121 AA631424 AA988296 AA631373
		AW891965 AW604749 BE080872 R15559 BE177623 AW883520 AW945343 AI246167 T07082 AW805679 W96278 AA135796 W32615 AW995418
		AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW801247 BE003239
		BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AJ378548
		AW690438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399
		AW885686 BE244086 BE005035 AW661913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939
		AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE087470 AW894935 BE082529 AI248811 BE179917 BE002200
		AW607506 AW392889 AW894560 AW861360 AI904206 AW883533 C00609 AW381372 BE082530 AW896120 BE075323 AW392799 AW601420
		AI695314 BE083790 AW858568 AW945550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW858979 AW794240 AW945566
		AJ688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW664582 AW867775 AW838449
		BE180466 AW858501 BE180464 AJ371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099
		BE011715 BE167842 BE011718 BE011724 AW383639 AW878658 AW878662 AW894887 BE082356 AW389211 AW804286 AW610312 AI904717
		AW610318 AW996909 AW610296 AW901923 AW880003 AJ762171 AW062582 AW368713 AW062593 AW176663 AW842084 AW842089
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		AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA325629
		BE089008 BE178350 BE178214 BE063291 AW820238 AW999653 BE089486 BE173126 BE171775 BE185787 AA582800 AI174840 AW999112
		BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972
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		AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172467 H92861
		AI524921 F02989 Z39328 F02705 F01414 T88878 AI215165 H87220 AW374781
65		BC013728 BI084032 BF090365 BE410706 N36391 W80436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK000826 BC008721
		BG744004 BG479141 BG823656 BG479061 AU121103 AU138176 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929
		BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AU139772 BG714385
		BF568538 BE304393 BF971755 BE267965 BE272012 AU135396 AU124535 BI551682 BG700612 AI815488 BG475195 BE388273 BE391517
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70		BE907957 W73238 BI711467 BG926027 AI816428 AA837518 AJ754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096
		AJ090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI979801 AI682636
		AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784
		AI918795 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA555116 AI097349 N22209 AA552917 N33151 D52422 BF477483
		AA476599 AA525787 AI279198 D53535 AA738063 AA558406 BI496334 AA999948 AA425847 BI496335 AA809624 BF197591 AW023259 AI652819
		T31424 AA088213 T31115 AI206650 AJ987996 AI948899 AW248762 AA49265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141
		BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111
		BM476906 BE293615 BE382443 BF155692 BE720638 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142
		BI667664 BG823325 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV727527 N67629 BG997927 BI915769 BG680692 R62777
		BE251116 H56358 AW369588 BG877759 BI044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384
80		AI654578 BF038102 H87151 H01574 T52573 N28881 AA301397 T92375 R68401 AW804066 AI268172 BE876949 D54019 AI909769
		AW798415 BI222383 AI393171 C15260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206
		BI093066 C14063 AL534349 BE255883 BE254088 AA428399 AW579360 AW579381 N53144 D50748 D54020 BG292106 H96705 D52423 T36174

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	426534	U58096	Hs.2051	testis specific protein, Y-linked	44.05
	423458	AI204212		ESTs	36.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	34.65
5	420367	AA259090	Hs.257028	ESTs	32.60
	451106	BE382701	Hs.25960	N-MYC oncogene	30.10
	437052	AA861697	Hs.120591	ESTs	29.35
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [Hsapi	29.05
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fs, clone HE	28.45
10	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	28.25
	407710	AW022727	Hs.23816	ESTs	26.86
	448981	AI968719	Hs.195387	ESTs	26.40
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	25.55
	420528	AF130728	Hs.98586	doublesex and mab-3 related transcript	25.10
15	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	23.70
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.95
	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	21.73
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	20.15
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	19.65
20	424578	AK001973	Hs.150890	hypothetical protein	19.16
	427335	AA448542	Hs.251677	G antigen 7B	19.05
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	18.95
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	18.86
	449322	AI638616	Hs.196566	ESTs	18.30
25	430691	C14187	Hs.157208	aristless-related homeobox protein ARX	18.00
	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (17.96
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	17.41
	418756	AA252254	Hs.226949	ESTs	17.20
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	16.20
30	447534	AW953935	Hs.288655	ESTs	16.04
	407122	H20276	Hs.31742	ESTs	15.95
	446979	AI654443	Hs.197683	ESTs	15.90
	406547			Target Exon	15.70
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.65
35	456847	AI360456	Hs.37776	ESTs	15.50
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	15.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	14.95
	408908	BE296227	Hs.250822	serine/threonine kinase 15	14.65
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
40	422828	AL133396		prion protein 2 (double)	14.08
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	14.05
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fs, clone H	14.05
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fs, clone NT	13.90
	418134	AA397769	Hs.86617	ESTs	13.85
45	454438	AA224053	Hs.172405	cell division cycle 27	13.70
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	13.40
	426427	M86699	Hs.169840	TTK protein kinase	13.35
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.20
	419384	AA490866	Hs.39429	ESTs	13.10
50	418477	AW022983		gb:df46h12.y1 Morton Fetal Cochlea Homo	12.85
	453922	AF053306	Hs.35708	budding uninhibited by benzimidazoles 1	12.80
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.78
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	12.72
	443068	AI188710		ESTs	12.65
55	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	12.60
	420401	AK001907	Hs.97454	hypothetical protein	12.50
	410361	BE391804	Hs.82661	guanylate binding protein 1, Interferon-	12.50
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	12.45
	406937	U14622		gb:Human transketolase-like protein gene	12.25
60	439451	AF086270	Hs.278554	heterochromatin-like protein 1	12.10
	404996			Target Exon	11.86
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	11.85
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-in	11.60
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	11.55
65	421241	X91817	Hs.102866	transketolase-like 1	11.50
	414972	BE263782	Hs.77695	KIAA0008 gene product	11.45
	426866	U02330	Hs.172816	neuregulin 1	11.37
	433159	AB035898	Hs.150587	kinesin-like protein 2	11.35
	433800	AJ034381	Hs.135150	lung type-I cell membrane-associated gly	11.24
70	440207	AI371978	Hs.128326	ESTs	11.12
	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.10
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	11.05
	449576	AW014631	Hs.225068	ESTs	10.95
	414251	AL042306	Hs.97689	VASA protein	10.95
75	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	10.90
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCI_CGAP_Su	10.85
	427521	AW973352		ESTs	10.81
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	10.80
	442832	AW206560	Hs.253569	ESTs	10.62
80	436899	AA764852		ESTs	10.60
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	10.55
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	10.45
	435206	AI432364	Hs.160594	ESTs	10.15
	433975	AA971953	Hs.122055	ESTs	10.10

	446791	AI632278	Hs.195922	ESTs	10.05
	422232	D43945	Hs.113274	transcription factor EC	10.00
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	9.71
5	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	9.50
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.44
	438188	AA779975	Hs.128859	ESTs	9.30
	418973	AA233056	Hs.191518	ESTs	9.25
	413627	BE182082	Hs.246973	intron of Bicucidal D homolog 1	9.25
10	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.15
	436508	AA628980	Hs.192371	down syndrome critical region protein DS	9.11
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	9.08
	426518	Z43039	Hs.170198	KIAA0009 gene product	9.05
	440968	N36327		gb:yx82b06.r1 Soares melanocyte 2NbHM Ho	9.05
	440952	AI291804	Hs.118101	ESTs	9.05
15	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	9.05
	442618	R56222	Hs.26514	ESTs	8.96
	419423	D26488	Hs.90315	KIAA0007 protein	8.95
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	8.80
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	8.76
20	444971	AI851116	Hs.148659	ESTs	8.75
	436513	AJ278110	Hs.125507	DEAD-box protein	8.60
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.59
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ111381 fis, clone HE	8.58
25	428847	AI954833	Hs.98881	ESTs	8.57
	408465	AW196940	Hs.253277	ESTs	8.54
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	8.53
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	8.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.50
30	450480	X82125	Hs.25040	zinc finger protein 239	8.50
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.42
	413318	AU076607	Hs.75285	Inter-alpha (globulin) inhibitor, H2 pol	8.35
	430835	AI240006	Hs.192326	ESTs	8.33
	416859	H43437	Hs.80305	hypothetical protein MGC14258	8.30
35	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	8.26
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	8.25
	449260	AA741180	Hs.29879	ESTs	8.25
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	8.18
40	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	8.17
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	8.14
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.14
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.03
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	7.98
	410420	AA224053	Hs.172405	cell division cycle 27	7.90
45	453878	AW964440	Hs.19025	DC32	7.75
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.66
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	7.65
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	7.65
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	7.65
50	451950	AW292317	Hs.213307	ESTs	7.60
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.59
	435514	AW592804		ESTs	7.55
	431041	AA490967	Hs.197955	KIAA0704 protein	7.55
55	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.51
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	7.38
	409421	AA199883	Hs.67624	ESTs	7.35
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	7.35
	458570	AW971698	Hs.12627	TJ6 protein	7.30
60	441287	AW293132	Hs.131373	ESTs	7.30
	434609	R76593		gb:yl60c11.r1 Soares placenta Nb2HP Homo	7.25
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	441425	AA933590	Hs.28937	homeobox protein from AL590526	7.25
	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	7.21
	414138	AA812434		SMC2 (structural maintenance of chromoso	7.20
65	409089	NM_014781	Hs.50421	KIAA0203 gene product	7.19
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.18
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	7.15
	452226	AA024898	Hs.157103	ESTs	7.15
	435918	AF283538	Hs.86232	growth differentiation factor 3	7.14
70	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.10
	436360	AI962796	Hs.156100	ESTs	7.10
	442950	AI500417	Hs.46764	ESTs	7.00
	415684	D69356		sorbitol dehydrogenase	7.00
75	448336	R53848	Hs.44976	ESTs	7.00
	453183	AW086185	Hs.223856	ESTs	7.00
	444434	NM_004849	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	6.95
	422665	AJ011812	Hs.119018	transcription factor NRF	6.95
	437421	AA917062		ESTs	6.95
80	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.94
	408045	AW138959	Hs.245123	ESTs	6.90
	448588	AI970276	Hs.155905	KIAA1676	6.89
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.85
	439780	AL109688		gb:Homo sapiens mRNA full length insert	6.85

	449911	AI262106	Hs.12653	ESTs	6.85
	417791	AW965339	Hs.111471	ESTs	6.80
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
5	453160	AI263307		H2B histone family, member L	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.73
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.70
	418379	AA218940	Hs.137516	fidgulin-like 1	6.70
10	407366	AF026942	Hs.17518	gb:Homo sapiens c1g33 mRNA, partial sequ	6.70
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	6.69
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	6.66
	428743	AL080060	Hs.301549	Homo sapiens mRNA: cDNA DKFZp564H172 (fr	6.65
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	6.65
	433247	AB040948	Hs.142856	KIAA1515 protein	6.65
15	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	6.65
	417885	AA214584		ESTs	6.64
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.62
	412537	AL031778		nuclear transcription factor Y, alpha	6.61
20	426614	AA411925	Hs.301960	ESTs	6.57
	457465	AW301344	Hs.122908	DNA replication factor	6.52
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	6.50
	440801	AA906366		ESTs	6.50
	453116	AI276680	Hs.146086	ESTs	6.50
	436909	AA907120		ESTs	6.50
25	402199			Target Exon	6.50
	419556	U29615	Hs.91093	chitinase 1 (chitinotrioidase)	6.46
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	6.41
	438494	AA908678	Hs.130183	ESTs	6.41
30	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	6.40
	408758	NM_003686	Hs.47504	exonuclease 1	6.40
	442671	AI005668	Hs.130673	EST	6.40
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.38
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.35
35	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	6.33
	441878	AI801869	Hs.127982	ESTs	6.31
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	6.31
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	6.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	6.30
40	421650	AA781795	Hs.122587	ESTs	6.30
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.28
	408291	AB023191	Hs.44131	KIAA0974 protein	6.26
	438180	AA808189	Hs.272151	ESTs	6.25
	412028	AA383618	Hs.73073	testis-specific ankyrin motif containing	6.25
45	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	6.20
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.20
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.18
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	6.12
	426223	AW977812	Hs.130391	ESTs	6.10
	445038	AI635444	Hs.143917	dJ467N11.1 protein	6.10
50	419197	N48921	Hs.27441	KIAA1615 protein	6.09
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	6.05
	436902	AW247145	Hs.192729	ESTs	6.05
	429228	AI553633		ESTs	5.99
55	457065	AI476318	Hs.192480	ESTs	5.90
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	5.90
	449132	BE045641	Hs.197573	ESTs	5.90
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.89
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.85
60	457289	AW573204	Hs.137078	ESTs	5.85
	433849	BE465884	Hs.280728	ESTs	5.85
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.80
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.77
65	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.77
	408460	AA054726	Hs.285574	ESTs	5.75
	442461	AW062564	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	5.75
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
	426249	AA130914	Hs.183291	zinc finger protein 268	5.74
70	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (5.72
	402145			Target Exon	5.71
	447178	AW594641	Hs.192417	ESTs	5.70
	458814	AA498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.65
75	442980	AA857025	Hs.8878	kinesin-like 1	5.65
	419131	AA406293	Hs.109526	ESTs	5.60
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor,	5.60
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	5.58
80	442333	AI650877	Hs.129302	ESTs	5.58
	453941	U39817	Hs.36820	Bloom syndrome	5.57
	415799	AA653718	Hs.225841	DKFZP434D193 protein	5.57
	413623	AA825721	Hs.246973	Intron of Bicaudal D homolog 1	5.55

	427147	AA398587	Hs.97414	ESTs	5.55
	451050	AW937420		ESTs	5.55
	450113	AJ583098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.54
5	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	5.54
	437812	AJ582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoqu	5.53
	431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransferase 3 be	5.51
	449592	AI655494	Hs.195718	ESTs	5.50
	445517	AF208855	Hs.12630	hypothetical protein	5.50
10	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	5.48
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.47
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	5.46
	409103	AF251237	Hs.112208	XAGE-1 protein	5.45
	420900	AL045633	Hs.44269	ESTs	5.45
15	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.45
	440738	AI004650	Hs.225674	WD repeat domain 9	5.45
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.45
	441122	H56777	Hs.121084	eppin-3	5.42
20	414151	AW976468	Hs.257245	ESTs	5.40
	435663	AI023707	Hs.134273	ESTs	5.40
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.39
	433701	AW445023	Hs.15155	ESTs	5.39
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.35
	440842	AA907288	Hs.130173	ESTs	5.35
25	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.34
	401837			NM_025109:Homo sapiens hypothetical prot	5.32
	423739	AA398155	Hs.97600	ESTs	5.31
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.31
30	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.30
	415717	AA167270	Hs.130435	ESTs	5.30
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	5.26
	427119	AW880562	Hs.272525	ESTs	5.25
	432117	AL036195	Hs.2909	protamine 1	5.24
35	446837	AW273055	Hs.156598	ESTs	5.23
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	5.21
	422797	AB033064	Hs.236463	KIAA1238 protein	5.19
	446258	AI283476	Hs.263478	ESTs	5.18
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	5.17
40	445413	AA151342	Hs.12677	CGI-147 protein	5.17
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	5.16
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.15
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	5.15
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	5.15
45	448038	AW015073	Hs.232026	ESTs, Weakly similar to ROS2_HUMAN 52 KD	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.14
	422094	AF129535	Hs.272027	F-box only protein 5	5.13
	420424	AB033036	Hs.97594	KIAA1210 protein	5.13
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.10
50	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	5.10
	453448	AL036710	Hs.209527	ESTs	5.10
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	5.06
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	5.05
	427961	AW293165	Hs.143134	ESTs	5.05
55	441553	AA281219	Hs.121296	ESTs	5.05
	429999	AI761902	Hs.99597	ESTs	5.04
	426496	D31765	Hs.170114	KIAA0081 protein	5.02
	410929	H47233	Hs.30643	ESTs	5.01
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	5.01
60	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	5.00
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.00
	407568	AA740964	Hs.62689	ESTs	5.00
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN IIII	5.00
65	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	5.00
	416350	AF188625	Hs.189507	phospholipase A2, group IID	4.99
	452197	AW023595	Hs.232048	ESTs	4.98
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.97
	403760			C4001759:gi1133250[sp]P19474[RO62_HUMAN	4.97
70	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	4.95
	418894	W73921	Hs.50743	ESTs	4.95
	426623	AA382826	Hs.132793	ESTs	4.95
	443537	D13305	Hs.203	cholecystokinin B receptor	4.94
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.94
75	453716	AA037675	Hs.152675	ESTs	4.90
	402299			Target Exon	4.90
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	4.89
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.87
	409066	AA062980	Hs.66960	ESTs	4.85
80	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.85
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	450375	AA009647		a disintegrin and metalloproteinase doma	4.85
	416201	AA467752	Hs.195161	ESTs	4.85
	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1128 (f	4.84

	423198	M81933	Hs.1634	cell division cycle 25A	4.82
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B)	4.81
	418971	AA360392	Hs.87113	ESTs	4.80
5	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.80
	409517	X90780		troponin I, cardiac	4.80
	424322	AL157491	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (I	4.80
	443169	AI038687	Hs.133338	ESTs	4.80
	438624	AA889055	Hs.123468	ESTs	4.79
10	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	4.76
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.76
	443715	AI583187	Hs.9700	cyclin E1	4.76
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	4.75
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.71
	444431	AW513324	Hs.42280	Homo sapiens, clone MGC:9010, mRNA, comp	4.71
15	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	4.71
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	4.70
	447175	AI365208	Hs.293606	ESTs	4.70
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.69
20	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	4.68
	416445	AL043004	Hs.79337	KIAA0135 protein	4.66
	429652	AA766810	Hs.259290	ESTs	4.65
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	4.65
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	4.64
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.62
25	427298	AA400495		ESTs	4.62
	412863	AA121673	Hs.59757	zinc finger protein 281	4.62
	446700	AW208257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.60
	446751	AA766998	Hs.79126	Human DNA sequence from clone RP11-16L21	4.60
30	432658	NM_000246	Hs.3076	MHC class II transactivator	4.60
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	4.60
	437915	AI637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	4.60
	421830	AA789269	Hs.122509	ESTs, Weakly similar to dJ1018D12.3 [Hs	4.59
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	4.58
35	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	4.58
	431721	AB032996	Hs.268044	KIAA1170 protein	4.55
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.55
	453529	AA036729	Hs.335639	ESTs	4.55
40	416209	AA238776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.55
	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.55
	428976	AL037824	Hs.194695	ras homolog gene family, member I	4.55
	449610	AI553154	Hs.328147	ESTs	4.55
	414725	AA769791		ring finger protein 21, interferon-respo	4.54
45	424153	AA451737	Hs.141496	MAGE-like 2	4.53
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA (choleste	4.52
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	458443	AV647010	Hs.27	glycine dehydrogenase (decarboxylating;	4.48
	453289	AI188161	Hs.144627	ESTs	4.48
50	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.45
	440196	N72847	Hs.125221	ESTs	4.45
	452338	AW608920	Hs.29169	zinc finger protein 75 (D8C6)	4.45
	428855	AI435901	Hs.89563	nuclear cap binding protein subunit 1, 8	4.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	4.45
	442240	AI791883	Hs.292719	ESTs	4.45
55	421917	AB028943	Hs.109445	KIAA1020 protein	4.45
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	4.44
	449676	AW380579	Hs.209657	ESTs	4.43
	433183	AF231338	Hs.222024	transcription factor BMAL2	4.40
60	439314	AA382413	Hs.178144	ESTs	4.40
	425312	AA354940	Hs.145958	ESTs	4.39
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.39
	430444	AW296421	Hs.121035	ESTs	4.35
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.35
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.34
65	418216	AA662240	Hs.283099	AF15q14 protein	4.32
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	4.32
	454073	AW206286	Hs.116727	ESTs	4.30
	417006	AW673606	Hs.80758	aspartyl-HRNA synthetase	4.30
70	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.30
	448877	AI583696	Hs.253313	ESTs	4.28
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	4.27
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	4.25
	430292	AK000634	Hs.238270	hypothetical protein FLJ20627	4.25
	427778	AA412323	Hs.105323	ESTs	4.25
75	418768	T39310		gb:ya04e09.r2 Stratagene lung (937210) H	4.25
	409268	AA625304		ESTs	4.25
	442010	AI032680	Hs.132213	ESTs	4.24
	452807	AA028933	Hs.162434	ESTs	4.23
80	401435			C14000397*:g[749898]pir[jT33295 hypoth	4.23
	447519	U46258	Hs.339665	ESTs	4.21
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (I	4.21
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	4.20
	453909	AW004045	Hs.203365	ESTs	4.20

5	431126	AF085243	Hs.283619	zinc finger protein 236	4.20
	429628	H09604	Hs.13268	ESTs	4.20
	415989	AI267700		ESTs	4.20
	421373	AA808229	Hs.46677	ESTs	4.20
	433979	AA620999		gb:ag03a08.s1 Soares_testis_NHT Homo sap	4.20
	408321	AW405882	Hs.44205	coristatin	4.19
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.17
	430335	D80007	Hs.239499	KIAA0185 protein	4.17
10	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.16
	438885	AI886558	Hs.184987	ESTs	4.15
	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	4.15
	432446	AA542845	Hs.294088	GAJ protein	4.13
	445076	AI206888	Hs.154131	ESTs	4.11
15	420218	AW958037		ribosomal protein L4	4.10
	453628	AW243307	Hs.83937	hypothetical protein	4.10
	418459	R85436	Hs.268814	ESTs	4.10
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.08
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	4.06
20	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.06
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	4.05
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	4.05
	449687	W68520		Intermediate filament protein syncoilin	4.05
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	4.05
25	401464			histone deacetylase 5	4.05
	444670	H58373	Hs.332938	hypothetical protein MGC5370	4.05
	415884	H22966	Hs.13471	ESTs	4.05
	442066	BE502147	Hs.128418	ESTs	4.04
	402098			ENSP00000217725*-Laminin alpha-1 chain p	4.02
30	404287			FGENESH predicted novel CUB-domain conta	4.01
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	4.01
	449704	AK000733	Hs.23900	GTPase activating protein	4.00
	445685	AW779829		gb:hn88a05.x1 NCI_CGAP_Kid11 Homo sapien	4.00
	444379	N99035	Hs.30352	ESTs	4.00
35	435373	AW665538	Hs.117689	ESTs	4.00
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	4.00
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	4.00
	418648	AW979223	Hs.292478	ESTs	4.00
	446074	AA079799	Hs.343103	hypothetical protein FLJ11896	4.00
40	447353	AI375701	Hs.25884	ESTs	4.00
	410100	AA081636	Hs.271916	ESTs, Weakly similar to S41044 chromosom	4.00
	428856	AA436735	Hs.183171	hypothetical protein FLJ22002	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	406367			NM_022357:Homo sapiens putative metallop	3.99
45	437834	AA769294		gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens	3.99
	453985	N44545	Hs.251865	ESTs	3.98
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434i143	3.97
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	3.97
	414713	BE465243	Hs.12684	ESTs	3.96
50	426067	AW664691	Hs.97053	ESTs	3.96
	456497	AW967956	Hs.123848	ESTs, Weakly similar to AF108460 1 ubiru	3.96
	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	3.95
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.95
	403137			NM_005381*-Homo sapiens nucleolin (NCL),	3.95
55	445730	AI624342	Hs.179082	ESTs	3.95
	451993	AA765776	Hs.122983	ESTs	3.95
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.92
	433583	AI817723	Hs.22678	hypothetical protein FLJ21832	3.91
	420812	AA715303	Hs.107369	ESTs	3.90
60	423806	AA331247	Hs.86617	ESTs	3.90
	437205	AL110232	Hs.278243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	3.90
	449211	AI922972	Hs.196073	ESTs	3.90
	409757	NM_001898	Hs.123114	cystatin SN	3.90
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	3.89
65	432512	NM_003284	Hs.3017	transition protein 1 (during histone lo	3.89
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	3.88
	449099	AI629041	Hs.46908	ESTs	3.88
	408092	NM_007057	Hs.42650	ZW10 Interactor	3.85
	423909	AJ223183	Hs.135194	Immunoglobulin superfamily, member 6	3.85
70	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.84
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.83
	433023	AW864793		thrombospondin 1	3.82
	452571	W31518	Hs.34665	ESTs	3.81
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	3.80
75	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.80
	420697	AA827705	Hs.26605	ESTs	3.80
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	3.80
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.80
	411856	H87899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.80
80	449529	AI990559	Hs.232033	ESTs	3.80
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.78
	444656	AJ277924	Hs.145199	ESTs	3.77
	448674	W31178	Hs.154140	ovary-specific acidic protein	3.77
	415829	AW450198	Hs.163742	ESTs	3.76

	436188	AK001049	Hs.48712	hypothetical protein FLJ20736	3.75
	402178			C19001998*.gij[5453813]ref[NP_008926.2] b	3.75
	418179	X51630	Hs.1145	Warms tumor 1	3.75
5	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.75
	429063	AW363845	Hs.322903	ESTs, Weakly similar to A46010 X-linked	3.75
	437440	AA846804		ESTs	3.75
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associate	3.74
	438456	AA913381	Hs.20594	ESTs	3.73
10	418821	AA436002	Hs.183161	ESTs	3.73
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.73
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.71
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	3.70
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	3.70
	414206	AW276887	Hs.46609	ESTs	3.70
15	427761	AA412205	Hs.140996	ESTs	3.69
	428728	NM_016625	Hs.191381	hypothetical protein	3.68
	452631	AJ188658	Hs.67496	ESTs	3.68
	427719	AJ393122	Hs.134726	ESTs	3.68
20	431869	AA521136	Hs.190176	ESTs	3.67
	429830	AJ537278	Hs.225841	DKFZP434D193 protein	3.67
	420297	AJ628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.66
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.66
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.65
25	456030	AA136106	Hs.184852	KIAA1553 protein	3.65
	402408			NM_030920:Homo sapiens hypothetical pro	3.65
	452387	AJ680772	Hs.306094	trinucleotide repeat containing 12	3.65
	416608	R11499	Hs.189716	ESTs	3.65
	417553	L09190		trichohyalin	3.65
30	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.65
	431077	AJ659133	Hs.115660	hypothetical protein FLJ12810	3.64
	452461	N78223	Hs.108106	transcription factor	3.60
	437660	W31708	Hs.55304	ESTs	3.60
	420552	AK000492	Hs.98806	hypothetical protein	3.60
35	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.59
	420161	AJ683069	Hs.120817	ESTs	3.59
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.59
	449571	AW016812	Hs.200266	ESTs	3.56
	424727	AW590378	Hs.152519	hypothetical protein FLJ20574	3.55
40	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein	3.55
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.55
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.55
	437700	AA766060	Hs.301209	myeloid/lymphoid or mixed-lineage leukem	3.55
	438176	AW138970	Hs.122113	ESTs	3.55
45	453062	AW207538	Hs.61603	KIAA1677	3.55
	447064	AB002350	Hs.17262	KIAA0352 gene product	3.55
	430056	X97548	Hs.228059	KRAB-associated protein 1	3.54
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.54
	434288	AW189075	Hs.116265	fibrillin3	3.54
50	439176	AJ446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.52
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.52
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	3.52
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	3.51
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.50
55	449467	AW205006	Hs.197042	ESTs	3.50
	405935			Target Exon	3.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	3.50
	411027	AF072099	Hs.67848	leukocyte immunoglobulin-like receptor,	3.50
	412140	AA219591	Hs.73625	RAB6 interacting, kinesin-like (rabkinnes	3.49
60	429183	AB014604	Hs.197955	KIAA0704 protein	3.49
	428878	AA436884	Hs.48926	ESTs	3.49
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.49
	435058	H16262	Hs.31415	ESTs	3.48
	442573	H93368	Hs.7567	branched chain aminotransferase 1, cytos	3.48
65	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.48
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.48
	406542			C19000728*.gij[12585552]sp[Q9Y2Q1]Z257_HU	3.47
	422406	AF025441	Hs.116206	Opa-Interacting protein 5	3.46
	402099			ENSP00000217725*:Laminin alpha-1 chain p	3.45
70	418826	AK000375	Hs.88820	HDCMC28P protein	3.45
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.45
	427617	D42063	Hs.199179	RAN binding protein 2	3.45
	428361	NM_015905	Hs.183658	transcriptional intermediary factor 1	3.45
	400268			NM_003292:Homo sapiens translocated prom	3.45
75	443596	AW026048	Hs.134124	ESTs	3.45
	442875	BE623003	Hs.22625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.45
	416031	T30290	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.45
	435244	N77221	Hs.187824	ESTs	3.45
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.45
80	453785	AJ368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.45
	420686	AJ950339	Hs.40782	ESTs	3.44
	429467	NM_004477	Hs.203772	FSHD region gene 1	3.43
	448769	N56037	Hs.38173	ESTs	3.43
	423453	AW450737	Hs.128791	CGI-09 protein	3.41

	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.41
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.41
	404068			Target Exon	3.40
5	401644			Target Exon	3.40
	422364	AF067800	Hs.115515	C-type (calcium dependent, carbohydrate-	3.40
	452907	BE256966	Hs.31652	ESTs, Moderately similar to IS4374 gene	3.40
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.39
	452404	AW450675	Hs.212709	ESTs	3.39
10	452255	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	3.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.39
	440606	AI828751		ESTs, Weakly similar to t38022 hypotheti	3.38
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.37
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.37
15	446214	AK001322	Hs.14347	hypothetical protein FLJ10460	3.36
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.36
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.36
	421533	AF121860	Hs.106260	sorting nexin 10	3.36
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.36
	436511	AA721252	Hs.291502	ESTs	3.35
20	402680			Target Exon	3.35
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.35
	449477	AI652602	Hs.197043	ESTs	3.35
	413686	AI469213	Hs.71404	ESTs	3.35
	401091			decay accelerating factor for complement	3.35
25	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.35
	433220	AI076192	Hs.131933	ESTs	3.34
	453200	AA033832	Hs.212433	ESTs	3.33
	427239	BE270447		ubiquitin carrier protein	3.33
30	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	3.33
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthase	3.31
	441243	AI767056	Hs.193002	ESTs	3.30
	440716	AW105245	Hs.146509	ESTs	3.30
	400587			C10000649:gi 7296574 gb AA151857.1 (AE	3.30
35	401148			Target Exon	3.30
	411752	AW236047	Hs.126497	ESTs	3.30
	433252	AB040957	Hs.151343	KIAA1524 protein	3.30
	434008	AA740878	Hs.112982	ESTs	3.30
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.30
40	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.30
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.29
	452761	BE244742	Hs.30532	CGI-77 protein	3.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.29
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.28
45	432809	AA565509	Hs.131703	ESTs	3.27
	449426	T92251	Hs.198882	ESTs	3.27
	425174	D87450	Hs.154978	KIAA0261 protein	3.25
	435159	AA668879	Hs.116649	ESTs	3.25
	446597	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	3.25
50	411554	W22895	Hs.112360	prominin (mouse)-like 1	3.25
	447555	AC391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	3.25
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	3.25
	445093	AI207197		ESTs	3.25
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.24
55	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.24
	453293	AA382267	Hs.10653	ESTs	3.24
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.23
	430552	AA176374	Hs.243885	nuclear autoantigenic sperm protein (hs	3.22
	411975	AI916058	Hs.144583	ESTs	3.22
60	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.22
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.21
	436515	AJ278111	Hs.195292	putative tumor antigen	3.21
	456505	AA504595		ESTs	3.21
	427658	AA298760	Hs.180191	hypothetical protein FLJ14904	3.21
65	452794	AI192444	Hs.25892	ESTs, Weakly similar to I37356 epithelia	3.20
	427314	AB033024	Hs.175475	KIAA1198 protein	3.20
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.20
	452028	AK001859	Hs.27595	hypothetical protein FLJ21142	3.20
	421002	AF116030	Hs.100932	transcription factor 17	3.20
70	422225	BE245652	Hs.118281	zinc finger protein 266	3.20
	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	3.20
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	442765	BE567353	Hs.99480	ESTs	3.20
75	410048	W76487	Hs.343874	proline oxidase homolog	3.20
	412008	NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	3.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.20
	453895	AA039843	Hs.61948	Homo sapiens, clone MGC:16466, mRNA, com	3.20
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.19
80	428612	AA770001		ESTs	3.19
	422805	AA436989	Hs.121017	H2A histone family, member A	3.19
	444371	BE540274	Hs.239	forkhead box M1	3.18
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.17
	451684	AF216751	Hs.26813	CDA14	3.17

5	452031	AA741314	Hs.855	RAP1A, member of RAS oncogene family	3.17
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	445528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H88923	Hs.270247	Homo sapiens cDNA FLJ11977 fis, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
10	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450405	AI694913	Hs.279637	ESTs	3.15
	414161	AA136106	Hs.184852	KIAA1553 protein	3.15
15	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
	441013	AI125252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
20	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.11
25	423419	R55336	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195631	ESTs	3.10
30	441795	N58115	Hs.21137	AD024 protein	3.10
	450553	S57498	Hs.76252	endothelin receptor type A	3.10
	403610			C3001199:gil7494834[pir]T15308 hypothet	3.10
	421281	AI299139	Hs.17517	ESTs	3.10
	429274	AI379772	Hs.99206	ESTs	3.10
35	438243	AI581311		ESTs	3.10
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.09
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	416443	N69469	Hs.194225	ESTs	3.08
40	421230	AW958439	Hs.105633	ESTs	3.07
	427906	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.06
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	AI343868	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
45	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102456	survival of motor neuron protein Interac	3.05
50	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.05
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
55	435726	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
60	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cel	3.00
	434776	AA648988		gb:ns41f11.s1 NCI_CGAP_GCB1 Homo sapiens	3.00
	414132	AI801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
65	433493	AA594915	Hs.155087	ESTs	3.00
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	3.00
	453416	NM_003037	Hs.32970	signaling lymphocytic activation molecu	3.00

TABLE 53B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	432666	144_7	AA558585 AA565499 AJ360576 AW204069 AA991648 AA864939
75	423458	30480_1	BC018070 BG702493 AJ204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
			BG215094 BG198867 BG196332 BG208220 BG212418
	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
			A1352469 BE061601 B1052752 AW818206 BF887722
80	422828	227063_1	BE671981 BE503379 A1655440 A1337054 A1288920 A1242370 A1825182 AA758081 BF855141 BF091068
	418477	4172_1	BC022538 A1990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
			A1623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 A1910424
	443068	18695_17	AV752763 A1032142 N30308 N22181 H95390 AW675632
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 A1690673

427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
436899	1000797_1	AA764852 AA736937
422689	874209_1	AW954733 AA315006 AW856665
440968	518029_1	AI964001 AI634418 AW236545 AI824860 BF223710 AW139686 AI672051 AI655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451
427486	684159_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
421974	864120_1	AA301270 AA301379 AA301366
435614	132288_1	AA683355 AW592804 AI150287
434609	14739_1	AF147390 R76593 R76594
414136	30243_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566634 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AU154486 AW605017 AW450072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812
415684	18695_18	BF666746 D59356 BG678312 N56640 AA166861
437421	978554_1	AA917062 AA757369 AW592218
439780	49082_1	AL109688 R23665 R26578
453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H07775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
412537	14066_1	AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI258215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
440801	2635916_1	AA906366 AA938956 AI910938
436909	596835_1	AW102570 AA907150 AA907120 AA737188 AI248890 AW977353
429228	215430_1	BC676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969605 AI553633
451050	11847_4	BM453041 AA760783 BE218582 AJ40046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115485 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839
418235	886897_1	BE072634 BE072653 AA830615 AA214736 AA331718
418378	1227421_1	AA218925 AW962081 AA354237
450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758
409517	4537_1	NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070 C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339
442582	39593_1	AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 AI653056 AW937309 AI653173 BG054997 AI266043 BI054879 AI658750 AI492830 AW021142 AI472184 AW170056 AI082443 AH67921 D59940 BI492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832
451105	1145037_1	BI015205 AI761324 AW880937 AW880941
424281	892055_1	AA338252 AA338213
430183	17316_1	AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038
427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
444386	1490237_1	BE065183 AI144398 BE065367 BF377924
414725	19377_1	NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112 BI054316
433641	35983_1	AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N29986 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA205262 AI365204 H77608 AW590511
418768	2293204_1	T39328 T39310 T39303 T39284
409268	109625_1	BE893356 AA625304 AI765607 AI624898 R76060 AA069651 BG998885 R35783 BF086499 AA428755 AI245055
415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469833 AW958465 AW953397 AA172056 BE940288 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
433979	2076469_1	N50454 AA620999 T16375
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 T65754 AA229658 AA229857
418866	245947_1	AK056550 AK056356 AI928212 AI742073 AW300558 BG058755 AA058343 AI554842 AW207438 BF509981 BF444954 AW026234 AI620104 AA973460 AI370934 N63066 AA493129 AW590888 AI682952 AI167202 AA631394 AI421915 AI222883 BF477519 AI208777 AA765849 AI675076 AI370922 AI339579 AA486224 AA453524 AW771805 AI492842 H54679 AA961022 AW023555 H06192 AA910222 AI680021 AI032525 AI375480 AI351860 AI032919 AA833599 BG057928 AA553913 AW235737 AA002124 AA913636 F04607 AI867699 AA648100 BE091446 AA486378
445685	381678_1	BE002022 H84627 BI059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG290981 AW954251 AA757126 H11545 AA353384 N48448 AA379845 AA004943 AA379928 AA002123 BM470118 AL598847 AL598830 BG899239 R57470 BF939179 AI650642 AI758851 BF352505 W68422 W35297 H11435 AA937499 AI783996 R12500 AI819557 N39093 Z41619 H22849 AA004942 R09436 R02403 T90942 T85823
413646	1525656_1	BG026683 AI248120 BI850480 AW779829 N22494
437834	294580_1	BE155042 BE155040 BE154987 BE155012 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573 AW813110 BF771370 BF771371 AW813113 AW003381 BI862319 AA204955 BF240507 BG212143 AW205739 BI760647 BI760482 AW300025 AI288591 AW236114 AI302852 AI038548 AI797207 AA534496 BG188194 AA921877 BG191846 BG182959 BE520243 BF217428 BC009514 BM463015 AL529077 BM051874 BG773269 BM314351 BM314660 AW629666 AA316207 AE123431 AA504153 AA314700 BG195449 BG614101 BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846676 AA927355 H80424 AW973235 R88209 F29868 BE928871 AA846804 AA757581 AI050950 AI092024 AA838807
437440	2497201_1	

5	417553	258857_1	AL545411 AI096369 BF431750 AJ130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AJ204699 W60115 N56751 N30878
	408065	101881_1	AJ769345 R71250 AI363766 R22777 R17009 R27985 R28243
	418049	12052_4	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
	430968	1237115_1	AJ314647 NM_052888 BI494693 AA835065 AI634477 AJ336678 AJ807696 BF477887 AJ701147 Z39187 R38979 F02234 AA984711 BI222234
	400268	840_4	AV731417 R42406 H04996 T98498 R12489 R12577 R42405
10			AW972830 AA489820 AA527647 AA570362
			U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AJ870824 BE973573
			BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687
			BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AJ765790 BF222859
			AW167268 AJ990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916
			AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450
			AL549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385625 BE175733 BE175727 BE175723 BF092430 BI061782
			AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532
			BE934857 BF925067 AW438446 R86246 AW179270 BE087782 BI832144
15	440606	10075_1	BC017350 BC021031 AI220219 AJ828751 AW134498 BE139642 AA894554 AI278594 AV747315 BE561749 BI085890 T80117 H69682 N70904
	427239	20459_2	AV741999 H70098
20			AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AJ307208 BE138953 BE049086 AI334881
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334809 AI802853 AI345036 AI348921 AJ340734 AJ307478
			AJ251289 AW302327 AW072520 AJ312145 AW073656 AW072513 AW071289 AJ307559 AA876186 T29587 AJ307483 AI255068 AI252868 AI252839
			AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073459 AW072901 AW072496 AW071420
			AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
			AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
			BF718773 BF718645 AW074866 BE857822
25	445093	175963_1	AI207197 BF773544 AW196462
	456505	15472_2	BC017965 AW969075 AA279982 AA504511 AJ219979 AA504595 AI245579 AA278181 BG485019 BI049312
	428612	1383189_1	AA770001 AA431112 AA432126
	437642	77594_1	AL079309 AA281819
	440129	2607882_1	AI732997 AA977633 AA865818
30	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
			AW840571
	438243	2532601_1	AI581311 AA781682 AA781678
	438869	52134_1	AF075009 R63109 R63068
35	434776	118129_1	AW974599 AA648988 R98760

TABLE 53C

40	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

45	Pkey	Ref	Strand	Nt_position
	406547	7711513	Minus	172780-174358
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	402199	8576116	Minus	84187-84744
	402145	8018280	Plus	113086-114800
50	401837	7630990	Minus	120993-121095,121660-121729
	403780	8076989	Plus	93160-93409
	402299	6693370	Plus	23367-25175
	401435	8217934	Minus	54508-55233
	401464	6682291	Minus	170688-170834
55	402098	8117697	Minus	44186-44330
	404287	2326514	Plus	53134-53281
	406367	9256126	Minus	58313-58489
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402178	8576912	Plus	391138-391711
60	403433	9719611	Minus	72225-72437
	402408	9796239	Minus	110326-110491
	405935	6758795	Minus	163112-163652
	406542	7711499	Plus	117335-118473
	402099	8117697	Plus	121553-121742,123265-123423
65	404068	3168621	Minus	18123-18766
	401644	8576138	Plus	82655-83959
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	401091	9958240	Plus	94760-94898
	400587	9887626	Plus	25435-25588,25668-25747
70	401148	2547238	Minus	22521-23053
	403432	9719611	Minus	68204-68392
	400592	9887642	Minus	24642-24815
	403610	8308266	Plus	157705-157860

TABLE 54A:

75	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
80	R1:	Ratio of normal testis to normal adult tissues
	R2:	Ratio of "average" normal testis to "average" testicular cancer

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
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401979			C17000767:gl 11990770[emb]CAC19651.1 (A	10.08	43.3
421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35	36.8
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74	32.0
441728	AI797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54	24.5
452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.85	22.0
415211	R64730	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93	19.8
418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	4.94	18.5
449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.94	17.5
420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75	15.6
436532	AA724299	Hs.304020	ESTs, Weakly similar to CRTC_HUMAN CALRE	6.51	14.9
418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96	14.6
406409			Target Exon	3.98	14.3
427060	AW378993	Hs.90286	ESTs	3.56	14.2
427310	AI613480	Hs.47152	taktin 3	4.50	14.0
427166	AA431576	Hs.99154	ESTs	4.28	13.9
427178	AA398866	Hs.97542	Homo sapiens testis-development related	10.19	13.7
410694	AL137538	Hs.65500	Homo sapiens mRNA; cDNA DKFZp434N2019 (f	5.76	13.4
424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24	13.3
427441	AA412605	Hs.343879	SPANX family, member C	10.45	12.6
438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORNI	18.57	12.3
422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	5.18	12.3
427293	AA705799	Hs.183714	ESTs	10.79	12.1
444983	AI916973	Hs.213603	ESTs	3.18	12.1
428608	AI699329	Hs.99168	ESTs, Weakly similar to AF132972.1 CGI-3	15.40	11.8
453178	AA496086	Hs.61648	ESTs	4.13	11.8
428618	AA885360		Target CAT	7.53	11.5
401741			Target Exon	10.41	11.5
422086	AW182930	Hs.250182	ESTs	4.39	10.7
426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04	10.6
442373	AI377758	Hs.164799	testes development-related NYD-SP17	8.23	10.3
427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax interacti	3.03	10.1
437248	AW449340	Hs.93090	ESTs	9.06	10.1
426608	AA444162	Hs.99344	hypothetical protein PRD2-NY3	3.68	10.0
427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70	9.8
422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85	9.7
451610	AW118604	Hs.207126	ESTs	5.63	9.7
410830	BE044562	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38	9.5
426677	AW949856	Hs.97165	ESTs	6.58	9.3
437558	AI126471	Hs.124112	ESTs, Moderately similar to HSJ2_HUMAN D	4.47	9.2
423088	NM_006687	Hs.123530	actin-like 7A	15.07	8.9
426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	18.55	8.9
421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	13.93	8.8
429877	W37337	Hs.103014	ESTs	6.97	8.7
413114	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78	8.6
412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	22.03	8.5
411844	AI807681	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	7.34	8.3
436868	AA974253	Hs.120319	Homo sapiens autoimmune infertility-rela	4.16	8.2
426599	AW183574		ESTs	6.29	8.1
426683	AI073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89	8.0
426930	AA393442		ESTs	5.06	8.0
427836	AA416842	Hs.116176	ESTs	4.79	8.0
407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11	7.9
430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26	7.6
434150	BE047007	Hs.116116	testis specific, 10	4.85	7.6
422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.29	7.5
422116	H64205	Hs.111850	mitochondrial capsule selenoprotein	9.12	7.5
433724	AI827749	Hs.144924	serine/threonine protein kinase SSTK	22.24	7.4
410187	AA860341	Hs.104680	ESTs	3.03	7.4
419584	AF053356	Hs.283764	F-box only protein 24	6.43	7.4
458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90	7.3
418665	T19204	Hs.195685	ESTs	7.14	7.3
426646	AA382787	Hs.122713	ESTs	7.03	7.3
420349	NM_016611	Hs.97174	potassium inwardly-rectifying channel, s	14.90	7.3
428624	AI125222	Hs.98712	hypothetical protein DKFZp434H0311	3.71	7.1
420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78	7.1
434317	AI674095		ESTs	3.98	7.1
443432	AI056863	Hs.339871	ESTs	3.46	7.0
425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21	7.0
426670	AA383047	Hs.310210	ESTs	6.92	7.0
408613	AW242086	Hs.253987	ESTs	5.77	6.8
452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23	6.7
434133	AI655275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46	6.7
427294	AA412594	Hs.125902	ESTs	3.44	6.7
427262	AA448509	Hs.128652	ESTs	5.66	6.5
429851	AA459935	Hs.120573	hypothetical protein DKFZp434K1172	9.01	6.5
406378			NM_021247*:Homo sapiens protamine 3 (PRM	3.96	6.4
425865	AA393491	Hs.183740	ESTs	9.15	6.4
428665	NM_017481	Hs.189184	ubiquitin 3	11.07	6.4
439379	AA835002	Hs.125611	ESTs	5.06	6.3
427520	BE467881	Hs.97489	ESTs, Weakly similar to B28096 line-1 pr	9.29	6.2
458940	BE149824	Hs.132888	KIAA1674	3.11	6.2
426620	AW450252		ESTs	12.27	6.2
429516	AI653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15	6.1

	426736	AA431615	Hs.130722	ESTs	3.58	6.1
	427843	AC005622	Hs.180943	hypothetical protein R30953_1	6.34	6.1
	426639	AI799059	Hs.112807	ESTs	6.93	6.0
5	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
	433795	AI216683	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
	441232	AI656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
	426955	AA393669	Hs.238094	ESTs	4.75	5.8
10	428918	AL036987	Hs.2324	protamine 2	38.40	5.8
	427851	AA846543	Hs.98257	ESTs	15.87	5.8
	428208	AA442327	Hs.104854	ESTs	6.34	5.7
	422207	AI828862	Hs.10964	ESTs	6.43	5.7
	431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
15	419350	AC005328	Hs.77823	Homo sapiens chromosome 19, cosmid R2666	14.94	5.6
	427107	AA895885	Hs.180346	ESTs	6.25	5.6
	429461	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	22.03	5.6
	434451	AW445179	Hs.121438	ESTs	7.89	5.5
20	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	11.26	5.5
	427214	AA442240	Hs.178213	ESTs	8.41	5.5
	458658	AI301117	Hs.122055	ESTs	4.35	5.5
	457034	AA398081	Hs.296587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
	423120	AW160551	Hs.124021	soggy-1 gene	8.88	5.4
25	438983	AF085884	Hs.20029	proacrosin binding protein sp32 precursor	22.69	5.4
	426619	AI357194	Hs.119284	ESTs	7.07	5.4
	440822	AI554897	Hs.119284	Homo sapiens clone 19187 placenta expres	3.60	5.4
	416205	AA176396	Hs.169624	ESTs	10.26	5.4
	426712	AW173177	Hs.197755	hypothetical protein MGC5355	8.17	5.3
30	427840	AI216654	Hs.98251	ESTs	6.44	5.3
	439314	AA382413	Hs.178144	ESTs	8.35	5.3
	426943	BE551631	Hs.20969	ESTs	6.31	5.2
	409209	AA460160	Hs.73217	ESTs	7.85	5.2
	441710	AI187883	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
35	420571	AA442366	Hs.98952	Human DNA sequence from clone RP1-39G22	9.39	5.1
	428563	AA431616	Hs.98660	ESTs	14.94	5.1
	433994	AL042483	Hs.335499	ESTs	6.84	5.0
	441856	AI674774	Hs.128014	ESTs	3.74	5.0
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
40	418957	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
	430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHUH ferrit	10.66	4.9
	421850	AW274576	Hs.121021	ESTs	12.27	4.9
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
	426699	AA383337	Hs.121269	ESTs	5.67	4.9
45	426627	AF012359	Hs.195685	ESTs	20.66	4.9
	427285	AA401664	Hs.97784	ESTs	4.72	4.8
	423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
	457019	AA421844	Hs.12830	hypothetical protein	3.87	4.8
	405264			NM_030813*:Homo sapiens suppressor of po	4.48	4.8
50	450606	AI686605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
	421378	L77584	Hs.103978	serine/threonine kinase 22B (spermogene	7.35	4.8
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
	427423	BE267041	Hs.177926	exonuclease NEF-sp	19.27	4.7
	438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
55	424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
	423284	AC005764	Hs.126496	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
	432117	AL038195	Hs.2909	protamine 1	55.33	4.7
	424426	AI476416	Hs.132888	KIAA1674	5.41	4.6
	437387	AI198874	Hs.28847	AD026 protein	5.04	4.6
60	420718	NM_002301	Hs.99881	lactate dehydrogenase C	9.18	4.6
	420768	AI468780	Hs.292503	ESTs, Weakly similar to T47142 hypothei	5.70	4.6
	423677	M86808	Hs.131361	pyruvate dehydrogenase (lipoamide) alpha	10.93	4.5
	436661	AI125270	Hs.128069	ESTs, Weakly similar to T19142 hypothei	3.82	4.5
	427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
65	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
	427877	AW138725	Hs.178067	ESTs	4.09	4.5
	426623	AA382826	Hs.132793	ESTs	26.62	4.5
	429965	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	3.88	4.4
70	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosom	3.46	4.4
	421938	AA405951		gb.zu66c01.r1 Soares_testis_NHT Homo sap	4.69	4.4
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
	426710	BE041517	Hs.143893	ESTs	5.57	4.4
	428710	AI890919	Hs.126780	ESTs, Weakly similar to T12519 hypothei	11.86	4.4
75	438641	AW138484	Hs.190653	ESTs	6.19	4.4
	420614	AL110291	Hs.99364	putative transmembrane protein	6.86	4.4
	422705	NM_006688	Hs.119287	actin-like 7B	9.73	4.4
	421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610712, mRNA,	6.77	4.3
80	426738	AA421097	Hs.291902	ESTs	3.49	4.3
	440403	AW685135	Hs.130531	ESTs	6.97	4.3
	456085	AI184560	Hs.130352	ESTs, Weakly similar to A47582 B-cell gr	8.30	4.3
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
	428909	AI190714	Hs.98945	ESTs	7.79	4.3

5	426735	T78716	Hs.120446	ESTs	5.10	4.3
	438653	AW188099	Hs.131813	ESTs	5.29	4.3
	443038	AI968058	Hs.209205	ESTs, Weakly similar to S38782 actin bel	7.29	4.2
	428677	AI657119	Hs.120036	troponin I, cardiac	10.73	4.2
	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.169222	acrosomal vesicle protein 1	4.87	4.2
	428871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTTS protein	7.29	4.2
10	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401692			C16000122:gij5689527[dbj]BAA83047.1}[A	6.37	4.1
	403783			NM_031956:Homo sapiens NYD-SP14 protein	3.74	4.0
15	421611	AA459841	Hs.97309	ESTs	11.51	4.0
	404271			ENSP00000244792*:Phosphoglycerate kinase	4.02	4.0
	418100	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RP5-860F19	4.84	4.0
20	420419	AA397796	Hs.11614	HSPC065 protein	4.07	3.9
	435897	AF269223	Hs.128322	I-complex 11 (a murine tcp homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400590	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRTD-NY3	10.07	3.9
25	452579	AA131657	Hs.23830	ESTs	5.24	3.9
	441443	BE465999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRIN protein	3.82	3.9
	435484	AA692756	Hs.88051	ESTs	5.10	3.9
30	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fls, clone L	4.61	3.8
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
35	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYC	7.69	3.8
40	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekli	3.46	3.7
	442589	BE409869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262951	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
	440487	AI203685	Hs.135763	ESTs	5.90	3.7
45	419455	AW172570	Hs.14600	ESTs	4.23	3.7
	436588	AA759233		ESTs	5.04	3.7
	421610	AA393168	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434I099	5.17	3.6
50	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CQ-	3.17	3.6
	438064	AI476330	Hs.234934	ESTs	3.56	3.6
	426558	AA397912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
55	431986	AA536130		Novel human gene mapping to chromosome 20	6.13	3.6
	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-281G23	4.04	3.6
	437896	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fls, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cylclin, basic protein of sperm head cyt	5.13	3.5
60	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
	437399	AI808626	Hs.121188	ESTs, Weakly similar to T29922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.135283	ESTs	4.47	3.5
65	423329	AF054910	Hs.127111	teklin 2 (testicular)	4.40	3.5
	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005281	Hs.98338	serine/threonine kinase 13 (aurora/IPL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-t	10.39	3.4
70	420482	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
	426988	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW628609	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
75	422782	AL133054	Hs.120369	hypothetical protein DKFZp434H2215	4.72	3.4
	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	collin	6.30	3.4
	435587	AF215924	Hs.97899	putative allantolcase	3.48	3.3
80	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotroph-regulated testicular RNA ho	10.76	3.3

5	412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypotheti	5.27	3.3
	441579	AW468847	Hs.127194	ESTs	7.13	3.3
	420519	AF130255	Hs.99430	testis zinc finger protein	5.19	3.3
	425368	AB014595	Hs.155976	cullin 4B	3.07	3.3
	425538	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
10	429338	BE295804	Hs.226377	phosphate cytidylyltransferase 2, ethano	3.03	3.3
	453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
	424468	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
	442084	H81173	Hs.34596	ESTs	4.78	3.3
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
15	434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
	428093	AW594506	Hs.104830	ESTs	6.95	3.3
	433882	AA724720	Hs.112941	ESTs	5.11	3.2
	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
	408415	AW418788		ESTs, Weakly similar to S43569 R01H10.6	3.49	3.2
20	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
	402857			Target Exon	3.19	3.2
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
	427748	AA421041		ESTs	4.57	3.2
25	422794	AJ011733	Hs.120857	synaptogyrin 4	4.23	3.2
	417488	AL040652	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
	440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
	437143	AW204056	Hs.8917	ESTs	4.16	3.2
	417473	M55268	Hs.82201	casein kinase 2, alpha prime polypeptide	4.02	3.2
30	426594	AA884317	Hs.97130	ESTs	3.45	3.2
	428733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
	440864	AI382142	Hs.132104	ESTs	8.48	3.2
	427141	AW528007	Hs.97643	testis-specific protein TSP-NY	5.60	3.2
	431534	AI137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
35	438670	AI275803	Hs.123428	ESTs	4.08	3.2
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.26	3.2
	452251	R37132	Hs.65009	ESTs	4.01	3.1
	444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
	428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
40	421621	AL045589	Hs.180197	ESTs	7.09	3.1
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
	457138	AW140059	Hs.98579	ESTs	13.17	3.1
	428524	AA429772		ESTs	4.40	3.1
	428726	AA432195	Hs.98694	ESTs	6.47	3.1
45	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	4.07	3.1
	428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
	424450	AL137526	Hs.147472	dynein intermediate chain 2	6.01	3.1
	433963	AI218808	Hs.187778	ESTs	5.68	3.1
50	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
	440933	AI208217		ESTs	3.44	3.1
	441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
	423313	NM_014269	Hs.126838	a disintegrin and metalloproteinase doma	6.36	3.1
	428530	AA431270	Hs.140646	ESTs	3.59	3.1
55	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	5.63	3.0
	434720	AI208541	Hs.189160	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
	436328	AI201145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
	429293	AI767879	Hs.99214	ESTs	5.69	3.0
	427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
60	440713	AA804448	Hs.126368	ESTs	6.28	3.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
	423218	NM_015896	Hs.167380	BLu protein	6.68	3.0
	444644	AW070634	Hs.144794	ESTs	5.00	3.0
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
65	427829	AI188225		ESTs	7.36	3.0
	426879	AI969340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
	427362	AA625582	Hs.97752	EST	4.38	3.0
	441973	T60072	Hs.10688	ESTs, Weakly similar to HRIHFB2157 [H.sa	4.06	2.9
	428989	AF104260	Hs.194712	pwl (Drosophila)-like 1	4.45	2.9
70	438735	M76676		ESTs	3.81	2.9
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
	427586	AA609661	Hs.190592	ESTs, Moderately similar to WASP-family	6.26	2.9
	427306	AI476743	Hs.229275	ESTs	3.00	2.9
	418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
75	456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.60	2.9
	433836	AA610065	Hs.179646	ESTs	3.33	2.9
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.22	2.9
	437426	AW136558	Hs.125246	ESTs	4.49	2.9
80	405528			C2002647:g[4507721:ref]NP_003310.1 [ti	6.03	2.9
	442977	AW291731	Hs.144090	ESTs	4.23	2.9
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	13.24	2.8
	424275	AW673173	Hs.144505	DKFZP566F0546 protein	5.60	2.8
	426667	AA770016	Hs.121192	ESTs	3.64	2.8
	410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
	428080	AI198656	Hs.98330	ESTs	4.09	2.8
	427252	AA400069	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

	458255	AW140126	Hs.132357	ESTs	3.23	2.8
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
	440582	AA993337	Hs.129082	ESTs	5.29	2.8
5	435566	AJ457958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
	433771	AI028794	Hs.112684	ESTs	3.36	2.8
	447924	AJ817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.30	2.8
	426703	AI221893	Hs.121549	ESTs	3.93	2.8
	430251	AA609246	Hs.181451	ESTs	4.04	2.8
10	427184	AJ969361	Hs.180471	ESTs	6.78	2.8
	439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
	448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 testi	3.34	2.7
	450340	AA442322	Hs.60288	ESTs	5.39	2.7
	428100	AW665592	Hs.190413	ESTs	5.32	2.7
15	449333	AI203021		ESTs	4.35	2.7
	429861	AJ989571	Hs.99510	ESTs	3.28	2.7
	426622	AL044400	Hs.25371	ESTs, Weakly similar to A37232 muchn, tr	5.38	2.7
	427256	AL042436	Hs.97723	ESTs	4.08	2.7
	408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
20	403328			Target Exon	4.26	2.7
	436264	AA707457	Hs.120014	ESTs	3.58	2.7
	427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci	3.68	2.7
	426640	AJ200981	Hs.98104	ESTs	4.60	2.7
	428789	AW296167	Hs.91930	ESTs	4.23	2.7
25	435274	AA887547	Hs.150905	ESTs	4.25	2.7
	426512	AA922057	Hs.184185	ESTs	7.17	2.7
	435110	M42688	Hs.81001	F-box only protein 25	4.85	2.7
	433792	AA778661		ESTs	4.06	2.7
	423278	AL117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
30	427284	AA400298	Hs.144696	ESTs	5.81	2.6
	423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.36	2.6
	422362	Z46967	Hs.115460	calicin	4.72	2.6
	439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
	409364	AJ480252	Hs.137368	ESTs	7.22	2.6
35	419224	NM_012189	Hs.314452	fibrousheathin II	13.86	2.6
	428915	AJ041278	Hs.87808	Snf2-related CBP activator protein	4.73	2.6
	427181	AJ183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
	442122	AJ932330		ESTs	3.07	2.6
	424812	AF059252	Hs.153299	DOM-3 (C. elegans) homolog Z	3.80	2.6
40	430956	AJ183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
	427234	AA399667	Hs.104675	ESTs	3.43	2.6
	423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
	428214	AA936282	Hs.120397	ESTs	4.14	2.6
	452613	AA461599	Hs.23459	ESTs	7.78	2.6
45	410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
	401712			Target Exon	4.51	2.6
	429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
50	438124	AA778610	Hs.122045	ESTs	3.43	2.6
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
	410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
	428625	W87565	Hs.18566	ESTs	5.29	2.6
	433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.5
	433760	AW592321		ESTs	3.26	2.5
55	431219	AJ190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.56	2.5
	445158	AJ992108	Hs.127206	ESTs	3.60	2.5
	440860	R10482	Hs.132876	ESTs	4.26	2.5
60	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.95	2.5
	433281	N48673	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
	429369	AJ269514	Hs.129802	ESTs	3.49	2.5
	433949	AJ674766	Hs.112877	ESTs	5.15	2.5
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	10.46	2.5
65	414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypotheti	3.87	2.5
	408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	6.10	2.4
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	5.64	2.4
	426956	AA393673		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
	429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
70	426247	U92992	Hs.98834	ESTs	5.40	2.4
	427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
	453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
	413372	H55532		tubulin, alpha 2	9.32	2.4
75	411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
	453868	NM_014433	Hs.35984	rhabdoid tumor deletion region protein 1	3.05	2.4
	427098	AA398161	Hs.97602	ESTs	3.21	2.4
	427165	AA429709	Hs.99336	ESTs, Weakly similar to T15446 hypotheti	4.27	2.4
	425808	AA364109	Hs.177990	ESTs	7.80	2.4
80	444790	AB030506	Hs.11955	B9 protein	3.32	2.4
	426718	AA383555	Hs.126413	ESTs	4.20	2.4
	411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
	450852	AJ983354	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
	427054	AA421240	Hs.97570	ESTs	3.10	2.3

5	438633	AI653327	Hs.123501	ESTs	3.46	2.3
	427199	AW015836	Hs.292919	ESTs	4.31	2.3
	440182	AA868919	Hs.250110	ESTs	3.03	2.3
	435517	AA928626	Hs.130177	ESTs	3.64	2.3
	446309	BE044261	Hs.149774	ESTs	3.52	2.3
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	4.23	2.3
	433829	AI190715	Hs.102021	ESTs	6.08	2.3
	429485	AW197086	Hs.99338	ESTs	3.14	2.3
10	423068	AW964568	Hs.111591	ESTs	3.36	2.3
	433822	AI218609	Hs.112772	ESTs	3.83	2.3
	442268	BE278064	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
	434298	AA860090	Hs.116290	ESTs	3.71	2.3
	440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
	427554	AW246578	Hs.179615	hypothetical protein FLJ10058	3.39	2.3
15	414251	AL042306	Hs.97689	VASA protein	11.25	2.3
	430254	AI809520		ESTs	3.27	2.3
	437418	AI478954	Hs.59459	ESTs	3.43	2.2
	437522	AA983844	Hs.121383	ESTs	4.15	2.2
	422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
20	436695	AA725655	Hs.120480	ESTs	5.26	2.2
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	6.78	2.2
	421625	AA405386	Hs.178004	ESTs	3.22	2.2
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
	428174	AA913321	Hs.126778	ESTs	3.09	2.2
25	409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
	444467	AI150368		ESTs	3.81	2.2
	433832	AA918018	Hs.172516	ESTs	6.94	2.2
	440036	AW593295	Hs.210956	ESTs	5.87	2.2
	415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
30	432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
	440882	AI205777	Hs.129538	ESTs	3.83	2.1
	436605	AI187742		ESTs	3.41	2.1
	422990	AF035620	Hs.122764	BRCA1 associated protein	5.66	2.1
35	432174	AW590264	Hs.132806	ESTs	3.05	2.1
	409267	NM_012453	Hs.52515	transducin (beta)-like 2	5.46	2.1
	423021	AL036111	Hs.292767	ESTs	3.87	2.1
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
	433812	AA725026	Hs.97165	ESTs, Weakly similar to T31611 hypotheti	3.62	2.1
40	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
	437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
	426038	AA368101	Hs.99052	ESTs	3.03	2.1
	427065	AA397903	Hs.236635	gb:z189f12.1 Soares_testis_NHT Homo sap	3.23	2.1
	428824	W23624	Hs.173059	ESTs	3.07	2.1
45	428224	X54017	Hs.183088	acrosin	3.18	2.1
	436954	AA740151	Hs.130425	ESTs	3.20	2.1
	444470	AA412195	Hs.13740	ESTs	4.27	2.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	5.30	2.1
	427886	AA417083	Hs.104789	ESTs	3.49	2.1
50	439273	AW139099	Hs.269701	ESTs	3.83	2.1
	434318	AW207552	Hs.116328	ESTs, Weakly similar to A39564 transcrip	4.01	2.1
	427015	AA397520		ESTs	4.28	2.1
	421598	AW630942	Hs.106061	RD RNA-binding protein	3.30	2.1
	427238	AA399959	Hs.148271	ESTs	3.07	2.1
55	434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
	456051	T85626	Hs.76239	hypothetical protein FLJ20608	3.11	2.0
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
	451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	4.73	2.0
60	420484	W32963	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
	414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
	424558	AF038847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 54B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

70	Pkey	CAT Number	Accession
	428618	2668_1	BC017998 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI652853 AI990773 AW665193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515652 H15004 AA909115 BI465310 BI462024 BI561578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272
	426599	10110_1	BE736800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 BI830957 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203683 BE041513 AA382260 AA382261 AL554887 BE273483 AI809889 AA393442 AI150574 AI200886 AI221692 AA608977 AA813213
75	426930	1310779_1	AI209094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW665317 AA629314 AA776691 AA906846
	434317	595987_1	AA974625 AA884357 AI808590
	426620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI636668 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI139837
80	419350	13086_1	AI218809 BC014609 BG724383 AI024359 AA904573 AI138595 AA868685 AI768931 BI828436 BG717350 BG719800 AW182303 AA448181 BI826670 BI827131 BI830254 BI824155 BI831745 T19190 BI830415
	440822	532608_1	BG207562 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA906867 AI873494 AI015039
	421938	863689_1	AA412383 AA300675 BG773248 AA412243 AA405951

442589	33097_2	NM_004157 X14968 BG480488 BE409869 BG723898 BG476313 AU121626 BE386516 A1969297 AW172340 AA89668 R23436 A1015037 BE250558 BF590945 AW385993 BF983000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899096 BG827945 BE741233 A1015465 AW370169 BE297350 AA093249 A122828 AA909991 AA759233 AL591713 BF197609 A1985094 AW448916 A1243277 AL449630 AL449629 AW241405 AW205071 A1671586 A1652354 A1638465 AW590359 AW662771 AW594067 BE502532 A1218894 BE466416 BF056295 A1247366 A1990484 A1917746 AW665925 A1216456 AW182169 AA969884 AAT23888 A1018419 BI602176 BI603138 BI459895 BI755030 AW418788 AA883999 AAT24858 A1480311 AW196355 A1004813 A1651117 BE814363 AW589856 AA448124 AA447982 BI461166 AA405629 A1208966 AA421041 AA815377 AA411954 BF980395 R51074 BF979883 A1539370 BM128735 AA993397 A1611039 AW593985 R41808 A1208080 AA442862 AA429772 A1125404 AW593312 A1247364 A1208217 AA910021 A1915307 A1190292 A1188225 AA416673 AA416596 AA952888 AA972172 AA906874 M76676 NM_022571 BG772522 BF516449 A1537485 AW517245 BF762536 AA634446 AW196331 A1203035 BG722281 AK056320 AL522040 BI793043 AW071691 A1433682 AA865414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA482563 N33446 N25222 Z41110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 A1655113 A1309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA364618 AA364851 AA421448 T74231 R52350 AA482415 A1203021 T88948 A1565842 A1024286 AA769898 AA776651 AA868572 AA609524 A1932330 A1190707 A1376782 AA976847 AA609179 AW592321 AA758282 A1214437 AW072537 AA781937 BI831486 AW190479 A1472793 AA460217 AA459937 BF082576 AA393673 AA398702 NM_006001 L11645 A1205604 A1207994 A187362 AA709190 BI462421 BG772170 BG722772 AA436991 BG771655 BI553260 BF126025 BF125857 BI462670 BG724164 BI562424 BG721652 BI559662 BG722455 BI596415 BG717561 BG722138 BG773507 BG720572 C03867 A1016802 AL042663 AA770436 AA435720 T19365 AA626698 AA759057 A1208021 BF507844 A1208058 AA412719 AA426374 A1208775 AA977217 AA758055 F34585 AA180062 BG700885 AA886017 AW341719 AA971332 A1688794 Z20462 A1808145 AW665263 AA884952 AA906136 AW663704 A1150368 A1216464 A1125340 A1125684 A1377949 A1126470 A1218351 AW665355 A1243952 AW663454 A1240603 A187742 AA884214 AA723933 AA857437 A1968733 A1968938 AA992784 AA397520 AW235244 BM479185 AL552795 AL577722 BF038888 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 A1806539 AW449522 AA993634 A1827626 AA904788
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TABLE 54C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401979	2828778	Minus	75693-75851,76977-77112
406409	9256364	Minus	141101-141256
401741	2982169	Plus	196686-196823,200241-200381
406378	9256142	Minus	126408-126800
405264	7329374	Plus	28556-28684
401692	3540172	Plus	26365-26510
403783	8081824	Plus	128412-128635
404271	9828129	Minus	56392-57645
401798	6730720	Plus	22831-23448
402857	9801539	Plus	13402-14133
405528	9581957	Minus	22418-22687
403328	8469086	Minus	120428-120703
401712	6682593	Minus	76410-76527,76692-76829,78737-78868,8024

TABLE 55A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
416680	AW245540	Hs.79516	brain abundant, membrane attached signal	48.80
423961	D13666	Hs.136348	perlestin(OSF-Zos)	43.30
412948	BE243313	Hs.334851	LIM and SH3 protein 1	42.50
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithell	36.80
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	29.80
414438	A1879277	Hs.76136	thioredoxin	29.40
406658	A1920965	Hs.77961	major histocompatibility complex, class	29.25
446899	NM_005397	Hs.16426	podocalyxin-like	28.70
411573	AB029000	Hs.70823	KIAA1077 protein	28.40
432730	A1066520	Hs.131358	ESTs	28.00
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	28.00
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	27.30
446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	26.80
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	25.00
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	24.15

	406856	AW515336	Hs.29797	ribosomal protein L10	23.66
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	23.60
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	23.60
5	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptide	22.35
	417426	NM_002291	Hs.82124	laminin, beta 1	21.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	21.50
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
10	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
	412636	NM_004415		desmoplakin (DPI, DPIP)	20.90
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	20.30
	414587	NM_004852	Hs.76507	LPS-induced TNF-alpha factor	19.45
	412915	AW087727	Hs.74823	NM_004541: Homo sapiens NADH dehydrogenas	19.30
	406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
15	412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
	424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
	415314	N88802	Hs.5422	glycoprotein M6B	16.80
20	406656	M16714	Hs.89643	major histocompatibility complex, class	16.75
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.25
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	16.00
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
25	417088	M54915	Hs.81170	pim-1 oncogene	15.60
	449338	H73444	Hs.394	adrenomedullin	15.51
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
	414420	AA043424	Hs.76095	immediate early response 3	15.30
	425543	R23313	Hs.334895	ribosomal protein L10a	15.10
30	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
	420754	W79431	Hs.346911	ribosomal protein L22	14.92
	410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
35	406786	AW161678	Hs.111334	ferritin, light polypeptide	14.57
	422105	AI929700	Hs.111680	endosulfine alpha	14.57
	422714	AB018335	Hs.119387	KIAA0792 gene product	14.25
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
40	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	13.95
	410185	BE294068	Hs.737	immediate early protein	13.85
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	13.60
	410611	AW954134	Hs.20924	KIAA1628 protein	13.60
45	448588	AI970276	Hs.156905	KIAA1676	13.40
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	13.10
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheri	13.00
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
50	454413	AI653672	Hs.40092	PNAS-123	12.90
	415221	W07418	Hs.78225	annexin A1	12.89
	425535	AB007937	Hs.158287	KIAA0468 gene product	12.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	12.45
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
55	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	12.19
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	12.12
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
	408437	AW957744	Hs.278469	lacrimal prolina rich protein	11.80
60	430542	AI557486	Hs.119122	ribosomal protein L13a	11.51
	424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
	432409	AA806538	Hs.130732	KIAA1575 protein	11.50
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	11.44
	425996	W67330		hypothetical protein AL110115	11.40
65	449961	AW265634	Hs.133100	ESTs	11.40
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	11.25
	407179	AA206465		thymosin, beta 4, X chromosome	11.21
	412623	R28898	Hs.74170	metallothionein 1E (functional)	11.10
	429978	AA249027		ribosomal protein S6	11.10
70	450377	AB033091		KIAA1265 protein	11.10
	418509	AB028624	Hs.85639	ATP synthase, H transporting, mitochondr	11.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
	451106	BE382701	Hs.25960	N-MYC oncogene	10.93
75	426552	BE297660	Hs.170328	moesin	10.91
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhotekin, clone	10.75
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
80	435056	AW023337	Hs.5422	glycoprotein M6B	10.70
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	10.70
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
	420676	AI434780	Hs.4248	vav 2 oncogene	10.60

	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
	436075	BE090176	Hs.179902	transporter-like protein	10.30
5	450139	AK001838		serum/glucocorticoid regulated kinase	10.30
	427691	AW194426	Hs.20726	ESTs	10.26
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	10.15
	448412	AJ219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
	440528	BE313555	Hs.7252	KIAA1224 protein	10.05
10	423184	NM_004428	Hs.1624	ephrin-A1	10.05
	450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
	417407	AA923278	Hs.290905	ESTs, Weakly similar to prolease [H.sapi	9.90
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	9.90
	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	9.89
15	435918	AF263538	Hs.86232	growth differentiation factor 3	9.89
	411251	R19774	Hs.22835	HHGP protein	9.80
	406791	AJ220684	Hs.347939	hemoglobin, alpha 2	9.75
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
	425580	L11144	Hs.1907	galanin	9.60
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	9.60
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.60
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	9.53
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
25	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	9.42
	416926	H03109	Hs.263395	HT018 protein	9.41
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
	428065	AJ634046	Hs.157313	ESTs	9.40
	441455	AJ271671	Hs.7854	zinc/ferritin regulated transporter-like	9.39
30	410325	AB023154	Hs.62264	KIAA0937 protein	9.30
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (tr	9.24
	447211	AL161961	Hs.17767	KIAA1554 protein	9.22
35	422068	AJ807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	8.93
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	8.90
	429490	AJ971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
40	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.84
	413886	AW958264	Hs.103832	similar to yeast Upt3, variant B	8.80
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	8.70
	426215	AW963419	Hs.155223	stanniocalcin 2	8.70
	446627	AJ973016	Hs.15725	hypothetical protein SBB148	8.60
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase II	8.60
	410023	AB017169	Hs.57929	sfil (Drosophila) homolog 3	8.50
	445245	AB032973	Hs.12461	LCHN protein	8.50
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
50	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
	410143	AA188169		KIAA1191 protein	8.35
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
	433208	AW002834	Hs.24095	ESTs	8.30
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.25
55	432559	AW452948	Hs.257631	ESTs	8.20
	450581	AF081513	Hs.25195	TGF-beta 4	8.10
	450157	AW961576	Hs.60178	ESTs	8.10
	444795	AI193356	Hs.160316	ESTs	8.10
	400288	X06256	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	8.05
60	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
	419970	AW612022		ESTs	8.00
	411975	AI916058	Hs.144583	ESTs	7.95
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
65	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	437103	AW139408	Hs.152940	ESTs	7.90
	432636	AA340864	Hs.278562	claudin 7	7.87
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
70	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	7.80
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.80
	450147	AW373713	Hs.146324	CGI-145 protein	7.75
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
	449571	AW016812	Hs.200266	ESTs	7.70
	429355	AW973253	Hs.292689	ESTs	7.70
	446488	AB037782	Hs.15119	KIAA1361 protein	7.70
75	414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
	422424	AI186431	Hs.296638	prostate differentiation factor	7.67
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
80	451812	X81889	Hs.152151	plateophilin 4	7.65
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
	422746	NM_004484	Hs.119651	glypican 3	7.60
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	7.57

5	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	7.50
	419223	XG0111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T18206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
10	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	7.40
	413686	AA69213	Hs.71404	ESTs	7.40
	408605	AF025374	Hs.46465	T-cell, Immune regulator 1	7.40
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.30
	444838	AV651680	Hs.208558	ESTs	7.30
15	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87136	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
20	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	7.00
25	449567	AI990790	Hs.188614	ESTs	7.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to t38022 hypot	7.00
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464964		gb:zz80f10.s1 Scores ovary tumor NbHOT H	7.00
30	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
	442492	AA528489	Hs.234518	ribosomal protein L23	6.84
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	6.80
35	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
	436684	NM_001290	Hs.4980	LIM domain binding 2	6.80
	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adiccan	6.76
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	6.75
40	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	6.74
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.72
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	6.70
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	6.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
45	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regl	6.70
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	6.70
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nuclear protein family A, member 3 (H/	6.66
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
50	406858	AI865720	Hs.29797	ribosomal protein L10	6.65
	435748	AA699756	Hs.117335	ESTs	6.63
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	6.62
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.61
55	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.60
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.55
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	H42587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
60	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	6.43
	402145			Target Exon	6.43
	414562	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436860	H12751	Hs.5327	PRO1914 protein	6.40
	438962	BE046594		gb:hm41c11.x1 NCI_CGAP_RDF2 Homo sapiens	6.40
65	435937	AA830893	Hs.119769	ESTs	6.40
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
	446173	BE565849	Hs.14158	copline III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242691	Hs.14947	ESTs	6.34
70	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
75	434423	NM_005769	Hs.3844	LIM domain only 4	6.30
	434524	AA635931	Hs.249716	ESTs	6.30
	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
	437374	AL359571	Hs.44054	nlnln (GSK3B interacting protein)	6.25
80	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	AI080042	Hs.180450	ribosomal protein S24	6.20

5	418840	AI321614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159651	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
	413840	AI301558		RNA binding motif protein, X chromosome	6.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
10	429109	AL008537	Hs.195352	neutrophil cytosolic factor 4 (40kD)	6.10
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) rmb	6.10
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
15	432805	X94630	Hs.3107	CD97 antigen	6.06
	441283	AA927670	Hs.131704	ESTs	6.06
	417632	R20855	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0456 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
20	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo sapien	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14295 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
25	447217	BE465754	Hs.17778	neurotrophin 2	5.90
	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGCA248	5.84
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.84
30	414483	R25513	Hs.10683	ESTs	5.82
	428570	AA430321	Hs.283945	ESTs	5.81
	443194	AI954968		matrix Gla protein	5.80
	429582	AI569068	Hs.22247	ESTs	5.80
	414405	AI362533		KIAA0308 protein	5.80
35	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 (H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
40	406745	AW511970	Hs.279850	tumor protein, translationally-controlled	5.70
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541.1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.68
45	444273	AI903474	Hs.230	fibromodulin	5.65
	441623	AA315805		desmoglein 2	5.63
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	5.60
	417621	AV654694	Hs.82316	Interferon-induced, hepatitis C-associat	5.60
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
	406699	L06505	Hs.182979	ribosomal protein L12	5.53
55	458965	AA010319	Hs.60389	ESTs	5.50
	430592	AJ224864	Hs.9688	leukocyte membrane antigen(IRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratillin	5.42
60	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
	417849	AW291587	Hs.82733	nidogen 2	5.40
	408989	AW361666	Hs.49500	KIAA0746 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
65	406819	AA908472		gb:oxg82a10.s1 NC1_CGAP_Ov8 Homo sapiens	5.39
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.38
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AI857607	Hs.181301	cathepsin S	5.32
70	429307	AU076592	Hs.198951	jun B proto-oncogene	5.30
	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
75	411165	NM_000169	Hs.69089	galactosidase, alpha	5.26
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435631	BE254088	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539674		ectinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
80	440703	AL137663	Hs.7378	Homo sapiens mRNA: cDNA DKFZp434G227 (tr	5.20
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185538	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430656	AW967807	Hs.13797	ESTs	5.16
5	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subun	5.15
	454227	AW963897	Hs.44743	KIAA1435 protein	5.15
	429357	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
10	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	5.10
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AI187945	Hs.199310	ESTs	5.10
	427641	AI270591	Hs.146116	ESTs	5.10
15	442806	AW294522	Hs.149991	ESTs	5.10
	442495	AI184717		ESTs	5.10
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.10
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.09
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 otogend	5.07
20	418117	AI922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE resequences, MAGL Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.06
	410570	AI133086	Hs.64593	ATP synthase, H transporting, mitochondr	5.03
25	431805	NM_014053	Hs.270594	FLVCR protein	5.00
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443634	H73972	Hs.134460	ESTs	5.00
30	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	5.00
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	4.97
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.95
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.94
35	452063	R53185	Hs.32366	ESTs, Weakly similar to TWST_HUMAN TWST	4.93
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.93
	429558	AI391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	4.92
	433162	AI025842		ESTs	4.92
40	406797	AI432224		ribosomal protein L6	4.91
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:gh88b01.s1 Soares placenta Nb2HP Homo	4.90
	447832	AI433357		ESTs	4.90
45	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
	413593	AA205248		gb:zq78c12.r1 Stratagene hNT-neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	4.90
	441224	AU076964	Hs.7753	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
50	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
	417308	H60720	Hs.81892	KIAA0101 gene product	4.90
	438763	AI583207	Hs.95029	CCAAT/enhancer binding protein (C/EBP),	4.89
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.89
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	4.88
55	421748	NM_014718	Hs.107809	KIAA0726 gene product	4.87
	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.86
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.82
	406867	AA157857	Hs.182265	keratin 19	4.81
	449378	AW664026	Hs.59892	ESTs	4.81
60	427202	BE272922	Hs.173936	Interleukin 10 receptor, beta	4.80
	418945	BE248762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.80
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.79
	441321	HI17182	Hs.7771	B-cell associated protein	4.75
65	448896	AL157484	Hs.22483	Homo sapiens mRNA: cDNA DKFZp762M127 (fr	4.75
	447232	AW499834	Hs.327	Interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.73
	436372	AW972301	Hs.310286	ESTs	4.71
70	422082	AA016188	Hs.111244	hypothetical protein	4.70
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomat	4.70
	446659	AI335361	Hs.226376	ESTs	4.70
	414829	AA321568	Hs.77436	pleckstrin	4.70
75	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.70
	432407	AA221036	Hs.13273	gb:zr03f112.r1 Stratagene NT2 neuronal pr	4.69
80	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.67
	406794	AI890243		ribosomal protein L6	4.66
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.155828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	A1766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
5	417535	AA203569	Hs.191482	ESTs	4.61
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	4.61
	408491	A1088063	Hs.7882	ESTs	4.60
	426398	A1249368	Hs.98558	ESTs	4.60
	410295	AA741357		nidogen (enactin)	4.60
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.60
10	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA: cDNA DKFZp586F1822 (I	4.60
	426141	C05886	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
15	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108288	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
20	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	4.53
	453330	A1268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
25	417750	A1267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
	440774	A1420611	Hs.153934	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlled	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	A1638640	Hs.220624	ESTs	4.51
30	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.50
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
35	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myo-responsive	4.47
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.47
	408307	A1761785	Hs.204574	ESTs	4.46
40	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibitor	4.46
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.45
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	4.45
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.44
	416297	AA157834	Hs.79172	solute carrier family 25 (mitochondrial	4.44
45	428773	BE256238	Hs.193163	bridging integrator-1	4.43
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	4.43
50	442232	AJ357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
	441612	AJ802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424868	A1568170	Hs.96886	ESTs	4.41
	408380	AF123050	Hs.44532	diubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
55	428782	X12830	Hs.193400	interleukin 6 receptor	4.40
	408360	AJ806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW891865		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
	422499	A1268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	4.39
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	4.39
60	427779	AA906997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75260	mitogen inducible 2	4.36
	452651	A1218918	Hs.30209	KIAA0854 protein	4.35
	453467	A1535997	Hs.30089	ESTs	4.35
65	435961	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963979	Hs.24723	ESTs	4.34
	435968	AW161481	Hs.111577	integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
70	421522	R48881	Hs.102991	hypothetical protein FLJ13956	4.33
	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.30
	408784	AW971350	Hs.63386	ESTs	4.30
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
80	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	408896	AJ610447	Hs.48778	niban protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

	406230		Target Exon	4.25	
	435655	AW105663	Hs.6947	HSPC069 protein	4.25
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
5	437386	W52452		ribosomal protein L10	4.24
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	4.23
	447341	AF105941	Hs.18142	arrestin, beta 2	4.22
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	4.22
	409453	AI885516	Hs.95612	ESTs	4.22
10	428453	AB011110	Hs.184367	GTPase activating protein-like	4.22
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.21
	416072	AL110370	Hs.79000	growth associated protein 43	4.20
	450937	R49131	Hs.26267	ATP-dependant interferon response protel	4.20
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.20
15	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	4.20
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	4.20
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFPz564K143 (fr	4.20
	431550	BE244135	Hs.260238	hypothetical protein FLJ10842	4.20
	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!	4.20
20	409245	AA361037		IRNA isopentenylpyrophosphata transferas	4.18
	437296	AA350594	Hs.20281	KIAA1700	4.17
	406877	AA226392	Hs.179943	ribosomal protein L11	4.17
	419652	AL157485	Hs.91973	hypothetical protein	4.17
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.15
25	452432	AW205008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	4.15
	448782	AL050295		KIAA0758 protein	4.14
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	4.14
	422960	AW890487		cadherin 13, H-cadherin (heart)	4.14
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	4.12
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	4.11
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.11
	419726	U50330	Hs.1274	bone morphogenetic protein 1	4.11
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	4.10
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.10
35	418699	BE539539	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.10
	443035	Z45822	Hs.6906	Homo sapiens clone 24889 mRNA sequence	4.10
	457415	AK000010	Hs.258798	hypothetical protein FLJ20003	4.10
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protel	4.10
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	4.10
40	444633	AF111713	Hs.286218	junctional adhesion molecule 1	4.10
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	4.10
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	4.09
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.09
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	4.07
45	417930	H81136	Hs.334604	Homo sapiens mRNA for KIAA1870 protein,	4.06
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.06
	424464	R68537	Hs.17962	ESTs	4.06
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.06
	412627	BE391959	Hs.74276	chloride intracellular channel 1	4.06
50	414890	BE281095	Hs.77573	uridine phosphorylase	4.05
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.05
	450887	AA011518	Hs.271778	ESTs, Weakly similar to 138022 hypotheti	4.05
	444224	AV648599	Hs.199438	ESTs	4.05
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
55	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.04
	439854	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.04
	408745	AW936356	Hs.300925	ESTs, Weakly similar to A46010 X-linked	4.03
	409132	AJ224538	Hs.60732	protein kinase, AMP-activated, beta 2 no	4.01
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.01
60	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	4.01
	426398	BE256390	Hs.169718	calponin 2	4.01
	417777	AJ823763	Hs.7055	ESTs, Weakly similar to 178885 serine/th	4.01
	446979	AI654443	Hs.197683	ESTs	4.00
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	4.00
65	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.00
	436394	AA531187	Hs.126705	ESTs	4.00
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.00
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFPz564B1264 (f	4.00
	446013	AI360167	Hs.152774	ESTs	4.00
70	452404	AW450675	Hs.212709	ESTs	4.00
	444736	AA533491	Hs.23317	hypothetical protein FLJ14681	4.00
	438590	AAB11465	Hs.123375	ESTs	4.00
	451838	AW005866	Hs.193969	ESTs	4.00
	449832	AA694264	Hs.60049	ESTs	4.00

TABLE 55B

Pkey: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
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413787	7612_1	BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 AJ082748 AJ470204 BI711078 BF350700 BI496963 AI087141 AA720684 AA862331 AA605146 BM313650 AI089749 AJ359738 N69107 AW995424 AI086917 AI083995 AW340217 N99662 AI829449 AI089839 AI608761 AI342365 AI199076 AA908944 AI248943 AU160053 AI191245 AI218477 AJ077943 AA864930 AI310394 AA872478 AI279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 AI469689 BE464590 AW654539 H67097 AL534332 C21397 AI085941 AW028427 BG339820 AI697089 AI039008 AH25315 AI655561 AW150042 L20422 X57345 BI458375 AU142852 BI666601 BE888276 AU119302 BI603754 BG705953 BI598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127798 AI124697 D54224 F08031 AA340253 BF923383 BM467808 BI546644 BG777200 BG705941 BG468577 AU127209 AW403970 BI597630 BI458091 AV689560 BI669267 BG506219 BI837163 BI667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 BI689271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 BI493502 AW273118 AJ473820 AA608668 AI359337 AV712091 AA084011 BF592036 H13301 AI864305 AA505883 AI423963 AW084401 AJ917740 R69658 AA033631 N79982 BE885276 AI635674 AA096126 AA700018 AV707753 AI082545 AU145681 AA629032 AI421367 AA740589 AA150830 AI248541 AA988608 AA150478 W65437 BM310234 AA262704 T26031 AI811116 BM272753 H21979 T15405 AA938406 F04963 AI188296 AW152629 AA905196 BG223058 AI831016 AJ766457 AI811102 AA776573 AI922133 AA775958 AJ261476 AA219489 AI688035 AI872093 BE537084 AW189078 D82630 AI23121 AL583492 BE350791 R69901 W65436 BE165392 BI089081 BE155394 AL120538 AW166100 AI359620 AI174338 N20527 W47413 AA155615 AJ272249 H25293 BE14558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W48459 AI866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R25253 AI809817 AI559406
5		M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA85212 AW366568 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW366175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG988845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BF089397 BF952276 BG005197 BF350086 BE715196 BE715165 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AJ392928 AU158477 BI467252 AU159919 AI760816 BF082516 AA439101 AA451923 AJ340326 AI509075 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AJ3404772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA025864 AI830049 AW780435 AI078449 AI819884 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AW182821 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AJ270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 BF745530 BI762796 BG287391 AW798780 BE706045 BE925470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067785 BF721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI685869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE706999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040931 BF747389 BI047320 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AJ284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG986267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BE880923 BG390191 AW470082 AW014585 AA423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AJ348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AW780704 AW008596 AI795964 AA917471 AI400531 AA668626 W22207 AI306482 AW440562 AI084687 AA347280 AA053536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA809614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627
426295	510_1	BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AJ521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI969980 BE857686 BE326711 AW953706 AI393749 AJ383821 W67199 AI431759 AI796526 AI521794 AI796380 AW117545 AI749657 AI537634 N50122 BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 W57017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 AW963196 C06195 AI678018 AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768485 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925899 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164 AK055070 AK055612 AK000174 BG619808 BG108086 AI741949 AI004176 BF891936 BF378565 AW197163 BE856860 BE245124 AW674411 AA490531 AW674981 AA740788 AW274758 BF512523 AI521278 AA548759 AI802431 AW051682 AI628247 AI799606 AW088103 AA236549 AI91529 AW273168 AI168451 AW073812 AW090611 AW003593 AI215845 AI799616 AW474940 AA954927 BM193740 AW662704 AW090127 AA969444 AI080438 AA552500 AW237538 AA481060 AI246378 AA565227 AA398921 AA207051 AA721378 BF438608 AI086295 AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766664 AI453279 AA435673 AI519515 AA879080 AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE782742 AW897470 W05809 AI1323 T83796 R68544 H88711 BI087136 AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI866459 AU155873 H04255 AW243386 AA557749 AI286227 R68691 R33453 AW388097 BE005398 AA628622 AA94155 AK000357 AI571830 AA579613 AA668790 BF939495 BF196886 AI990982 BF591561 AI809189 AW410232 BF739769 AI144392 BF438721 AI707495 AI423359 N52503 BE855784 N94367 AI023931 AA553662 AI744624 AI221298 AI299523 AI299520 BI491312 AI452711 AI360730 AA622643 AW195955 AA470473 AW392767 AI218127 AA873430 AA906005 AA748160 H89523 AW020252 AW664988 AA970424 AA879079
429978	35194_2	
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444060	6315_1	
450139	34017_1	
434280	1474904_1	
410143	MH1244_8	

			AJ581622 AJ361357 AA468498 AW008694 AA903275 AI187724 AI187718 AA890505 BF092771 AI066555 BE714172 BG289028 AW080390 BE001197 BF132049
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	409208	10117_2	AK074047 AJ144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236295 AW236606 AW081031 AA765843 BM144372 AA989341 AJ824838 AJ963970 AJ637671 AW196330 BG427526 BM148789 BF893644 BF881946
	430068	1177709_2	AA947566
	444207	9172_3	BE739425 AA514221 AA865491 AJ828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AJ432496 AJ470335 AI247243 BG533994 AA513783 AJ887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AJ521413 AJ669583 BE932521 AI581370 BE180238 AW088750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AJ735658 AW393133 AW073080 AJ707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524564 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 AJ565004 AW819026 BE843092 AV688437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AJ962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006582 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 H45942 H55897 AV657718 BG563497 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE177661 H06215 BE144709 BE144829
10			AI207343 BF813684 BF928775 AA282585
15			BC020284 AW953495 AW402677 BF890739 Z44378 AI660081 AI769242 T84954 C05886 AI224851 AI568340 AI024026 AW015010 AI032051 AA505095 AA830304 H98001 H63431 BG249610 AI284792 AA205732 AI598130 AW516813 AI123905 AA132557 AI140199 H53399 AA928496 AI200299 AI400044 BE940512 BE940609 H28028 BF913868 AJ01558 D79095 AI762695 AA311547 AI673408 AI673002 N67358 AA885913 AI288094 N67347 Z40311 T94918 AV722693 AW170339 AW975566 AA452774 AA504759 AA370643 T79706 AA721063 BF588887 BG982917 AI343373 AW236167 BE568091 BF747959 BF241262 BE940663 AJ435278 R05794 AW027091 AI860259 AI268890 T94871 AW182884 N67183 AW149083 H42473 AI678254 R26706 AI19684 R24905 AW386568 AW363261 N31299 H63489 AW195475 AA452592 BE044216 T91205 H64955 BF858811 AW962778 AW388295 BF857615 BF858552 BF855548 BF857611 AW866752
20	413497	1518002_1	BG926557 AW965540 R76280 AA335645 BF370246 BE835794 AA725102 AW152576 BF055494 AI743398 BE464853 AI391675 AI453078 BE017970 AI803141 AI417070 AA489488 BE835818 AW050475 BE835826 AI015220 AW300496 AA33881 H98062 AA554989 N32774 AA012825 BF989549 AL576463 W60527 AW576215 N32000 AA450065 AW137525 AI290944 T16431 T50379 AA830657 N78847 T51070 AW505288 AI446370 AA100988 AA824552 BE835780 AA770659 BF370223 H03890 R76557
25	450944	36100_1	AA558585 AA565499 AI360578 AW204069 AA991648 AA864939 AI744949 AW062361 BF919486 AW813419 AW816041 AA354572 BI754027 BF696071 AI351939 BG151298 AI919334 AJ401620 BI770165 W72057 T86158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758956 AI598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG121015 BG184149 BG200180 BG212590 BI761222 BG182079 AW338822 AI295631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568964 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AI188162 AA864282 BI493352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439999 AW023269 BE813871 AW999947 BE839108 AV707983 AI369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785 BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 FZ7582 AA614748 D56545 F20774 F30660 F25646 AW023542 AA827300 AA582214 AI701289 AA228293 AJ06950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518 AV704158 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA51625 AA916141 AL572719 AV707258 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926530 AA081013 AA553696 AA916094 BG924321 AI039722 AI954958 AI372839 AI401406 AI538215
30	432666	144_7	AL047596 AA393792 AI870731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545
35	425291	298763_1	AK056315 AI015524 AA724079 BI713619 AJ377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI051872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
40	443194	19335_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706728 BE706558 BE153312 BE706705 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI823661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32582 AI358102 AW241694 AI038448 AI672071 AJ018369 AA576391 AA977874 AW183692 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW687496 AA149420 BE706307 BE539395 BE748765 AI373653 BF75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG496559 BF248373 BG494800
45			AA908472
50	414405	112689_1	BM469076 AA533027 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AI671356 AA962403 BF808010 AA663911 AA847058 AA513301 AA369069 AA377265 BG291208 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701502 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA255558 H15928 BI087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605
55	441623	3362_1	AI184717 AW518883 AF121173 AW972842 AA516061 AA630205 AI742311 AI025842 AA578843 AI432224 AW276890 AI499348 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640 R36075 R36167 AI366546 AI628543 AI433357 AW772732 AA205248 AA204737 AI130658 BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433 AI890243
60	406819	0_0	BG402852 BG545068 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 BI524854 BI497111 BF940043 AI129268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448 W76547 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268
65	418905	517_1	
70			
75	442495	928718_1	
	431824	1237125_1	
	433162	2167905_1	
	406797	0_0	
	447197	2176805_1	
	447832	1036795_1	
	413593	2949482_1	
80	427486	684159_1	
	406794	0_0	
	410295	2817_1	

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413703 376077_1
406870 0_0
456629 207_22

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437386 5541_2

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439403 4937_10
409245 3189_2

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448782 34980_1

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422960 11862_2

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TABLE 55C
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nl_position: Indicates nucleotide positions of predicted exons.

65

Pkey	Ref	Strand	Nl_position
401466	6682292	Plus	28748-29023
401192	9719502	Minus	69559-70101
402474	7547175	Minus	53528-53628, 55755-55920, 57530-57757
402145	8018280	Plus	113085-114800
406230	4760409	Plus	71716-72515

70

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TABLE 56A:
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

80

Pkey	ExAccn	UnigenelID	Unigene Title	R1
414438	A1879277	Hs.76136	thioredoxin	47.30

	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
5	417088	M54915	Hs.81170	plm-1 oncogene	31.10
	430542	AI557486	Hs.119122	ribosomal protein L13a	29.60
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	28.13
10	433800	AI034361	Hs.135150	tung type-I cell membrane-associated gly	28.10
	406658	AI920965	Hs.77961	major histocompatibility complex, class	27.85
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
15	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
	429978	AA249027		ribosomal protein S6	25.40
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	AI371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
20	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	24.10
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	24.05
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
25	406856	AW515336	Hs.29797	ribosomal protein L10	22.77
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
	412636	NM_004415		desmoplakin (DPL, DP11)	22.40
	420676	AI434780	Hs.4248	vav 2 oncogene	22.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.40
30	446627	AI973016	Hs.15725	hypothetical protein SBB148	21.20
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	21.10
	420754	W79431	Hs.346911	ribosomal protein L22	20.98
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.90
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	20.80
35	429490	AI971131	Hs.23689	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.50
	422714	AB018335	Hs.119387	KIAA0792 gene product	19.15
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.00
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
40	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.50
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.00
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.90
	448588	AI970276	Hs.156905	KIAA1676	17.70
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.50
45	428782	X12830	Hs.193400	interleukin 6 receptor	17.40
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	17.20
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.15
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.10
	440528	BE313555	Hs.7252	KIAA1224 protein	17.06
	410143	AA188169		KIAA1191 protein	17.05
50	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.90
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.70
	450937	R49131	Hs.26267	ATP-dependant interferon response protel	16.60
55	449571	AW016812	Hs.200266	ESTs	16.50
	432730	AK066520	Hs.131358	ESTs	16.20
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.15
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.90
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	15.80
60	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.80
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	15.50
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	14.90
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	14.90
	406656	M16714	Hs.89643	major histocompatibility complex, class	14.85
65	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.71
	450377	AB033091		KIAA1265 protein	14.70
	425996	W67330		hypothetical protein AL110115	14.60
	430332	R51780	Hs.239483	Human clone 23933 mRNA sequence	14.60
70	427691	AW194426	Hs.20726	ESTs	14.42
	428614	AI371172	Hs.211539	hypothetical protein MGC4248	14.35
	451106	BE382701	Hs.25960	N-MYC oncogene	14.21
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor 1	14.13
	436860	H12751	Hs.5327	PRO1914 protein	13.90
75	446899	NM_005397	Hs.16426	podocytin-like	13.90
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	13.75
	408380	AF123050	Hs.44532	diubiquitin	13.70
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.40
	427521	AW973352		ESTs	13.30
80	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.25
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.23
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.70
	426552	BE297660	Hs.170328	moesin	12.69

	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
	436398	H87136	Hs.5174	ribosomal protein S17	12.50
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.30
5	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.30
	410275	U85658	Hs.61795	transcription factor AP-2 gamma (activat	12.28
	414587	NM_004852	Hs.76507	LPS-induced TNF-alpha factor	12.25
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
10	419384	AA490856	Hs.39429	ESTs	12.20
	410185	BE294068	Hs.737	immediate early protein	12.15
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	12.05
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	11.90
15	408989	AW361666	Hs.49500	KIAA0746 protein	11.80
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.80
	410325	AB023154	Hs.62264	KIAA0937 protein	11.70
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	11.70
20	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	11.61
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	11.60
	454413	AI653672	Hs.40092	PNAS-123	11.60
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	11.40
	428065	AI634046	Hs.157313	ESTs	11.40
25	432805	X94630	Hs.3107	CD97 antigen	11.36
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
	444060	AA340277	Hs.31447	Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
	452436	BE077546	Hs.250857	ESTs, Moderately similar to A46010 X-lin	11.30
	409963	AA133590		calcium/calmodulin-dependent protein kin	11.11
30	402474			NM_004079:Homo sapiens cathepsin S (CTSS	11.00
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.00
	406786	AW161678	Hs.111334	fertilin, light polypeptide	10.95
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
	444656	AI277924	Hs.145199	ESTs	10.90
35	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	10.85
	440774	AI420611	Hs.153934	ESTs	10.82
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	10.80
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
40	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	10.65
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	10.43
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
45	446682	AW205632	Hs.211198	ESTs	10.40
	447211	AL161961	Hs.17767	KIAA1554 protein	10.31
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
	422105	AI929700	Hs.111680	endosulfine alpha	10.21
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	10.20
50	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
	452651	AI218918	Hs.30209	KIAA0854 protein	10.15
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
	427761	AA412205	Hs.140995	ESTs	10.10
55	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
	402145			Target Exon	9.82
	413686	AI469213	Hs.71404	ESTs	9.80
	446488	AB037782	Hs.15119	KIAA1361 protein	9.80
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
60	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
	407179	AA206465		thymosin, beta 4, X chromosome	9.72
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	9.70
	446795	AI797713	Hs.156471	ESTs	9.70
65	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
	451864	N20370	Hs.69547	ESTs	9.65
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
	419904	AA974411	Hs.18672	ESTs	9.60
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
70	409208	Y00093		Integrin, alpha X (antigen CD11C (p150),	9.52
	424950	AA602917	Hs.156974	ESTs	9.50
	447534	AW953935	Hs.288555	ESTs	9.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
75	422950	AW890487		cadherin 13, H-cadherin (heart)	9.33
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	9.32
	408784	AW971350	Hs.63386	ESTs	9.30
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.30
	432409	AA806538	Hs.130732	KIAA1575 protein	9.30
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
80	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.20
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.20
	434524	AA835931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
5	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.03
	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
10	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	8.90
	442806	AW294522	Hs.149991	ESTs	8.90
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	408437	AW957744	Hs.278469	lacrimal proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
15	431187	AW971146	Hs.293187	ESTs	8.80
	421098	AI697901	Hs.192425	ESTs	8.70
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	8.70
	401091			decay accelerating factor for complement	8.62
20	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	438089	W05391		nuclear receptor subfamily 1, group 1, m	8.60
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.60
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (tr	8.59
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	8.56
25	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.50
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.45
30	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.43
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.38
	425284	AF155568		NS1-associated protein 1	8.33
35	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.33
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methyleneletrahydrofolate dehydrogenase	8.30
	453716	AA037875	Hs.152675	ESTs	8.30
40	418840	AI821614	Hs.185831	ESTs	8.20
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
	449656	AA002008	Hs.188633	ESTs	8.20
	425535	AB007937	Hs.158287	KIAA0468 gene product	8.17
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.13
45	432559	AW452948	Hs.257631	ESTs	8.10
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.10
	420099	D80011	Hs.95140	KIAA0189 gene product	8.01
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
50	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
	437886	BE284111	Hs.31314	retinoblastoma-binding protein 7	8.00
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.92
	433655	AL036559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.89
	434511	R28982	Hs.18106	ESTs	7.88
55	423523	AW299828	Hs.193580	ESTs	7.86
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	7.84
	411960	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	AI381900	Hs.159212	ESTs	7.80
60	406699	L06505	Hs.182979	ribosomal protein L12	7.75
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.68
	426759	AI590401	Hs.21213	ESTs	7.66
	406776	T18206	Hs.237164	ESTs, Highly similar to LDH_HUMAN L-LAC	7.62
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	7.60
65	444795	AI193356	Hs.160316	ESTs	7.60
	406663	U24683		immunoglobulin heavy constant mu	7.59
	442821	BE391929	Hs.8752	transmembrane protein 4	7.56
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.52
	407252	AA659037	Hs.163780	ESTs	7.50
70	414405	AI362533		KIAA0306 protein	7.50
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	429999	AI761902	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.50
75	420943	AI718702	Hs.279930	major histocompatibility complex, class	7.46
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.43
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.42
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.41
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	7.40
80	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	7.40
	419839	U24577	Hs.93304	phosphatase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	7.40
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	7.40
	432598	AI341227	Hs.157106	ESTs	7.38

	447484	AA454839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AI802629	Hs.113560	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
5	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AI184717		ESTs	7.30
	445929	AI089660	Hs.323401	dpy-30-like protein	7.30
	446013	AI360167	Hs.152774	ESTs	7.30
10	436075	BE090176	Hs.179902	transporter-like protein	7.20
	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:cg82a10.s1 NCL_GAP_Ov8 Homo sapiens	7.16
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
15	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
20	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.10
	438980	AW502384		gb:U1-HF-BR0p-aka-1-12-0-ULr1 NIH_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	7.10
	441878	AI801869	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
25	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
	417315	AI080042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12461	LCHN protein	7.00
30	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.00
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
35	418134	AA397769	Hs.86617	ESTs	6.90
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.89
	451838	AW005866	Hs.193969	ESTs	6.88
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	6.87
	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
45	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
50	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	6.80
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mito	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
55	425277	NM_001241	Hs.155478	cyclin T2	6.72
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016625	Hs.191381	hypothetical protein	6.70
	430299	V28873	Hs.106747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA608955	Hs.109653	ESTs	6.70
60	430556	AW967807	Hs.13797	ESTs	6.69
	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AI922013	Hs.83496	linker for activation of T cells	6.67
	417558	AF045229	Hs.82290	regulator of G-protein signalling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
65	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PRO0641 protein	6.60
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.57
70	415221	W07418	Hs.78225	annexin A1	6.56
	450256	AA285887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	catumenin	6.50
75	443749	R38828	Hs.143463	ESTs	6.50
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
80	421633	AF121860	Hs.106260	sorting nexin 10	6.40
	435937	AA830893	Hs.119769	ESTs	6.40
	445612	N94126	Hs.12969	hypothetical protein	6.40
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlled	6.39

5	434817	AA082118	Hs.102737	golliath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	6.35
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW953897	Hs.44743	KIAA1435 protein	6.30
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.30
10	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447687	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
15	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.27
	411975	AJ916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	6.25
	433162	AI025842		ESTs	6.23
20	449322	AI638616	Hs.196566	ESTs	6.22
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.191146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
25	427968	AI857607	Hs.181301	cathepsin S	6.18
	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.16
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	6.16
	406870	AA075144		gb:zm85f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
30	445493	AJ915771		metallothionein 1E (functional)	6.15
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
35	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
	406797	AI432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	AI277367	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
40	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
45	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
	412949	AA71639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AI418466	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
50	441623	AA315805		desmoglein 2	5.98
	416926	H03109	Hs.263395	HTO18 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.95
55	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	5.91
	433891	AA613792		gb:nc97h03.s1 NCI_CGAP_Pr2 Homo sapiens	5.90
	406542			C19000728*:gij12585552:spjQ9Y2Q1J257_HU	5.90
60	406858	AI865720	Hs.29797	ribosomal protein L10	5.90
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
65	441321	H17182	Hs.7771	B-cell associated protein	5.88
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW086535		ribosomal protein, large, P0	5.87
	416987	D86957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
70	428773	BE256238	Hs.193163	bridging integrator 1	5.83
	406794	AI890243		ribosomal protein L8	5.82
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
75	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
	412528	AI123478	Hs.32112	ESTs	5.80
	424875	AI187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AI459554	Hs.161286	ESTs	5.80
80	449961	AW265634	Hs.133100	ESTs	5.80
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JCS238 galactosy	5.79
	422773	AB028962	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc-finger regulated transporter-like	5.78

	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363857	Hs.155029	ESTs	5.73
5	414890	BE281095	Hs.77573	uridine phosphorylase	5.72
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne)	5.71
	435961	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGE Homo	5.70
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
	446659	A1335361	Hs.226376	ESTs	5.70
	457250	AA811987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	A1985897	Hs.125293	ESTs	5.67
15	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
	451812	X81889	Hs.152151	plakophilin 4	5.65
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [Hs	5.63
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	5.60
20	431770	BE221880	Hs.268555	5'-3' exonuclease 2	5.60
	436511	AA721252	Hs.291502	ESTs	5.60
	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X69392	Hs.91379	ribosomal protein L26	5.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.57
25	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	5.56
	437296	AA350994	Hs.20281	KIAA1700	5.56
	453985	N44545	Hs.251865	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	A1583696	Hs.253313	ESTs	5.53
30	435748	AA699756	Hs.117335	ESTs	5.52
	420732	AA789133	Hs.63525	ESTs	5.51
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	5.50
	430915	AA488953		gb:aa55e05.r1 NCL CGAP_GCB1 Homo sapiens	5.50
	436716	A1433540		gb:ti69g05.x1 NCL CGAP_Kid11 Homo sapien	5.50
35	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
	449625	NM_014253		odx (odd Oz/Jan-m, Drosophila) homolog 1	5.50
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associa	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
40	427640	AF058293	Hs.180015	D-dopachrome tautomerase	5.47
	420552	AK000492	Hs.98806	hypothetical protein	5.45
	449338	H73444	Hs.394	adenomedullin	5.42
	427176	AW381569	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
45	421568	W85858	Hs.99804	ESTs	5.40
	423961	D13666	Hs.136348	periostin(OSF-2os)	5.40
	440719	AA150869	Hs.26267	ATP-dependant Interferon response protei	5.40
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	5.40
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	5.39
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
55	457465	AW301344	Hs.122908	DNA replication factor	5.37
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.36
	409485	S80990	Hs.252136	ficolin (collagen/fibrinogen domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
60	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
	412623	R28898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
65	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.30
	422900	AA641201	Hs.222051	ESTs	5.30
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein Interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	5.30
70	430177	AW969233	Hs.302746	MSTP028 protein	5.30
	430835	A1240006	Hs.192326	ESTs	5.30
	433009	AA761668		gb:zn24c08.s1 NCL CGAP_GCB1 Homo sapiens	5.30
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
75	415995	NM_004573		phospholipase C, beta 2	5.29
	424578	AK001973	Hs.150890	hypothetical protein	5.27
	441303	AW293081	Hs.241801	ESTs	5.27
	427816	AA159248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.26
80	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	5.24
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	5.23
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405086			NM_006662:-Homo sapiens Snf2-related CBP	5.20

	413401	AI361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0051 protein	5.20
5	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.20
	434372	AA631373		gb:mp86c01.s1 NCL_CGAP_Thy1 Homo sapiens	5.20
	436812	AW298067		gb:U1-H-BWD-ctg-g-09-0-U1.s1 NCL_CGAP_Su	5.20
	441390	AI692560	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
10	453127	AI696671	Hs.294110	ESTs	5.20
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.20
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	5.19
	451814	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	5.18
15	406799	AA908548		gb:og83g12.s1 NCL_CGAP_Ov8 Homo sapiens	5.16
	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.15
	422293	X94453	Hs.114366	pyroline-5-carboxylate synthetase (glut	5.14
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
20	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.12
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.186704	ESTs	5.11
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
25	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HTO	5.10
30	436137	AI058769	Hs.133512	ESTs	5.10
	440948	AW188311	Hs.128619	ESTs	5.10
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0524	5.09
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.09
	424868	AI568170	Hs.96886	ESTs	5.08
35	418905	BE539674		actinin, alpha 4	5.08
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.07
	442618	R58222	Hs.26514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
40	406813	AW276131		ribosomal protein L13a	5.06
	454128	AL031259	Hs.41639	programmed cell death 2	5.05
	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.05
45	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.04
	418876	AA740616		gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens	5.03
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	AI133095	Hs.64593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
50	431451	AA761378	Hs.192013	ESTs	5.00
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
	435655	AW105663	Hs.6947	HSPC069 protein	5.00
	435919	AI052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
55	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	5.00
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.00
60	447197	R36075		gb:yt88b01.s1 Soares placenta Nb2HP Homo	5.00
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.00
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to I38022 hypotheti	5.00
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4064156, mRNA,	5.00
65	457068	X69391		ribosomal protein L6	5.00
	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.97
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.95
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.94
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.92
70	400281			Eos Control	4.91
	414420	AA043424	Hs.76095	Immediate early response 3	4.90
	415789	AA653718	Hs.225841	DKFZP434D193 protein	4.90
	434666	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
75	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
	451598	N29102	Hs.118078	ESTs	4.90
	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.88
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.86
80	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.86
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.85
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

	406781	AA639388		gb:nq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
	449810	AB008681	Hs.23994	activin A receptor, type IIB	4.82
	410323	AJ241708	Hs.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
5	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	4.81
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.81
	400424	AJ276316	Hs.287374	zinc finger protein 304	4.80
	411573	AB029000	Hs.70823	KIAA1077 protein	4.80
	421045	BE144608	Hs.55533	ESTs	4.80
10	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.80
	438590	AA811465	Hs.123375	ESTs	4.80
	442071	BE048433	Hs.276043	ESTs	4.80
	449567	AJ990790	Hs.188614	ESTs	4.80
15	453213	AA082650	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
	437802	AJ475995	Hs.122910	ESTs	4.77
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.77
	421932	W51778	Hs.323949	kangal 1 (suppression of tumorigenicity	4.74
20	428453	AB011110	Hs.184367	GTPase activating protein-like	4.74
	413441	AJ929374	Hs.75367	Src-like-adaptor	4.74
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
	435541	AA687361	Hs.221318	ESTs	4.71
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	4.70
25	412766	BE544475	Hs.54347	ESTs	4.70
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
	418973	AA233056	Hs.191518	ESTs	4.70
	421433	AJ829192	Hs.22380	ESTs	4.70
	432925	AA878324	Hs.264750	ESTs	4.70
30	438869	AF075009		gb:Homo sapiens full length insert cDNA	4.70
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
	447198	D61523	Hs.283435	ESTs	4.70
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.70
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.66
35	444598	AJ094221	Hs.135150	lung type-I cell membrane-associated gly	4.66
	447817	BE620775	Hs.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
	416062	AA724811	Hs.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (the	4.64
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	4.64
40	411165	NM_000169	Hs.69089	galactosidase, alpha	4.63
	435905	AW997484	Hs.5003	KIAA0456 protein	4.63
	445776	NM_001310	Hs.13313	cAMP responsive element binding protein-	4.62
	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	4.62
45	410668	BE379794	Hs.159651	hypothetical protein	4.61
	406774	AW518383	Hs.177592	ribosomal protein, large, P1	4.60
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.60
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.60
	415682	AJ347128	Hs.191870	ESTs	4.60
50	417621	AV654694	Hs.82316	Interferon-induced, hepatitis C-associat	4.60
	419970	AW612022		ESTs	4.60
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	4.60
	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	4.60
	432586	AA568548		ESTs	4.60
55	437438	AL359820	Hs.14217	hypothetical protein DKFP762P2111	4.60
	441355	AJ822034	Hs.137097	ESTs	4.60
	444539	AJ955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	4.60
	458965	AA010319	Hs.60389	ESTs	4.60
	406655	M21533	Hs.277477	major histocompatibility complex, class	4.60
60	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	4.60
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59
	423766	AA303799	Hs.300141	ribosomal protein L39	4.59
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	450043	AA885699	Hs.24332	CGI-26 protein	4.56
65	447742	AF113925	Hs.19405	caspase recruitment domain 4	4.54
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.54
	426395	BE151985		hypothetical protein FLJ23316	4.53
	418300	AJ433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
	423799	AW026300	Hs.132906	19A24 protein	4.53
70	445093	AJ207197		ESTs	4.52
	428044	AA093322	Hs.301404	RNA binding motif protein 3	4.52
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	4.51
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	4.50
	427747	AW411425	Hs.180655	serine/threonine kinase 12	4.50
75	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	4.50
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	4.50
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.50
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	4.50
	429687	AJ875749	Hs.211608	nucleoporin 153kD	4.50
80	436566	BE545588	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
	437634	AW293046	Hs.255158	ESTs	4.50
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	4.50
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	4.50
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	4.50

	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447687	AL117811	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
5	413856	O13639	Hs.75586	cyclin D2	4.49
	419556	U29615	Hs.91093	chitinase 1 (chitinotriosidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
10	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protei	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
15	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
	436623	AI417073	Hs.107265	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypotheti	4.41
20	436671	AW137159	Hs.183291	ESTs	4.40
	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, non	4.40
25	429109	AL008637	Hs.195352	neutrophil cytosolic factor 4 (40kD)	4.40
	430280	AA361258	Hs.237868	interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gb:hn41c11.x1 NCL_CGAP_RDF2 Homo sapiens	4.40
30	444794	AI419991	Hs.145225	ESTs	4.40
	445100	AW188205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
35	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.37
	406742	AI468091	Hs.279860	tumor protein, translationally-controlled	4.35
	425095	AW014160	Hs.182585	KIAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.34
40	442333	AI650877	Hs.129302	ESTs	4.33
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp66780711 (f	4.30
45	408875	NM_015434	Hs.48604	DKFZP434B168 protein	4.30
	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
50	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
55	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regl	4.30
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k8	4.30
	452994	AW962597	Hs.31305	KIAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.30
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
60	440910	H97875	Hs.117974	ESTs	4.29
	406853	AA614553	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
	413518	BE149455	Hs.75415	beta-2-microglobulin	4.28
65	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
	406746	AA580395	Hs.279860	tumor protein, translationally-controlled	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.26
	450201	T97838	Hs.25722	ESTs	4.25
	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
70	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
	404854			Target Exon	4.21
75	406653	AA574074	Hs.77861	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N57334	Hs.50158	ESTs	4.20
	418304	AA215702		gb:zr97g10.r1 NCL_CGAP_GC81 Homo sapiens	4.20
80	423180	AF068302	Hs.125031	choline/ethanolaminephosphotransferase	4.20
	424684	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW945871		gb:RC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

	451952	AL120173	Hs.301663	ESTs	4.20
	455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
	453247	T80198	Hs.111806	ESTs	4.19
5	430451	AA838472	Hs.297939	cathepsin B	4.19
	414283	AW960011	Hs.154993	ESTs	4.18
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
	450746	D82673	Hs.278589	general transcription factor II, I	4.16
10	444797	AB018333	Hs.12002	KIAA0790 protein	4.16
	445718	H79791	Hs.15227	ESTs	4.15
	425783	AI026740	Hs.1948	ribosomal protein S21	4.15
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
	406710	AI708347	Hs.184014	ribosomal protein L31	4.15
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
15	422343	AI628633	Hs.346823	gb:ty77d05.x1 NCI_CGAP_Kid11 Homo sapien	4.13
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
	406724	C14071	Hs.234518	ribosomal protein L23	4.12
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.12
	413828	L19067		v-rel avian reiculoendotheliosis viral	4.11
20	416819	U77735	Hs.80205	pim-2 oncogene	4.11
	436674	AA725002	Hs.272018	low molecular mass ubiquitome-binding pr	4.11
	405266			Target Exon	4.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
25	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.10
	423096	AA732684	Hs.278428	progesterone induced protein	4.10
	428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypotheti	4.10
	429355	AW973253	Hs.292689	ESTs	4.10
30	433308	AA582718	Hs.291650	ESTs	4.10
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
	450850	AA648866	Hs.151999	ESTs	4.10
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
	406854	AA613705	Hs.252259	ribosomal protein S3	4.10
35	410768	AF038185	Hs.65187	Homo sapiens clone 23700 mRNA sequence	4.09
	419612	AI498267	Hs.110613	KIAA0421 protein	4.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
	441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp554C1216 (f	4.08
40	443415	AI056523	Hs.133472	ESTs	4.08
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
	422305	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.07
	400233			Eos Control	4.06
	421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
45	442622	NM_000435	Hs.8546	Nolch (Drosophila) homolog 3	4.06
	424795	AW102850	Hs.153177	ribosomal protein S28	4.05
	446231	NM_002163	Hs.14453	Interferon consensus sequence binding pr	4.05
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	4.05
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfam	4.05
50	409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fis, clone C	4.03
	413891	BE271020		tumor suppressor deleted in oral cancer-	4.03
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	4.02
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.02
	410584	AB011112		KIAA0540 protein	4.01
55	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
	423645	AI215632	Hs.147487	ESTs	4.00
	430048	T65054	Hs.73605	ESTs	4.00
	431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
	434170	AA626509	Hs.122329	ESTs	4.00
60	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12607 fis, clone NT	4.00
	435391	AA704588	Hs.58934	ESTs	4.00
	446768	AV660305	Hs.110286	ESTs	4.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
	451831	NM_001674	Hs.460	activating transcription factor 3	4.00

TABLE 56B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947832 AI276125 AI185720 AW510698 AA987230 BE487708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268839 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40188 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552

			BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 B1039626 B1037700 R00353 BF155184 N98343 N79072 H01812 T55581
429978	35194_2		B0738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA805547 AV682125 H93575 AW071172 AW769904 AI853985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 B1260621 AI767525 R31653 B1918664 AW963196 C06195 AI678018
442562	39593_1		AK066585 BG399272 AA187635 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 A1653056 AW973709 AI653173 BG054997 AI266043 B1054879 AI565750 AI492830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 B1492088 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832
412636	1438_1		M77830 NM_004415 AF139065 BG681115 BG740377 BF12964 BG000656 AA128470 B1438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE040047 AA857316 B1039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 B1090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 B1036306 BG990973 B1040954 BF919911 AU140155 A1951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 B1039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873593 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG858845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603118 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927535 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 BF752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 B1467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 B1791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 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 AI609836 AI340650 AI312472 BF054840 AI802838 AI345448 AI336508 AI313098 AI312293 AI312277 AJ254912 AW302091 AW074788 AI611968
 AI611948 AI583362 AI583284 AI583245 AJ379398 AJ371935 AI340564 AW301840 AI662239 AI612025 AI611859 AI609852 AI345449 AI312375
 AI312318 AI311993 AI310895 BF057960 BE178604 AI802860 AI612115 AI611886 AI370059 AI313286 AI802856 AI611438 AI311587 AI802821
 AI312997 BF054711 AI611889 AI376483 AI252445 AI611577 AJ349139 BF054925 AI802840 AI583286 AI340739 AI612041 AI345196 BF054833
 AI308909 AI611883 AI313275 BF477097 AI609466 AI348792 AI340468 BG944254 BG941457 AW302007 BG944413 BG941475 D58042 AA328428
 BG429596 BE395392 BM424161 BF663310 AV727364 BM473884 BG531178 AA307591 BF965435
 BG009500 AI376551 AA897445 T87714
 BE564506 Z47727 BF028489 B1597545 AA152273 AA730753 W07504 AA406507 AA316220 AA424683 N35844 N72473 AA442109 W01788
 AA747605 AA235894 N41438 AA382786 AI906934 AJ906935 BF091197 N85572 N75678 AV758098 BE719745 BE719744 BE719735
 AA639388 AA584945 AA776364 AA776365 AA865528
 AI732997 AA977633 AA865818
 AF075009 R63109 R63068
 AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 B1497126 AW903775 B1917368
 AW150900 BF244813 H79201
 BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548
 AK057067 BF111915 AW249706 AI222199 AI887251 AI818753 AI244687 AW135782 BF476693 BF060935 AI197928 AW251092 AI685636
 AI685630 BE673458 AA932894 AW205200 AA720784 BG236866 AI583152 BE677464 AW149338 AI926439 BG303125 BF915924 BG982583
 B1060025 BG991393 BE830027 BE151985 BE152208 BE152002 BE818337 BE717581 BE818354 BE830030 AA377477 T51255 BF920761
 BG170636 N90052
 AI207197 BF773544 AW196462
 AI207343 BF813684 BF928775 AA828585
 AF070570 BF439282 BF109960 AI480268 AJ038060 AW082339 BF516290 BE218214 AJ469956 AA039955 BE444674 AI861871 AA766231
 AA845840 W85716 AA676253 AI087188 AA022908 AW953178 T33195 BF594711 AA488969 R55652 D81245 D80778 D81560 AW960933
 BF930897 BE698103 AA040024 BF515960 BE168475 AA453247 AI267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109
 AA004849 H41852 W88634 BF031932 BM423354 AL041825 H29654 AJ908178 W85754 AJ905762 AA309860 C04540 AA340248 H84669
 BM476605 B1545004 B1834636 BG112453 B1199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AJ734997 AA931168 AA429766
 NA7913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990
 BE857200 AA932598 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA427777 AA603724 AA873347 AI056717 AI092185 AI032895
 AA535689 BF806025 BF806081 BF806082 BF746099 BF746097 AI309259 AI597603 BF806068 AI090653 AI129205 AI248410 H72931 AW615341
 BF806590 BF806582 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76397
 T65754 AA226568 AA229857
 X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579
 AA449679 AA740864 NM_001111 H18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475
 BE890249 AW406263 BE074258 AV729485 BF809610 BG056819 AA677244 BE179838 AA622264 AI460106 AA740411 AA99168 AI078223
 AI682923 BE695559 AW375385 AA788739 BG984978 Z40874 T17054 F09569 AW844043 U10439 B1711870 AW245957 AI158567 AA679305
 AA679316 W72610 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI707980 AI049397 AI042115 AI200901
 BE328452 AA644678 AA551209 BE351065 AA970781 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664483 AI218710
 AW020650 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE465703 AW512940 AW241366
 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073 AA548255 AI569630 BE710031 AA244182 AI341697 AA563904
 AI537990 AW517908 AW172943 Z39498 AI70294 AW150414 AI253293 BE825720 T31860 AW150775 BE202101 AA150892 AU133933 BE781148
 AL038957 BF910979 AA352297 BG988142 AW372175 BF229105 AW866705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502
 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 B1021048 BMD48783 AW501366 AW501342 AW501549
 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 B1919250
 B1253018 AW130996 BE074249 BE895428 B1034862 BE083277 BF952166
 BE883520 B1057842 AA215702 AA215703 AA368006 BE008876 BE066655

438141	1173217_1	AA778849 AW946871 AW945782 AW946955
455397	1163608_1	AW936332 AW936341
413828	9453_1	BC011603 BG479117 AU124990 BG829759 AU143705 BG701663 BG699781 AU131718 BE515064 AU121812 BG898850 AL558461 BM151887
5		AU128758 BM263692 AU099013 A1241350 U88318 AW058358 AW469340 BF683967 A1470140 AU150993 AA633376 AW150821 AA536142
		AU148749 A1620547 AU151769 AU153404 AW070666 A1457758 AU153077 N99566 AW050940 BG055674 AA506657 AW301529 A1918646
		AJ511235 A1266081 A1334542 AW071277 A1312434 AW303114 A1436544 A1436466 R22972 A1472987 N77886 AW072883 AA318683 D19761
		AW050566 A1312433 AA328444 R72435 AA430721 A1425599 AA582290 AU148896 AA721233 AW628132 R93935 AA100710 B1520773 A1934172
		BG222461 H85359 AW074639 AA017117 B1026412 AL582142 AA443547 AA586793 AA777535 AA693844 A1018661 AA577422 AA522800
10	410704	1054673_1
		BF054818 AA102378 AA757993 AA687769 R55540 AA505784 B1820705 B167939
		AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
		BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
		AW840571
15	400233	11259_1
		BC004324 NM_001020 BC007977 M60854 BM050828 BG829809 BE385504 BG744451 B1826914 BE440007 B1260656 BE395117 BE389334
		BE255792 B1194169 B1668218 B1194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 B1828267 AW958606 BG831252
		BE392943 BE394033 B1858915 B1668334 BE621019 BG706995 BE791985 BF967484 B1193635 BG761859 BM466537 BG747165 BG827488
		A1133550 BM011511 B1227282 BG489212 BG478388 BE727789 B1160880 BG831707 BG324692 BM470427 B1083889 BG831605 BG754114
		BG420536 BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 B1193807 B1159866 BG473786 BG397178
		B1194428 B1117210 BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145
20		BM017978 B1193934 B1160764 B1160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 B1192794 BG831002 BG830459
		BG764737 BG761808 BG481705 BG104314 BM464565 B1261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762
		BG480900 BG419627 BG248771 BF975542 BM042233 B1161149 BG831302 BG830033 BG829626 BM050064 B1193014 B1161360 BG822729
		BG110091 BG106500 B1258369 BG831982 BM458301 BM019513 B1161350 B1114178 BG481969 BG474870 BF974048 BF971122 BE741405
		BE395269 BG832027 BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 B1258301
		B1160946 BG105893 BF183072 BM459542 B1193881 BG832043 BG831323 B1194545 B1160568 BG755930 BG706018 BE743865 BM465145
25		BG831227 BG774290 BF683451 BE907161 BM045391 B1194396 B1161269 BG747091 BG546643 BF984863 B1160206 B1226402 B1226336
		AW328236 BG339458 BF972634 BE909808 B1160988 B1160251 BG828764 BG826860 BG758350 BF568228 B1818282 B1457127 BG831491
		BG759884 A1830010 BF568381 BE907238 B1161172 B116773 BG827153 BG825088 BG335419 BG109404 A1929068 BE906354 BE408564
		BM045000 BG339617 BG287294 BG335767 BE907263 BF568921 BG829961 BG479305 BG260397 A1922228 BE301975 AW516055 BG480919
		BG480626 AW196817 BG336261 BE906157 BE395717 BE391427 B1192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344
30		A1433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 A1871761 BE744523 B1192663
		BG831669 A1000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297
		BE391448 BE390780 BE388821 BE258477 BE905970 BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA550542
		BE744156 BE394125 BE742207 BE395265 BE392942 BE894336 BE378222 BE906928 BE904650 BE393704 BE620999 BE515162 BE378753
		BE272370 BE907458 BE512801 BE392484 BE907636 BE907353 BE910491 BE909796 BE905331 AW248173 A1683576 BE908826 BE520180
35		BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA955746 BE561195 BE908825
		BE906472 BE906509 BE906017 BE910442 BE614657 B1261969 BE741707 BE392216 BM042793 BF570283 B1262119 BE395707 BE378298
		AW327827 BE394422 BF569178 BE263240 A1700512 BG830290 BF569308 BF569156 B1194587 BE390831 BG745096 A1681675 BE395674
		AA136372 BE279892 AA442822 BE384898 AA313519 A1878866 AA305804 F33366 BE394852 F29153 F33618 A1133637 AA300009 F34063
40	413891	823_1
		F29455 AU099691 A1905085 A1906856 AA343249 BE388691 AW404280 AA379888 F29022 BF089981 F31013 F24305
		BE271020 A1925430 A1806151 AW129911 AA828002 AW003539 BE042625 A1287859 AW778973 A1621173 A1991000 AA846016 AW150029
		AW169748 AA649945 A1358486 A1470921 BF434211 AW513748 AW451232 A1953739 A1249448 A1040580 A1655280 A1637976 AW194345
		AW611997 A1367197 BF064039 F29558 A1537342 BF593207 AW879538 AA973211 A1674328 AW879559 BF061961 AA481914 AA426532
		AA426653 AA480106 AW243290 BF513102 BF346057 A1763358 AW003726 A1139045 A1570748 AW237602 T57492 BE887212 A1969311
		AA133045 F23464 AA576416 T15590 A1650891 A1950958 A1983931 AW515101 A1650820 H81989 AA508473
45	410584	35319_1
		BF828833 A1968217 A1651409 A1760574 A1147562 AW001418 A1146791 A1650589 A1952939 A1432373 A1964094 A1963870 A1420438 A1336803
		AA809634 BF590826 AA741075 B1712639 AL134637 BM264338 AA527993 A1867208 A1439038 A1684987 A1631696 A1587126 A1637622 A1651931
		A1867525 A1783674 A1638281 A1825752 A1339197 A1653411 A1341372 A1673213 A1673191 AW779768 A1627934 A1921836 A1741634 A1382284
		A1741624 A1401569 AW190430 AW196390 A1829182 A1523816 A1760522 BE505014 A1917343 BG818909 AW009307 AA927544 AA825621
		AA829400 AA527307 A1887999 A1865022 AA865063 AA653458 AA483816 AA836167 AA505879 AA421004 AA252626 A1380678 AW196980
50		AA549133 A1742276 A17015700 AA595019 AA877835 A1701658 AA729793 AA535004 AA926792 AA505131 AA603726 W68390 N90130 AA489461
		AA830462

55	TABLE 56C
	Pkey: Unique number corresponding to an Eos probe set
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand: Indicates DNA strand from which exons were predicted.
60	NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402474	7547175	Minus	53526-53628,55765-55920,57530-57757
402145	8018280	Plus	113086-114800
401091	9958240	Plus	94760-94898
401466	6682292	Plus	28748-29023
401113	9966541	Minus	19419-19959
406542	7711499	Plus	117335-118473
405086	8072509	Plus	73664-73841,74081-74217,74510-74779,7492
401846	7712190	Minus	82775-82823,82912-83022
404854	7143420	Plus	14260-14537
405266	4156171	Minus	63337-63552

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TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

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Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Alfymetrix HuO1 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
5	Pred.Protd.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
	UniGene Title:	UniGene gene title
	R1	95th percentile of testicular cancer AIs divided by the 50th percentile of normal tissues AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
10	Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Protd.Domains; R1	
	424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23	
	440119; AA865455; Hs.125331; ESTs, Moderately similar to unknown [H.sapiens]; ESTs, Moderately similar to unknown [H.s; 27.37	
15	421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89	
	431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription factor 1; 25.03	
	435918; AF263538; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88	
	432666; AW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product [H.sapiens]; ESTs, Weakly similar to unnamed protein; 17.74	
	419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); chitinase 1 (chitotriosidase); 17.64	
20	452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in melanoma; 17.06	
	417886; AA214584; ESTs; ESTs; 15.95	
	412265; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93	
	425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcript; 15.82	
	423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11	
25	419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08	
	427584; BE410293; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogene; 14.17	
	418696; AW959433; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58	
	416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20	
	414034; U89277; Hs.305985; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog of; 12.93	
30	454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90	
	432730; AJ066520; Hs.131358; ESTs; ESTs; 12.84	
	446293; AI420213; Hs.149722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74	
	423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2delta subunit 2; calcium channel, voltage-dependent, alpha; 12.46	
	450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42	
35	450719; AJ096837; Hs.21349; ESTs, Weakly similar to RB88_HUMAN RAS-RELATED PROTEIN RAB-8B [H.sapiens]; ESTs, Weakly similar to RB88_HUMAN RAS-R; 12.26	
	431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96	
	431354; BE046956; Hs.251673; DNA (cytosine-5-)-methyltransferase 3 beta; DNA (cytosine-5-)-methyltransferase 3 be; 11.91	
	402199; ; Target Exon; Target Exon; 11.85	
	424578; AK001973; Hs.150890; hypothetical protein; hypothetical protein; 11.81	
40	416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67	
	439979; AW600291; Hs.6823; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57	
	410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42	
	442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42	
	414812; X72755; Hs.77367; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38	
45	421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15	
	440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; NALP2 protein; PYRIN-Containing APAF1-like; 10.92	
	414683; S78296; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91	
	423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage; 10.74	
	433800; AJ034361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68	
50	429120; AK001673; Hs.195530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48	
	444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46	
	411553; AA281219; Hs.121296; ESTs; ESTs; 10.37	
	426534; U58096; Hs.2051; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28	
	441878; AI801869; Hs.127982; ESTs; ESTs; 10.06	
	432117; AL036195; Hs.2909; protamine 1; protamine 1; 10.01	
55	425427; AI852662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97	
	416201; AA467752; Hs.195161; ESTs; ESTs; 9.97	
	410929; H47233; Hs.30643; ESTs; ESTs; 9.91	
	427486; AA974433; Hs.352432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81	
60	427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68	
	402680; ; Target Exon; Target Exon; 9.68	
	409208; Y00093; Hs.172631; Integrin, alpha X (antigen CD11C (p150), alpha polypeptide); Integrin, alpha X (antigen CD11C (p150); 9.46	
	443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42	
	440207; AJ371978; Hs.128326; ESTs; ESTs; 9.41	
65	433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41	
	447534; AW953935; Hs.288655; ESTs; ESTs; 9.33	
	442333; AJ650877; Hs.129302; ESTs; ESTs; 9.28	
	421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425); Homo sapiens mRNA; cDNA DKFZp434B0425 (f; 9.24	
	423458; AL204212; Hs.351113; ESTs; ESTs; 9.23	
70	431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta); 9.23	
	422938; NM_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21	
	411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; 9.21	
	425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18	
	428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17	
75	428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3 (RAIG1); metabo; 9.11	
	447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11	
	422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10	
	449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86	
	441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 8.86	
80	440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86	
	409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83	
	420367; AA259090; Hs.257028; ESTs; ESTs; 8.82	
	415947; U04045; Hs.78934; mitS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); mitS (E. coli) homolog 2 (colon cancer; 8.73	
	418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase 1; mitogen-activated protein kinase kinase; 8.71	

- 417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapiens]; 8.64
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; 8.58
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55
 412140; AA219591; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkinesin 6); 8.52
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group 1, member 3; nuclear receptor subfamily 1, group 1, m; 8.51
 424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45
 447188; H65423; Hs.17631; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45
 430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); midkine (neurite growth-promoting factor 2); 8.40
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope protein RIC-3 (env) gene, complete cd; gb:Homo sapiens envelope protein RIC-3; 8.38
 420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.38
 406621; X57809; Hs.181125; immunoglobulin lambda locus; immunoglobulin lambda locus; 8.37
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25
 423198; H81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 [p95], lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 [p95], ly; 8.17
 453968; AA847843; Hs.62711; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromosomal); 8.16
 453985; N44545; Hs.251885; ESTs; ESTs; 8.14
 451108; BE382701; Hs.25960; N-MYC oncogene; N-MYC oncogene; 8.10
 420347; AL033359; Hs.97124; Human DNA sequence from clone RP1-309H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, STSs, GSSs and a CpG Is; Human DNA sequence from clone RP1-309H15; 8.03
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.02
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90
 421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobulin); 7.89
 432407; AA221036; gb:z03f12.1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN.; mRNA sequence; gb:z03f12.1 Stralagene NT2 neuronal pr; 7.83
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80
 433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73
 446528; AW076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71
 447350; AJ375572; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 7.71
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked moi; 7.71
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1); ectonucleotide pyrophosphatase/phosphodi; 7.62
 443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; interferon, gamma-inducible protein 30; 7.55
 410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD); eukaryotic translation initiation factor; 7.53
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein; 7.52
 411975; AJ916058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like 1; 7.50
 439864; A1720076; Hs.291897; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 7.47
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4669, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47
 407710; AW022727; Hs.23616; ESTs; ESTs; 7.45
 445093; AJ207197; Hs.374149; ESTs; ESTs; 7.41
 418113; AJ272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37
 429469; M64590; Hs.111801; glycine dehydrogenase (decarboxylating); glycine decarboxylase, glycine cleavage system protein P; glycine dehydrogenase (decarboxylating); 7.33
 422726; U11690; Hs.1572; faciogenital dysplasia (Aarskog-Scott syndrome); faciogenital dysplasia (Aarskog-Scott sy; 7.33
 430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32
 448981; AJ968719; Hs.195387; ESTs; ESTs; 7.28
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121; 7.25
 434414; A1798376; gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN.; mRNA sequence; gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens; 7.24
 428977; AK001404; Hs.194598; cyclin B2; cyclin B2; 7.19
 434274; AA628539; Hs.57783; ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1_HUMAN A; 7.19
 445700; AW206257; Hs.155326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelinoligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L22; 7.16
 420524; AB010575; Hs.98547; amiloride-sensitive cation channel 3, testis; amiloride-sensitive cation channel 3, te; 7.15
 439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14
 445076; AJ206888; Hs.154131; ESTs; ESTs; 7.14
 448588; AJ970278; Hs.156905; KIAA1676; KIAA1676; 7.13
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E. coli RecA homolog); RAD51 (S. cerevisiae) homolog (E. coli Ra; 7.04
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; interferon-stimulated protein, 15 kDa; 7.02
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA; 6.96
 416658; U03272; Hs.79432; fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2 (congenital contractural ara; 6.92
 438450; AJ050866; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90
 444381; BE387333; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89
 447582; BE293520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89
 424779; AL046851; Hs.153053; CD37 antigen; CD37 antigen; 6.89
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pro; 6.84
 427268; AA400495; ESTs; ESTs; 6.82
 414732; AW410976; Hs.77152; minichromosome maintenance deficient (S. cerevisiae) 7; minichromosome maintenance deficient (S.; 6.81
 424959; NM_005781; Hs.153397; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81
 426866; U02330; Hs.172818; neuregulin 1; neuregulin 1; 6.80
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80
 427521; AW973352; ESTs; ESTs; 6.75
 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein; 6.75
 427719; AI393122; Hs.134726; ESTs; ESTs; 6.74

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein; 6.70
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63
 441031; AJ110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57
 414161; AA136108; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete; 6.55
 452363; AJ582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55
 422785; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mifolin); minichromosome maintenance deficient (S.; 6.50
 418918; JO7871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A; 6.44
 427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43
 409142; AL136877; Hs.50755; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42
 430280; AA361258; Hs.237868; Interleukin 7 receptor; Interleukin 7 receptor; 6.42
 425938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3_HUMAN TUBBY; 6.40
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39
 441384; AA447849; Hs.288650; retinoic acid induced 3; retinoic acid induced 3; 6.38
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; 6.31
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright; 6.31
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mif5, S. pombe) 6; minichromosome maintenance deficient (mif; 6.31
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcript; 6.30
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30
 415829; AW450198; Hs.163742; ESTs; ESTs; 6.28
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25
 428918; AL036957; Hs.2324; protamine 2; protamine 2; 6.24
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19
 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19
 407245; X90568; Hs.172004; titin; titin; 6.18
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino; 6.09
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA, transcript (FBL), mRNA; NM_001436; Homo sapiens fibrillarin (FBL); 6.09
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05
 422283; AW441307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); interferon, alpha-inducible protein (clo; 6.04
 402678; ; Target Exon; Target Exon; 6.03
 453884; AA355925; Hs.38232; KIAA0186 gene product; KIAA0186 gene product; 6.01
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 216812; hypothetical protein from EUROIMAGE 2168; 6.01
 420596; NM_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01
 420676; AJ434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95
 417777; AJ823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/thr; 5.94
 449589; AJ656634; Hs.195389; ESTs; ESTs; 5.92
 436576; AJ458213; Hs.77542; ESTs; ESTs; 5.90
 438746; AJ885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89
 420005; AW271108; Hs.133294; ESTs; ESTs; 5.89
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88
 403171; ; C2001472:g[5809678]g[AB41848.2] (U64675) sperm membrane protein BS-63 [Homo sapiens]; C2001472:g[5809678]g[AB41848.2] (U64; 5.87
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA, VERSION NM_000178.1 GI; NM_000179; Homo sapiens mutS (E. coli) h; 5.85
 423787; AJ295745; Hs.236204; nuclear pore complex protein; nuclear pore complex protein; 5.85
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84
 452796; AB011100; Hs.30650; KIAA0528 gene product; KIAA0528 gene product; 5.84
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80
 447359; NM_012093; Hs.18268; adenylate kinase 5; adenylate kinase 5; 5.79
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78
 420297; AJ628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1_HUMAN ALU S; 5.75
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5_HUMAN LEUKE; 5.74
 436251; BE515065; Hs.296585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73
 421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspartate; 5.69
 401704; ; NM_021195; Homo sapiens claudin 6 (CLDN6), mRNA. VERSION NM_020982.1 GI; NM_021195; Homo sapiens claudin 6 (CLDN6); 5.66
 425358; AL079558; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin associated protein 1; 5.65
 402677; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.64
 409264; NM_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63
 432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63
 409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63
 430252; AI638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61
 452816; AA131789; Hs.61509; ESTs; ESTs; 5.60
 402679; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.59
 414291; AI289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58
 453028; AB006532; Hs.31442; RecQ protein-like 4; RecQ protein-like 4; 5.58
 453905; NM_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-associated kinesin); 5.55
 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino acid transporter, y system), member 7; 5.55
 446979; AI654443; Hs.197683; ESTs; ESTs; 5.54
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kinase; 5.53
 418962; AA714835; Hs.271863; ESTs; ESTs; 5.53
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, complete cds; 5.52
 427247; AW504221; Hs.174103; Integrin, alpha L (antigen CD11A (p180)), lymphocyte function-associated antigen 1; alpha polypeptide; Integrin, alpha L (antigen CD11A (p180)); 5.52
 449322; AI638616; Hs.196566; ESTs; ESTs; 5.51
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51
 415141; AA189099; Hs.268171; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7_HUMAN ALU S; 5.48
 454048; H05626; Hs.6921; ESTs; ESTs; 5.46
 417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 fis, clone HE; 5.44
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; 5.44
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class II, DQ alpha 1; 5.44
 427668; AA288760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43
 449437; AF702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 5.41
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40
 450746; D82673; Hs.278589; general transcription factor II, t; general transcription factor II, t; 5.40
 425966; NM_001761; Hs.1973; cyclin F; cyclin F; 5.39
 418134; AA397769; Hs.86617; ESTs; ESTs; 5.38
 432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, member 3; 5.36
 428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328.2 [H.sapiens]; ESTs, Moderately similar to R27328.2 [H.sapiens]; 5.35
 406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; 5.34
 415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII), 1; 5.33
 448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33
 424762; AL119442; Hs.183884; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor 4 gamma, 2; 5.32
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypeptide 1; 5.32
 429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32
 455373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); 5.30
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30
 422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; 5.28
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26
 416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer antigen NY-BR-81; 5.21
 450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20
 409670; AI368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20
 429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20
 408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); 5.19
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, member 3; 5.16
 437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated protein 1; 5.15
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15
 436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor type, C; 5.14
 426752; X69490; Hs.172004; titin; titin; 5.13
 415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2; 5.13
 400263; ; Hs.75309; Eos Control; Eos Control; 5.13
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; 5.12
 427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10
 407347; AA829847; ; gb:0404007.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gb:0404007.s1 NCL_CGAP_GCB1 Homo sapiens; 5.10
 458933; AI638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10
 450431; AW136797; Hs.266041; ESTs; ESTs; 5.09
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08
 410423; AW404232; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-receptor type 6; 5.08
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05
 412723; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog) 1; 5.02
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha 2 (RAG cohort 1, importin alpha 2); 5.00
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00
 414809; AA34699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99
 402145; ; Target Exon; Target Exon; 4.99
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, complete cds; 4.88
 419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NTZRP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96
 448569; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of transcription 1; 4.94
 426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91
 440129; AA855818; Hs.369523; ESTs; Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-like; 4.91
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1; 4.90
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88
 445333; BE537641; Hs.44276; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating protein; 4.87
 416000; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG51) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIG51); 4.87
 421350; AF017002; Hs.278188; ESTs; Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene; 4.87
 409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86
 424304; NM_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86
 437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase transporters), member 1; 4.84
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor; 4.81
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; 4.80
 409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G protein), alpha 14; 4.79
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79
 447250; AB78909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), magnesium-dependent; 4.79
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78
 448950; AF268687; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78
 412926; AB79076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C kinase substrate; 4.78
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); 4.76
 421905; AB60247; Hs.32699; ESTs; Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; 4.75
 413880; AB60842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related kinase 2; 4.74
 418355; L42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; ATPase, H7 transporting, nongastric, alpha polypeptide; 4.74
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74
 428024; Z29067; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related kinase 3; 4.74
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bamacan); chondroitin sulfate proteoglycan 6 (bamacan); 4.70
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); 4.69
 449475; AB348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69
 420062; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; 4.68
 436856; AB469355; Hs.127310; ESTs; ESTs; 4.68
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds; gb:Human transketolase-like protein gene; 4.67
 411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67
 426726; AA488915; Hs.171955; trophinin associated protein (tastin); trophinin associated protein (tastin); 4.67
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 non-catalytic subunit; 4.67
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, alpha polypeptide; 4.65
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64
 415724; NM_003580; Hs.76587; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activation associated factor; 4.63
 435045; BE297155; Hs.143698; ESTs; ESTs; 4.62
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62
 414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62
 436585; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); 4.62
 449515; AB653378; Hs.302012; ESTs; ESTs; 4.61
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61
 420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD), member 4; 4.61
 438469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61
 413441; AI929374; Hs.75367; Src-like-adaptor; Src-like-adaptor; 4.60
 456847; AB360456; Hs.86088; ESTs; ESTs; 4.58
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57
 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L ORF; 4.55

- 443058; A1188710; Hs.374480; ESTs; ESTs; 4.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54
 453227; AW135862; Hs.243991; ESTs; ESTs; 4.52
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51
 422555; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascin homolog like); singed (Drosophila)-like (sea urchin fas); 4.51
 453613; F06838; Hs.374476; ESTs; ESTs; 4.50
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H); 4.50
 412507; L36645; Hs.73964; EphA4; EphA4; 4.50
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo); 4.49
 406547; ; Target Exon; Target Exon; 4.49
 443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47
 448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46
 446238; NM_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46
 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (TIT3 complex); CD32 antigen, zeta polypeptide (TIT3 com); 4.46
 413426; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt); 4.44
 421819; NM_013403; Hs.108665; zlnedin; zlnedin; 4.44
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; 4.43
 434551; BE387162; Hs.280856; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 (H.sapiens); ESTs, Highly similar to A35661 DNA excis; 4.43
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42
 413186; AW077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic); 4.42
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40
 424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi); 4.37
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35
 400440; X83957; Hs.83870; nebulin; nebulin; 4.35
 437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34
 430478; NM_014349; Hs.241535; apolipoprotein L 3; apolipoprotein L 3; 4.34
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re); 4.30
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfam; 4.29
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29
 427337; Z46223; Hs.176563; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled receptor; 4.28
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28
 426108; AA622037; Hs.166488; programmed cell death 5; programmed cell death 5; 4.28
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component ; 4.27
 437908; A1082424; Hs.351043; ESTs; ESTs; 4.27
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26
 439334; A1148976; Hs.112062; ESTs; ESTs; 4.26
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25
 413869; NM_000878; Hs.75598; interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24
 447528; A1612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22
 449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated); 4.22
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21
 444535; AF011466; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21
 417088; M54915; Hs.81170; pim-1 oncogene; pim-1 oncogene; 4.20
 421707; NM_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20
 408717; AF045458; Hs.47061; uno-51 (C. elegans)-like kinase 1; uno-51 (C. elegans)-like kinase 1; 4.20
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19
 419452; U33635; Hs.90672; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18
 418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17
 413686; A1469213; Hs.71404; ESTs; ESTs; 4.17
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus); 4.16
 408482; NM_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15
 409421; AA199883; Hs.67624; ESTs; ESTs; 4.15
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to M; 4.13
 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbonate; 4.13
 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondria; Ts translation elongation factor, mitochondria; 4.13
 420253; A1656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 95; 4.12
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12
 400205; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM_006265; Homo sapiens RAD21 (S. pombe); 4.12
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11
 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10
 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31611 hypothetical; 4.10
 432512; NM_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to ; 4.10
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription factor; 4.09
 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09
 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G protein) alpha 12; 4.09
 425003; A119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/apyrimidinic endonuclease(APEX); 4.08
 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08
 423841; Hs.93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-receptor; 4.08
 452069; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08
 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker-; 4.07
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic; 4.07
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12169 fis, clone MA; 4.07
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe co; 4.06
 446791; A1632278; Hs.195922; ESTs; ESTs; 4.06
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), catalytic; 4.06
 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta; 4.06
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory sub; 4.06
 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, delta; 4.05
 408892; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrate; 4.04
 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 pr; 4.04
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule; 4.04
 410068; A1633888; Hs.58435; FYN-binding protein (FYB-120/130); FYN-binding protein (FYB-120/130); 4.03
 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03
 427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03
 451050; AW937420; Hs.351869; ESTs; ESTs; 4.02
 449667; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02
 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01
 437527; A1241019; Hs.145644; ESTs; ESTs; 4.01
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylene tetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase; 4.00
 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF1210; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00
 412939; AW411491; Hs.75068; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor; 4.00
 409581; U65243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99
 433577; AW007080; Hs.284192; ESTs; ESTs; 3.99
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrolase; 3.99
 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98
 402398; ; C19000263.gij3108023[gibAAC15755.1] (AC004659) BC62940_2 [Homo sapiens] [66335; C19000263.gij3108023[gibAAC15755.1] (AC0; 3.97
 408414; A114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell; 3.97
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97
 416084; L16991; Hs.79008; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kin; 3.95
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial; 3.95
 447887; A114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine pr; 3.95
 430770; AA765894; Hs.123296; ESTs; ESTs; 3.94
 442994; A1026718; Hs.16954; ESTs; ESTs; 3.94
 420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); lymphocyte antigen 94 (mouse) homolog (a; 3.94
 438456; AA913381; Hs.279763; ESTs; ESTs; 3.94
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A); 3.93
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93
 424829; NM_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR super; 3.93
 447574; AF162666; Hs.18895; lousled-like kinase 1; lousled-like kinase 1; 3.93
 425797; AF002988; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93
 421910; NM_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associated; 3.92
 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenase; 3.92
 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92
 400262; Hs.75309; Eos Control; Eos Control; 3.90
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90
 409799; A111928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90
 435206; A1432364; Hs.160594; ESTs; ESTs; 3.90
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90
 413627; BE182082; Hs.246973; Intron of Bicaudal D homolog 1; Intron of Bicaudal D homolog 1; 3.90
 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89
 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89
 407013; U65637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89
 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88
 400261; Hs.1802; Eos Control; Eos Control; 3.88
 450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88
 422293; AA94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glut; 3.87
 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87
 417767; BE242241; Hs.82542; acyltoxacyl hydrolase (neutrophil); acyltoxacyl hydrolase (neutrophil); 3.87
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor; 3.87

- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino : 3.86
419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86
427022; AW245839; Hs.17325; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86
443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86
5 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86
410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85
450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85
418978; T85295; Hs.266806; ESTs; ESTs; 3.84
10 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84
442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84
447232; AW499834; Hs.327; interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84
434689; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83
432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83
15 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83
451598; N29102; Hs.79658; ESTs; ESTs; 3.82
449433; A1672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82
426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81
435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80
20 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80
422753; A1928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79
421508; NM_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79
414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79
25 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79
439568; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; frizzled (Drosophila) homolog 8; 3.79
411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78
429170; NM_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78
425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78
30 423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78
429687; A1675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77
414177; A1351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77
414135; NM_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77
445817; NM_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77
35 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76
412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repa; 3.76
413011; AW068115; Hs.821; biglycan; biglycan; 3.76
428157; A1738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76
40 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor, alpha polypeptide); Integrin, alpha 5 (fibronectin receptor,; 3.75
427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75
405484; : C3002124*gi12737280|ref|XP_006682.2| keratin 18 [Homo sapiens]]|6633; C3002124*gi12737280|ref|XP_006682.2| k; 3.75
450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75
432460; H12912; Hs.274691; adenylyate kinase 3; adenylyate kinase 3; 3.75
428816; AA040498; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74
431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
45 to ALU8_HUMAN ALU S; 3.74
453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74
426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74
438330; AW450572; Hs.257316; ESTs; ESTs; 3.74
50 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74
452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73
442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypotheti; 3.73
451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73
410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73
55 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54); human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72
449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpo; 3.71
423523; AW299828; Hs.193580; ESTs; ESTs; 3.71
413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71
448336; R53848; Hs.44976; ESTs; ESTs; 3.70
60 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70
416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70
442200; AW590572; Hs.235768; ESTs; ESTs; 3.70
414280; BE410769; Hs.75873; zyxin; zyxin; 3.69
409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69
65 415276; U88666; Hs.78353; SFPS protein kinase 2; SFPS protein kinase 2; 3.69
439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69
446522; NM_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69
422785; AJ824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68
401083; : NM_016582*Homo sapiens peptide transporter 3 (LOC51256), mRNA, VERSION NM_016579.1 GI; NM_016582*Homo sapiens peptide transpor; 3.68
413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68
70 452690; A1536070; Hs.15085; ESTs; ESTs; 3.68
428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
to ALU2_HUMAN ALU S; 3.68
415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68
428579; NM_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68
75 446430; AA345837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66
442013; AA508476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG islands. Contains the NIFS gene for
cystine desulfurase, two genes for novel proteins and the gene for the Human DNA sequence from clone RP11-353C1; 3.66
416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65
80 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;
3.65
413076; U10584; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65
429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C; 3.65
452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN20), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

- 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65
 450256; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyros; 3.64
 437669; AJ358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA667999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep; 3.64
 444368; AB033056; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63
 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc; 3.62
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62
 411165; NM_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61
 438785; AA825792; Hs.377119; gbod84b11.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone, mRNA sequence; gbod84b11.s1 NCL CGAP_Ov2 Homo sapiens ; 3.61
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61
 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60
 444965; AL677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_023929); zinc finger protein RINZF (NM_023929); 3.59
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59
 415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel
 glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57
 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57
 423576; NM_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57
 404976; ; NM_014323; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM_014323; Homo sapiens zinc finger prot; 3.57
 449656; AA002008; Hs.188633; ESTs; ESTs; 3.56
 413795; AL040178; Hs.142003; ESTs; ESTs; 3.56
 406859; AL581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; 3.56
 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high aff; 3.55
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; inducible Ik; 3.55
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55
 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55
 425836; AW955696; Hs.90960; ESTs; ESTs; 3.54
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54
 440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53
 421652; NM_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53
 427232; AA577455; Hs.24937; transformer-2 alpha (hra-2 alpha); transformer-2 alpha (hra-2 alpha); 3.53
 424870; T15545; Hs.244624; ESTs; ESTs; 3.52
 442794; AL744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51
 419971; AA400027; Hs.295234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A1 - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51
 421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil); 3.50
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50
 429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211_HUMAN ZINC; 3.47
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77
 430439; AL133561; DKFZP434B061 protein; DKFZP434B061 protein; 2.76
 435697; AF269223; Hs.128322; I-complex 11 (a murine top homolog); I-complex 11 (a murine top homolog); 2.53
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosome; 2.46
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33
 426627; AF012359; Hs.195685; ESTs; ESTs; 2.12
 438963; AF065884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precursor; 2.07
 425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99
 433724; AB827749; Hs.144924; serine/threonine protein kinase SSTK; serine/threonine protein kinase SSTK; 1.68
 420710; NM_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT Number	Accession

417886 1031334_1 AA210987 D57294 AA214584 AA207006 D56572
 432407 MH1429_12 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
 5 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AJ732411 BG778834 BG283641 BE748279
 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 B1851466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AJ075321 L13823 AA216700 BF771864 AW861859
 BE537058 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
 10 434414 35978_1 AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
 AF134164 BF809407 AA218567 BF842853 A1267168 BF876178 BG999253 AW861851 AW858352 AJ817548 BF771300 AA113928 AA223422
 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 A1694265 AA045564 BG950256 A1829309 BG987850 BE093175
 BF854337
 15 427298 115241_1 AA933717 BF061897 AW628327 AA641788 AA400495
 427521 513212_1 AW973352 BF222929 AW016853 BF059130 A1651829 BE551767 AA558414 A1339359 BF059601 A1961162 A1341422 A1206248 A1206165
 407347 810943_1 AA548736 AA768578 A1539081 AW025957 AA736837 N79575 AW594357 AA480892
 430439 6750_2 T23514 A1655785
 AL133561 AL117481 AL122069 AW439292 A1968826 AL041090

TABLE 57C

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 25 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768,139702-139893,140475-14059
402260	3399665	Minus	113765-113910,115653-115765,116808-11694
402678	8113438	Plus	37395-37514,37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3097841	Plus	24712-25374
402677	8113438	Plus	22135-22309,23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4092817	Minus	24019-24973
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

50 Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

55 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 60 UniGene Title: UniGene gene title
 R1 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Prod.Domains; R1

65 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 35.25
 422282; AF019225; Hs.114309; apolipoprotein L; MoLA_ExbB;TM=Y;SS=M; 33.25
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 31.68
 415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3; aldo_ket_red;TM=M; 31.04
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 28.50
 70 439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 27.43
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 25.98
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT,none; 25.38
 418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT,none; 25.28
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolV,HATPase_c;SS=M; 23.58
 75 421733; U24389; Hs.1420; fibroblast growth factor receptor 3 (ach; lg, pkinase;TM=Y;SS=M; 21.24
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 20.45
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 19.78
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 18.90
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M; 18.75
 80 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 18.63
 444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypohetic; Collagen;TM=M;SS=M; 18.60
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; Ig_Rhbd_glycop;TM=Y;SS=M; 18.55
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate trans; PHO4,LIM;TM=M; 18.25

- 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic; PKI; SS=M; 17.73
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; Ig; TM=Y; SS=M; 17.68
 450746; D82673; Hs.278589; general transcription factor II, t; none; SH3, PX; 17.12
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase, PLAT; TM=M; 16.88
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone_rec, zf-C4; TM=M; 16.78
 439941; AI392640; Hs.18272; amino acid transporter system A1; Aa_trans; TM=Y; 16.75
 431846; BE019924; Hs.271580; uropod 1B; transmembrane4; TM=Y; SS=M; 16.56
 424247; X14008; Hs.234734; lysosome (renal amyloidosis); lys, Ig, FAD_Synth, Idh, C, pkinase; SS=M; 16.43
 414883; AA926960; CDC28 protein kinase 1; CKS; 16.20
 438091; AW373062; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 15.80
 439953; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH, Lpase, GDSL; TM=M; 15.70
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1, pkinase; TM=M; 15.63
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 15.45
 434293; NM_004445; Hs.3798; EphB6; EPH, lbd, fn3, pkinase, SAM; TM=Y; SS=M; 15.43
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF, lectin, c_sushi; TM=M; SS=M; 15.28
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD, SK_channel, ion_trans; TM=Y; SS=M; 15.10
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; Ig; TM=Y; SS=M; 14.90
 432308; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib; CBM_21; TM=M; 14.80
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; 14.73
 429345; R11141; Hs.199695; hypothetical protein; K_tetra, SAM; 14.58
 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; Ig, lsdh, Ribosomal_L6, F-box; TM=Y; SS=M; 14.55
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN, HIN; TM=M; 14.53
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none; TM=M; SS=M; 14.35
 429556; AW139399; Hs.99988; ESTs; none; TM=M; 14.18
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding; ehand; SS=M; 14.13
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y_phosphatase, Band_41, PDZ; SS=M; 13.90
 426657; NM_015865; Hs.171731; solute carrier family 14 (urea transport; UT; TM=Y; 13.83
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2, none; 13.80
 400843; ; NM_003105; Homo sapiens sortilin-related; EGF, fn3, ldl_recept, a, ldl_recept, b, granulin, BNR; TM=Y; SS=M; 13.78
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA, ABC_tran, CoaE; TM=M; 13.38
 432314; AA533447; Hs.312989; ESTs; Xlink, none; 13.25
 413109; AW389845; Hs.110855; ESTs; PHO4, none; 13.15
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; 13.13
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC, PAS; TM=M; 12.93
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 12.43
 440249; AI246590; Hs.249175; ESTs; TatD_Nase, pkinase, death, none; 12.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; SS=M; 12.38
 440942; U30825; ; splicing factor, arginine/serine-rich 9; CD36; TM=Y; SS=M; 12.03
 439569; AW602166; Hs.222399; CEGP1 protein; EGF, TNFR_c6, granulin, CUB, Keratin_B2, TIL; TM=M; SS=M; 11.93
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 f1s, clone NT; Aa_trans, none; 11.88
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehand, spectrin, GAS2, SH3, Plectin, RA_Xylose_Isom, FliD, bZIP, Tropomyosin, Myc-LZ, M, Idh, C, CH, AIP3; TM=M; 11.88
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; mm, hormone_rec, zf-C4, sugar_tr; 11.85
 433470; AW960564; ; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 11.80
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding, THF, DHG_C, YH, THF, DHG_C, CAP, GLY, AAA, LON, Peptidase_C9, bZIP, M, xan_ur_permease, HCO3_cotransp; TM=M; 11.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1, 7tm_2; TM=Y; SS=M; 11.50
 426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (f; none; TM=Y; SS=M; 11.48
 439760; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA; IMPDH_C, IMPDH_N, CBS, Integrin_B, Ricin_B, lectin; 11.38
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none; TM=Y; SS=M; 11.23
 436729; BE621807; ; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 11.18
 409960; BE261944; Hs.339673; hexokinase 1; none, none; 11.02
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3, PDZ, Guanylate_kin; TM=M; 10.78
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofillin_ADF; SS=M; 10.63
 427654; AA410183; Hs.137475; ESTs; ion_trans, vwc, lGFBP, lisp_1; 10.58
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldehyde; TM=M; SS=M; 10.53
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (f; SH3, PH, RhoGEF; TM=M; 10.53
 449437; AJ702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone K; none, none; 10.52
 436856; AI469355; Hs.127310; ESTs; pkinase, rrm; TM=M; 10.48
 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand, CH, Adaptin_N; SS=M; 10.38
 418299; AA279530; Hs.83988; Integrin, beta 2 (antigen CD18 (p95); ly; integrin_B, EGF, PSI; TM=Y; SS=M; 10.35
 431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwc, Integrin_A, FG-GAP; TM=Y; SS=M; 10.34
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA, NB-ARC, PAAD_DAPIN, NA; NA; 10.25
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5; TM=Y; SS=M; 10.18
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365012.1 (Hsa; GPS, 7tm_2; TM=Y; 10.13
 400752; ; NM_003105; Homo sapiens sortilin-related; EGF, fn3, ldl_recept, a, ldl_recept, b, granulin, BNR; TM=Y; SS=M; 10.08
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese, DSPc; TM=M; 10.05
 426728; NM_007118; Hs.171957; triple functional domain (PTPRF Interact; SH3, Ig, pkinase, PH, spectrin, RhoGEF; TM=M; 10.05
 400496; ; ENSP00000224716; GTP-binding protein SAR; none; TM=Y; 10.01
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3, PDZ, Guanylate_kin; TM=M; 10.00
 404568; ; NM_022071; Homo sapiens hypothetical pro; SH2; TM=M; 10.00
 444823; BE262989; Hs.12045; putative protein; Mra1, MBOAT; TM=M; SS=Y; 9.93
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehand, kazal, arf, ltm_1; TM=M; 9.90
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2, SH3; TM=M; 9.90
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53, WD40, IRK; TM=M; 9.88
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase; TM=M; 9.85
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept, a, PKD, MHC_1; TM=M; SS=Y; 9.83
 429238; NM_002849; Hs.19828; protein tyrosine phosphatase, receptor t; Y_phosphatase; TM=Y; SS=M; 9.80
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese, DSPc, Y_phosphatase; TM=M; 9.73
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none, none; 9.73
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPc; TM=M; 9.72
 403912; ; C5000394; gll12737280 (refXP_006682.2) k; none; TM=M; 9.70
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none, spectrin, SH3, PH, CH; 9.70

- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase;TM=M; 9.68
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinasin;fn3_Y_phosphatase;TM=M; 9.63
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M; 9.63
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_P14_kinase;FAT;FATC;TM=M; 9.55
 430259; BE550182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 9.50
 428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none;TM=M; 9.50
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M; 9.50
 448913; AA194422; Hs.22564; myosin VI; mm,zf-RanBP,pkinase,GST_C,Ests,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-
 C2H2,PHD,BTB,TFIS,AT_hook,SAM;TM=M; 9.50
 414911; NM_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40,homeobox,UIM;TM=M; 9.48
 415295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase,DAG_PE-bind,pkinase_C,OPR;none; 9.45
 402328; ; Target Exon; pkinase;TM=M; 9.44
 443710; AI928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha;none; 9.42
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 9.42
 434375; BE277910; Hs.3833; 3-phosphoadenosine 5-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kin;SS=M; 9.40
 418827; BE327311; Hs.47166; HT021; none;TM=M; 9.40
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase;none; 9.35
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20;SS=M; 9.28
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 9.25
 430024; AI808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 9.23
 452656; AI826645; Hs.211534; ESTs; ArfGap,PH,ank,Guanylate_kin,PDZ,SH3; 9.13
 434263; N34895; Hs.44646; ESTs; Ig;none; 9.13
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal_S14,ank,pkinase,death;none; 9.10
 429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase,metalho;TM=M;SS=M; 9.08
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nlem,Integrin_B;SS=M; 9.08
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22,Claudin;none; 9.07
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoeE; 8.98
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M; 8.93
 438000; AI825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M; 8.90
 446620; AA128608; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.90
 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 8.88
 437056; AI147061; ; gbok33a11.s1 Soares_NSF_F8_BW_OT_PA_P_S; none,spectrin,SH3,PH,CH; 8.78
 445496; AB007860; Hs.12802; development and differentiation enhancer; SH3,ank,PH,ArfGap;TM=M; 8.78
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 8.70
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.68
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 8.65
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept; Y_phosphatase;SS=M; 8.65
 430397; AI924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp;TM=Y; 8.64
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD;TM=M; 8.60
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.60
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M; 8.60
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8_HUMAN ALU S; none,7tm_1; 8.55
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG_PE-bind,RBD; 8.43
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none;none; 8.40
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (ma; ank; 8.39
 448209; AW160489; Hs.20709; tetraspan 5; transmembrane4;TM=Y;SS=M; 8.33
 450139; AK001838; Hs.295323; serum/glucocorticoid regulated kinase; none;none; 8.33
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M; 8.31
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm_1;TM=Y;SS=M; 8.30
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK;none; 8.28
 446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA,SK;TM=M; 8.23
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none;none; 8.20
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, for; Ig,pkinase;TM=Y;SS=M; 8.18
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none;none; 8.15
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS,zf-C2H2,SET; 8.15
 417386; AL037228; Hs.82043; D123 gene product; NUDIX_secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 8.13
 431236; AV656840; Hs.285116; interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 8.10
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none;TM=M;SS=M; 8.09
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase,UBA,KA1;TM=M; 8.08
 422573; AW297985; Hs.295726; Integrin, alpha V (vitronectin receptor; FG-GAP,Integrin_A;none; 8.05
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 8.03
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase;SS=M; 8.03
 404891; ; Target Exon; none;none; 7.95
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none;none; 7.93
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin;fn2;TM=Y;SS=M; 7.93
 433211; H11850; Hs.12808; MARK; pkinase,UBA,KA1;SS=M; 7.91
 438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase,ABC1;none; 7.90
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.90
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan_w permease,RA; 7.88
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like,pkinase,Recep_L_domain,YLP;TM=Y;SS=M; 7.86
 405036; ; NM_021628; Homo sapiens arachidonate lip; lipoxigenase,complex1_49kd,PLAT;TM=M; 7.83
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmicn,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 7.83
 431912; AI660552; Hs.76549; ESTs, Weakly similar to A56154 Abl subst; none,Acyl-CoA_dh,Acyl-CoA_dh_M,Acyl-CoA_dh_N; 7.80
 432981; NM_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS,Aa_trans;TM=M; 7.78
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo; Sec7,PH,ANF_receptor,Ig_chan,WD40,IRK; 7.78
 446636; AC002563; Hs.15767; citron (rho-interacting, serine/threonin; CNH,DAG_PE-bind,PH,Involutrin,M;TM=M; 7.78
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept;TM=M;SS=M; 7.78
 400845; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,kil_recept_kil_recept_b,granulin,BNR;TM=Y;SS=M; 7.73
 409142; AL135877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,M,SMC_N,SMC_C,DUF164;none; 7.73
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ_con,Y_phosphatase,SH2; 7.70
 403212; ; NM_018959; Homo sapiens Intersectin 2 (IT; SH3,ethand,C2,PH,RhoGEF;TM=M; 7.70
 441190; H09073; Hs.25046; ESTs; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;none; 7.68

- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7m_1,zf-C3HC4,f3,SPRY,KRAB,zf-C2H2,ve,zf-8_box;TM=Y;SS=M; 7.68
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,pkinase;SS=M; 7.65
- 447898; AW969638; Hs.112318; 6.2 kd protein; none;none; 7.65
- 5 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 7.63
- 401927; ; ; C17000914*.gij8394367[ref]NP_058549.1] s; none; 7.60
- 407347; AA829847; ; gb:rod40d07.s1 NCI_CGAP_GCB1 Homo sapiens; RhoGAP,SH2,pkinase,POLO_box,none; 7.58
- 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3,none; 7.57
- 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 7.55
- 10 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, ty; none;none; 7.55
- 421489; AJ922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
- 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
- 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylatekinase,SRP54;TM=M; 7.50
- 430570; AJ417881; Hs.292464; ESTs; 7m_2,Fz.Frizzled,none; 7.50
- 15 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
- 420676; AJ434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-blind,none; 7.48
- 444252; R21135; Hs.54985; ESTs; none;none; 7.47
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_PI4_kinase;TM=M; 7.47
- 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
- 20 418546; AA224827; ; gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens; vwa,Integrin_A,FG-GAP,none; 7.45
- 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43
- 452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypothet; none,pkinase; 7.40
- 432407; AA221036; ; gb:z03f12r1 Stratagene NT2 neuronal pr; DEAD,helicase_C,rrm,Ndr,Cys_kno1,TIL,vwa,vwc,vwd,IQ,Rila,abhydrolase,TGF-beta,DUF139,TPR,OSPC,isp_1,Ribosomal_S21,rvp;TM=M; 7.40
- 25 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dENN,DENN,uDENN;TM=M; 7.40
- 421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-l; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
- 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 7.38
- 30 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
- 422813; AV656571; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
- 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (; none,spectrin,SH3,PH,CH; 7.25
- 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M; 7.24
- 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
- 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 7.19
- 407591; NM_000910; Hs.37125; neuropeptide Y receptor Y2; 7m_1;TM=Y; 7.18
- 35 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
- 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
- 403344; ; NM_000341;Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
- 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage_CLC;TM=Y; 7.14
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar_br;TM=Y;SS=M; 7.14
- 404875; ; NM_022819;Homo sapiens phospholipase A2; phospholip;SS=M; 7.11
- 40 433618; AA602539; Hs.345494; ESTs; G-alpha_A_deaminase; 7.10
- 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.08
- 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05
- 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05
- 45 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7m_2,HRM,CSD;TM=Y;SS=M; 7.03
- 400211; ; NM_003899;Homo sapiens PAK-interacting ; SH3,PH,RhoGEF,Terpene_synth;TM=M; 7.03
- 438150; AA037534; Hs.342874; transforming growth factor, beta receptor; zona_pellucida,none; 6.93
- 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M; 6.93
- 405275; AB029899; ; mitogen-activated protein kinase 8 inter; Cys_kno1,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
- 50 415392; Z44057; Hs.10957; ESTs; PIP5K,none; 6.89
- 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo_seg,none; 6.88
- 429663; M69874; Hs.211587; phospholipase A2, group IVA (cytosolic ; C2,PLA2_B;TM=M; 6.85
- 427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2_N,helicase_C,Armadillo_seg,HEAT;TM=M; 6.83
- 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M; 6.80
- 55 400158; ; ENSP00000244302; cDNA FLJ11591 fis, clone; Sm;SS=M; 6.78
- 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,Ion_trans,PAC,PAS,none; 6.78
- 400844; ; NM_003105;Homo sapiens sortilin-related; EGF,f3,lJl_recept_a,lJl_recept_b,granulin,BNR;TM=Y;SS=M; 6.73
- 457238; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase; 6.73
- 404440; ; NM_021048;Homo sapiens melanoma antigen.; MAGE;TM=M; 6.73
- 60 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Ets,SAM_PNT;TM=M; 6.70
- 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Priboyliran,OMPdecase;TM=M; 6.70
- 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
- 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;SS=M; 6.64
- 408638; AW451353; Hs.173328; ESTs; B56,none; 6.63
- 65 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
- 401057; BE563198; ; eukaryotic translation elongation factor; Ion_trans,IQ;TM=Y; 6.60
- 446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none;none; 6.60
- 400528; ; NM_020975;Homo sapiens rel proto-oncoge; cadherin,pkinase;TM=Y;SS=M; 6.58
- 418562; R60669; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
- 70 453826; AL138129; ; gb:DKFZp547F152_r1 547 (synonym: htfb1) ; PK,PK_C,none; 6.55
- 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane,none; 6.54
- 415088; AJ077288; Hs.296323; serum/glucocorticoid regulated kinase; none,none; 6.50
- 453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Ets,F5_F8_type_C,pkinase,Ets; 6.47
- 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46
- 75 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46
- 441712; AW391927; Hs.7946; KIAA1288 protein; AIP3;TM=M; 6.44
- 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7m_1; 6.43
- 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 6.43
- 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
- 438941; AF075047; Hs.31864; ESTs; Ca_channel_B,SH3,ar1,none; 6.40
- 80 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB,none; 6.33
- 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothet; lipoygenase,PLAT,none; 6.33
- 433255; AJ274270; Hs.96840; KIAA1527 protein; MHCK_EF2_kinase;TM=M;SS=M; 6.33
- 427801; AW979155; Hs.298275; amino acid transporter 2; Aa_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin, BAG, Tropomyosin; 6.30
 438464; AA659735; Hs.324743; protein phosphatase 4 regulatory subunit; none; none; 6.30
 453977; AA886006; Hs.250427; ESTs; pkinase, P2X_receptor, E1-E2_ATPase, Hydrolase; 6.30
 412491; W31589; Hs.73957; RABSA, member RAS oncogene family; ras, arf, PP2C; TM=M; 6.30
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA_gyraseB, DNA_topoisolV, HATPase_c, DNA_gyraseB, DNA_topoisolV, HATPase_c; 6.29
 404342; ; C7002192*gi|7295207|gb|AA54404.1| (AE0; none; TM=M; 6.27
 409274; NM_003930; Hs.52644; SKAP55 homologa; SH3, PH; SS=M; 6.25
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1, PLM, MAT8; TM=Y; SS=M; 6.23
 405429; ; Target Exon; Y_phosphatase, none; 6.23
 404975; AL042279; ; uncharacterized hypothalamus protein HT0; kringe; TM=Y; SS=M; 6.20
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin, EGF, Ig, Neuregulin, EGF, Ig; 6.18
 446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD, helicase_C, rrm, Ndr, Cys_kno1, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, lrp_1, Ribosomal_S21, rvp; TM=M; 6.18
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3, zf-C3HC4; TM=M; 6.15
 458791; BE154543; Hs.346509; dedicator of cyto-kinesis 1; none; TM=Y; 6.15
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none; none; 6.14
 447727; AI421079; ; tumor necrosis factor receptor superfamily; none, synaptobrevin; 6.13
 401536; ; NM_002530; Homo sapiens neurotrophic ty; lg, pkinase, LRR, LRRNT, LRRCT; TM=M; SS=M; 6.11
 444317; AI140568; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H]; PAN, kringe, trypsin, PI-PLC-X, C2, SH2, PH, SH3, PI-PLC-Y, PAN; 6.10
 427557; NM_002659; Hs.178657; plasminogen activator, urokinase receptor; UPAR, LY6, ET, PLA2_inh; SS=M; 6.08
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; 6.08
 450107; AI873287; Hs.257812; ESTs; ICE_p20, DED; TM=M; 6.05
 418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypotheti; zf-C2H2, BTB, K_tetra, Syntaxin; none; 6.05
 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC_tran, ABC_membrane, PRK, Bac_export_3; TM=Y; 6.05
 439738; BE245502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PS1, Integrin_B; TM=Y; 6.03
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none; none; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese; none; 6.03
 446650; AB016625; Hs.15813; solute carrier family 22 (organic cation; sugar_tr; TM=Y; SS=M; 6.03
 405102; ; C15001220*gi|4469558|gb|AAD21311.1| (AF; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 6.03
 400121; ; Eos Control; SH3, PH, RhoGEF, Terpene_synth; TM=M; 6.03
 415327; H22769; ; gbyrn54c02.r1 Soares Infant brain 1N1B H; SH3, PDZ, Guanylate_kin; SS=M; 6.03
 404148; ; NM_002944; Homo sapiens v-ros avian UR2; ; fn3, pkinase, DUF139; TM=Y; SS=M; 6.03
 405531; ; Target Exon; PDZ, CARD, Guanylate_kin; TM=M; 6.00
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B); NDK; none; 6.00
 427270; H47921; Hs.174139; chloride channel 3; voltage_CLC, CBS; none; 5.99
 423774; L39064; Hs.1702; interleukin 9 receptor; none; TM=M; SS=M; 5.98
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked; pkinase, TBC; 5.98
 411040; AF007393; Hs.177574; protein-kinase, Interferon-inducible dou; HLH; TM=M; 5.95
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer, 7tm_1; none; 5.88
 453902; BE502341; Hs.3402; ESTs; none; none; 5.88
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans; TM=Y; 5.86
 436154; AA764950; Hs.119898; ESTs; efrand, DAG_PE-bind, DAGKa, PHD, DAGKc, PSI; none; 5.85
 455358; AW902641; ; gb:QV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase, Somatomedin_B, Phosphodiesterase; none; 5.83
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxyesterol_BP, pkinase; TM=M; 5.82
 452547; AA335295; Hs.74120; adipose specific 2; LEA; TM=M; 5.82
 415204; T27434; ; gb:hbc2294 Human pancreatic Islet Homo s; Na_Ca_Ex, Calx-beta; none; 5.80
 435563; T210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; 5.78
 456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene; dsrm, FKBP; 5.78
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; TM=Y; 5.77
 436246; AW450563; Hs.119991; ESTs; none, DNA_gyraseB, DNA_topoisolV, HATPase_c; 5.75
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC_tran, PRK; TM=Y; SS=M; 5.75
 425854; AA749190; ; ESTs; RhoGAP, SH2, pkinase, POLO_box; none; 5.74
 424160; T74062; ; gbyc81f01.r1 Soares Infant brain 1N1B H; ROK; none; 5.70
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN, MK; TM=M; SS=Y; 5.69
 437613; R18892; Hs.10267; MIL1 protein; none; none; 5.68
 410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4; TBC; SS=M; 5.68
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase, PBD; TM=M; 5.68
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; 5.63
 406930; U04691; ; gb:Human olfactory receptor (OR17-219) g; none; TM=Y; SS=M; 5.60
 401044; ; Target Exon; none, ICE_p20, ICE_p10, CARD, Peptidase_M1; 5.56
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 5.55
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RRT; none; none; 5.53
 426248; T18988; Hs.293658; ESTs; pkinase; none; 5.50
 418426; NM_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase, death; TM=M; 5.43
 417086; AA194446; ; ESTs, Weakly similar to S55024 nebulin; ; ank, death, ZUS, EGF, kringe, trypsin, Nebulin, LIM; SS=M; 5.43
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupl; 7tm_1, SH2; TM=Y; SS=M; 5.40
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF; SS=M; 5.40
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, com; pkinase, TBC, Rhodanese; TM=M; 5.38
 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 5.35
 411188; BE161168; ; gb:PM04-HT0425-170100-002-a10 HT0425 Homo; adenylatekinase; none; 5.35
 422461; NM_003417; Hs.117077; zinc finger protein 264; zf-C2H2, KRAB, TFIIS; TM=M; 5.28
 426348; BE466586; Hs.17433; hypothetical protein FLJ20967; none; none; 5.25
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPc, Y_phosphatase, Ribosomal_S3_N; TM=M; 5.23
 429592; AB029041; Hs.209646; KIAA1118 protein; Tropoin, Exo_endo_phos, IQ; TM=M; 5.22
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER_lumen_recept, Ribosomal_L11, Ribosomal_L11_N; TM=Y; SS=M; 5.21
 434368; AW519020; Hs.73893; dopamine receptor D2; pkinase, SH3; none; 5.15
 405586; ; NM_000299; Homo sapiens plakophilin 1 (ec; Armadillo_seg; TM=M; 5.13
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase; none; 5.12
 407443; AF227138; ; gb:Homo sapiens candidate taste receptor; none; TM=Y; SS=M; 5.11
 416817; AA398045; Hs.104679; ESTs; Furin-like, pkinase, Recep_L_domain, fn3; none; 5.10
 401888; ; NM_021783; Homo sapiens XEDAR (XEDAR), mR; TNFR_c6; TM=M; SS=M; 5.08
 410314; AW680708; Hs.18851; hypothetical protein FLJ10875; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 5.08

- 401579; AL031447; ; Homo sapiens, clone IMAGE:4053044, mRNA; ; Neur_chan_LBD, Neur_chan_memb, none; 5.05
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-t; PABP, m, pkinase, 14-3-3; 5.05
 417529; AA203634; ; gbzx58b09.r1 Soares_fetal_liver_spleen; ; pkinase, UBA, KA1, none; 5.03
 417527; AA203524; ; gbzx58b10.r1 Soares_fetal_liver_spleen; ; SH3; SS=M; 4.88
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB; TM=M; 4.96
 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid_phosphat; none; 4.93
 404298; ; C6001238*gi121715|p26697|GTA3_CHICK; none, GST_C, GST_N, pkinase; 4.85
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; ; none; TM=M; 4.82
 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran, ABC_membrane; TM=Y; 4.73
 422366; T83882; Hs.97927; ESTs; pkinase, none; 4.64
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; 4.48
 426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fts, clone H; Esterase, enolase, Peptidase_S9; TM=M; 4.45
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 4.40
 400749; ; NM_003105; Homo sapiens sortilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.38
 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4; TM=Y; SS=M; 4.33
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a, PKD, MHC_1; TM=M; SS=Y; 4.31
 400751; ; NM_003105; Homo sapiens sortilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.18
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; SS=M; 3.90
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none, none; 3.88
 458760; AA98631; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3_cotransp, SH3, RhoGAP, xan_ur_permease, FCH; SS=M; 3.85
 441218; BE327561; Hs.202345; ESTs; none, WD40, E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; 3.78
 419073; AW372171; Hs.183918; Homo sapiens cDNA: FLJ12797 fts, clone NT; death, ZU5; SS=M; 3.76
 451385; AA017656; ; gbze39h01.r1 Soares retina N2b4HR Homo; ; Alrophin-1, enolase, Alrophin-1_Y_phosphatase, SH2, fibrinogen_C, TIM; 3.60
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; 3.30
 409582; R27430; Hs.271565; ESTs; none, Neur_chan_LBD, Neur_chan_memb; 3.28
 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1_LC3; SS=M; 3.23
 438740; AW975133; ; gbEST387239 MAGE resequences, MAGN Homo; none, EPH_b, fn3, pkinase, SAM; 3.20
 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked; none, IRK; 3.20
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none, NA; NA; 3.13
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit; none, none; 3.10
 400846; ; sortilin-related receptor, L(DLR class); EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 3.09
 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (f; none, Na_H_Exchange; 3.03
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glx, sugar_tr; TM=Y; SS=M; 3.02
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK, none; 2.98
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death, TNFR_c6; TM=Y; SS=M; 2.93
 401279; ; C13000351*gi12494033|pQ64398|KGDG_MES; none, none; 2.88
 406671; AA12547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema, pkinase, TIG, PSI, none; 2.83
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK; TM=Y; 2.80
 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase; TM=M; 2.75
 441699; AW511126; Hs.127572; ESTs; none, Aa_trans; 2.73
 458781; AJ444821; Hs.63085; ESTs, Weakly similar to MPP3_HUMAN MAGUK; SH3, PDZ, Guanylate_kin, L27; TM=M; 2.73
 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (let; transmembrane4; TM=Y; SS=M; 2.70
 453487; R31770; Hs.56562; ESTs; 7tm_1, none; 2.68
 421279; AW664878; Hs.106645; ESTs; pkinase, none; 2.68
 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none, none; 2.65
 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc; TM=M; 2.63
 422247; U18244; Hs.113602; solute carrier family 1 (high affinity x SDF; TM=Y; 2.62
 425212; AW962253; Hs.171618; ESTs; pkinase, none; 2.60
 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 2.58
 423629; AW021173; Hs.18612; Homo sapiens cDNA: FLJ21909 fts, clone H; voltage_CLC, CBS, none; 2.55
 456737; BE247203; Hs.124831; CGI-67 protein; abhydrolase_2; TM=M; SS=M; 2.53
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1; TM=Y; SS=M; 2.53
 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fts, clone Y7; none, none; 2.50
 448324; A1571356; Hs.34174; ESTs, Moderately similar to ALU8_HUMAN A; ICE_p20, CARD, ICE_p10, none; 2.50
 402256; ; Target Exon; pkinase, UBA, none; 2.43
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fts, clone HE; GDI, 7tm_1, none; 2.40
 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothet; none, spectrin, SH3, PH, CH; 2.40
 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP_binding, lon_trans; TM=Y; 2.35
 419630; W57756; ; gbzd20g10.r1 Soares_fetal_heart_LbNH19W; zf-C3HC4, none; 2.35
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 2.35
 400704; ; Target Exon; lig_chan, SBP_bac_3, ANF_receptor; TM=Y; SS=M; 2.33
 400149; ; Eos Control; acid_phosphat; TM=Y; SS=M; 2.30
 459327; AW149706; Hs.7859; gbzd41d02.x1 NCLCGAP_Bm50 Homo sapien; PHD, PWWP, SET, pkinase, lg; 2.30
 452220; BE158006; Hs.212296; ESTs; Integrin_AFG-GAP, none; 2.25
 416690; H84078; Hs.108551; ESTs; pkinase, none; 2.23
 408354; A1382803; Hs.159235; ESTs; none, none; 2.23
 452203; X57522; ; transporter 1, ATP-binding cassette, sub; ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 2.21
 405093; ; C12001101*gi17522643|p1r|T32733 AMPA g; none, none; 2.20
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; 2.20
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 2.18
 417185; NM_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; Para, fer4_NitH, ArsA_ATPase; TM=M; 2.18
 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 2.18
 413627; BE182082; Hs.246973; ESTs; Armadillo_seg, IBB; TM=M; 2.18
 407415; AF073328; ; gb; Homo sapiens tetracycline transporter-; none, none; 2.15
 450592; A1701555; Hs.202562; ESTs; pkinase, none; 2.15
 428767; A1421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1; ; none, pkinase, lg; 2.15
 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 2.15
 419122; AK01360; Hs.44410; ESTs; ABC_tran, ABC_membrane, none; 2.10
 446420; AW015693; Hs.135614; ESTs; lon_trans, none; 2.05
 420076; AA827860; Hs.293717; ESTs; DUF59, pkinase; 2.05
 409416; AW388359; Hs.10667; ESTs; transmembrane4; TM=Y; SS=M; 2.03
 428766; AA477989; Hs.98800; ESTs; TPR, 7tm_1; 2.03
 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; TM=M; 2.03

453709; AL119133; ; protein kinase C substrate 60K-H; none,histone; 2.03
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00
 456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7m; 1; 1.65
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 588

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

15	414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910644 AA583187 BM272167 AI828996 AA527373 AW972459 AI831360 AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871 AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887 AA455292 AI494230 BF507531 AI492600 AA952596 AW613002 AA293140 AA235549 BF108854 AA954344 NA9682 AI457100 AW589407 AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
20	438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646384 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI070807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H0720 T83523 BI039628 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292856 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA577735 AA037696 AI769516 AW772283 AD010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547950 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 AI133917 BG288151 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA54099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553098 AL548700 AL550751 AL547978 AL545286 AL540843 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE819182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
60	436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA577735 AA037696 AI769516 AW772283 AD010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547950 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 AI133917 BG288151 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA54099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553098 AL548700 AL550751 AL547978 AL545286 AL540843 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895

			AW651691 BM048974 BM043805 BG142185 AA315188 A446615 C06300 BG497644 AA088544 A1815987 BG526631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316986 AA343799 B1870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 AW976398 A1147061 AA765223 AA743380 A1803927 BC012771 BG397153 BF366196 AA337277 AA319285 AW843252 B1030997 AA921874 AW188822 B1027852 A1347618 A1361453 A1088754 AW207491 AAD77391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150780 B1033518 B1027818 BG015789 B1033807 AA341445 T23514 A1655785 T59708 AA224827 T59843 BE156903 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AWB18104 AWB47519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057263 B1861466 AA663341 AA57591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 ALD41698 BF959013 R87170 C16859 BF770411 BF771298 A1075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592 L13288 AA928785 A1608912 AW872978 AA565855 A1022915 A1304920 A1564366 A1568793 A1094557 T60038 R72302 H45409 AA508805 A46356 AA418798 BM129553 BM129126 BM129292 BM128865 A1808418 A1589932 A1806573 BF431808 AW872885 AW166269 H73241 T18182 A1264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 A1797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H450598 AA961010 R73210 R46451 AW884085 B1022902 B1763932 B1910138 NM_003899 D63476 BM456434 AA778936 AA52871 A1052466 AW014138 AA448725 BE673088 AW028198 B1856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333658 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 A1032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 ALD44534 AA258853 B1037915 AA448037 BM461769 B1825965 BE763352 AW167531 Z45588 AV721881 AA527273 A1573219 AA457036 AW439651 AW264418 AA577618 A1802954 AA902292 AA468752 A1380374 AA722690 A1867708 AA916982 A1291576 AW190427 A1338089 A1653744 A1306665 AW513541 AW440077 A1370014 AA904269 AW188378 A1671644 AW193386 A1261832 AA775336 BF436811 A1582703 A1278635 BE440186 AA617898 AA648948 B1491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 A1369564 AW503675 AA777194 BE501048 BF222087 AA042973 A1868087 AA911460 Z41274 A1919082 T16746 AA447634 A1282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916698 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 B1833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG986865 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030 BC000486 BC001930 U15008 NM_004597 BG326561 AV761269 BF212132 BG113313 B1838038 BG944198 BG255198 BG164334 BM013507 AV682717 BF028761 BG755489 BG030141 BG105499 BE440103 BF727449 BM454228 BG912181 BM015197 BG385995 A126579 AW248204 B1857394 B1857319 BG944205 BG323958 B1092930 AV756576 AA280959 BF033078 BE539360 AW247174 BG107836 BE796975 BG170920 A1148142 A1092009 A1336349 AV713409 BF685591 BE160229 AV713166 BE909458 BE743868 BM018218 A1340153 BE792567 BE206806 A1159916 A1184271 BE208585 B1862288 C18760 BG219364 A112677 BE207297 BF754798 AA314384 BE873951 BG207294 A148198 A1338189 A141094 A1308985 BF220098 A143289 BE856397 AA644001 BE675402 A1346708 A1052809 A140082 BF081542 A1342428 A1479625 AA278456 A1750163 BE707501 BG944510 AA314616 AA315774 BF360721 BE738404 AA814194 AA477195 AA932107 F36859 AA363159 BE865458 AA354147 AW904224 A1055855 AA380365 F28474 D59140 AA341946 AA993339 AA323350 F24344 AA374436 BG942061 AA636015 AA852919 T31486 F36334 BG943190 T30319 BG943153 BG941836 T32569 T31160 AA311749 BE710086 BE709911 W23826 BG941639 BF769034 AA026407 AA229555 AV756340 AV714380 AL138129 BG003205 AL138179 B1021773 BE084231 AL520734 B1666852 BF870571 BF945361 BF945354 A1770086 B1861138 A1421079 AL043200 BG683612 AW946265 NM_003899 D63476 BM456434 AA778936 AA52871 A1052466 AW014138 AA448725 BE673088 AW028198 B1856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333658 AW503767 AA305470 AW504819 AA978194 AW500776 BE872488 A1032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 ALD44534 AA258853 B1037915 AA448037 BM461769 B1825965 BE763352 AW167531 Z45588 AV721881 AA527273 A1573219 AA457036 AW439651 AW264418 AA577618 A1802954 AA902292 AA468752 A1380374 AA722690 A1867708 AA916982 A1291576 AW190427 A1338089 A1653744 A1306665 AW513541 AW440077 A1370014 AA904269 AW188378 A1671644 AW193386 A1261832 AA775336 BF436811 A1582703 A1278635 BE440186 AA617898 AA648948 B1491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 A1369564 AW503675 AA777194 BE501048 BF222087 AA042973 A1868087 AA911460 Z41274 A1919082 T16746 AA447634 A1282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916698 AW444935 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 B1833627 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG986865 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030 BM048470 BG983877 N92089 Z43544 F05783 R35182 H22769 H71928 H63921 R94394 AW195830 AA630220 F02030 R60760 R08204 H71929 BE46731 R62568 H63520 H77840 AL515501 F01971 T17168 N55275 AA883505 AW606824 AA704682 N74193 W57593 AW753776 H60439 A1076352 R31485 BE160931 AW130730 BE160869 AW580258 AW902073 BE702158 AW382079 N76884 BF431013 H38156 AW648937 H80573 AW902569 AW902557 AW902654 AW902641 AW902650 AW902741 AW902644 Z25288 R85077 F00323 D82802 T27434 BF184345 AA364846 B1494468 AA775693 BF195801 AA749190 A1480223 BE327332 A1470017 AW628345 A1917472 A1972264 A1375571 A1652583 A1656167 A1983110 BE550378 AW015085 BE552318 A1631475 A1433447 AA534540 A1865480 A1468119 BF110875 AW512059 W58721 AA827482 R59357 AW370493 AA923304 A1660828 AA502611 B1017370 AA039704 W65393 BE938514 W65295 BF919826 B1759440 B1838879 AA336207 F12441 BF171187 BE185031 T74062 AW904410 AA280078 BF919629 AK056605 AK056969 AW380724 AA195950 F21243 Z17422 AA176595 AA176955 AA194350 BC005933 BC017866 AA196396 Z24810 AA181361 AA193115 AA086465 F25194 F30130 AA180013 A1346143 F20589 F20620 F29371 F32439 F25153 F32146 F26110 F28508 F25307 F27533 F20375 F32370 AA653078 BF574897 Z24852 F00172 T30560 AW448925 A1620346 BG986374 BE706521 C02691 AL596834 F31902 F26078 AA670099 BF475555 F30818 F37524 A1346558 F28050 F17933 F31637 C03413 A1092152 AA180743 AA085730 F21998 F20854 F18944 F31180 F37937 F37738 AA193162 Z17344 AA192546 AW821260 BE162466 BE161168 AA203634 AA203524 W88451 AA019761 AA017656 AA017374 AW975133 AA805813 AA729943 BF223647 AA204668 AA256086 BF574707 W57756 AA249070 B1906494 AA248011 BC003160 NM_001610 X12548 BG386685 B1760868 B1559619 BG323829 AU135543 B1834101 AU142120 AU124511 AU124889 AL558171 AU117286 B1824000 BG386610 B1753285 B1223475 AU134828 BM126369 BE206493 BF751498 AL544274 AY007137 B1828921 BE870130 BF771242 B1835451 B1765655 B1820955 B1223344 BG015924 B1759894 AL527413 BF310588 N31870 N23974 BE514914 T48863 AW860257 BF334625 AA883860 AU144168 AA442562 AU159491 AU148353 AA564123 AU148667 A1377256 AW664004 A1871712 A1141486 A1332351 A1339094 BE206109 AW519033 A1817729 A1332490 A1149455 A1857411 A1763154 A1751608 A1377222 A1081956 AW664229 A1275872 AW168546 AA975270 A1367408 A1887729 A1269164 AW105344 BM193081 BE550930 A1082116 AA854691 A1056249 A1221062 A1290113 D51818 AA732409 BG055125 N85878 AU156121
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 5 BF093671 AA053070 T28548 AL570460 BI006862 BI007207 AA373620 W95069 AA629136 AA708164 AJ014885 AW168697 D51623 AA577168
 AI094208 AA028946 AA975078 R16815 BG151132 AI276297 D51676
 BC014081 NM_000593 X57522 L21208 L21207 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519
 BI770023 AL554969 BI489906 AJ304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470
 BG742981 AA279585 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429
 BE858232 AA838610 AI539114 AJ719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404
 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220
 AI819778 AI348733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184
 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619
 BE874601 BF804669 AI574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256
 AW361447 BE788505 AI682892 AA830989 AA852356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601
 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586
 AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H80793 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239
 AA074615 AI291059 AI681053 AA702355 BF439899 AW055166 AI056957 BF223853 AL119659 AI692209 BM312961 AI869297 BE466252 AI292024
 AA402764 AI214620 AA765312 BF380770 AA442682 AL519746 AW295039 AI037878 AW473433 AI499437 AI401618 AI130631 AA427406 AI042138
 BG272488 AI828769 AI828764 AI189390 W84635 AA398496 AA761672 AA699520 AI200406 N68093 AI143913 AA993133 AA613306 AI050971
 AA661905 AA722687 AI749577 AA829345 BG057324 BF001339 AA910169 AA765133 AI360722 AI701849 AI365083 H95974 AI830377 AI312866
 AI370491 BE858907 N62185 AA705746 BE379632 W93803 AI440333 AW367670 AW367640 N77131 BF993216 AI858263 W52329 N68106 R83113
 R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851
 AW367707 AA630879 AA28420 R76236 BG567847 N26931 AA173568 AI073567 AA004957 AI539585 N95093 H99798 H95072 H96853 AA215712
 AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 AI693577 BE181027
 AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734
 R58506

TABLE 58C

Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36461
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84974-85125
405036	7543748	Minus	121957-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03
 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the
 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50th percentile amongst non-malignant tissues. In order to remove gene-specific
 background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the
 ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probe set identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420923	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
416854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	AI093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microseminoprotein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	54.6
428398	AI249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7

5	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	slx transmembrane epithelial antigen of	39.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
15	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	39.0
	447726	AL137638	Hs.19368	matrilin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417087	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
20	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
25	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415539	AI733881	Hs.72472	BMP-R1B	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
30	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AI918950	Hs.123642	EphA3	32.7
35	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
40	406380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	31.4
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H777 transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
45	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023630	Hs.48786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
55	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
	407202	NS8172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
65	403047			NM_005656*:Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AI267700	Hs.317584	ESTs	26.8
	430639	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
70	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
75	400292	AA250737	Hs.72472	BMP-R1B	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448105	AI800470	Hs.171941	ESTs	25.5
80	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW957646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothe	24.5
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
5	418398	AI765805	Hs.26691	ESTs	24.1
	412088	AI689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	24.0
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
10	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypothe	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	22.9
	440260	AI972867	Hs.7130	copine IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
20	450642	R39773	Hs.7130	copine IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970872	Hs.46638	chromosome 11 open reading frame 8	21.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190542	ESTs	21.2
	430887	N56801	Hs.260287	KIAA1841 protein	21.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
40	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157646	Hs.153506	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420611	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
50	411800	N39342	Hs.103042	microtubule-associated protein 18	20.5
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
	424897	D63216	Hs.153684	frizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263:HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	20.3
	429918	AW873986	Hs.119383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
65	441690	R81733	Hs.33106	ESTs	19.9
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PND099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431556	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_008769	Hs.3844	LIM domain only 4	19.2
80	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
	409082	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp5648182 (f	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latadin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001529	Hs.86149	phosphoinositide 3-phosphate-binding prot	18.9

	445929	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
5	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteglycin (osteolinductive factor, mime	18.7
	418819	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443966	Hs.31595	ESTs	18.4
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
20	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439569	AW602166	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424682	AW604804	Hs.151717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
30	431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (tr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	polysium intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
45	421823	N40850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76560	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.159983	ESTs	16.9
55	432966	AA650114	Hs.325198	ESTs	16.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF085833	Hs.135624	ESTs	16.8
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
60	442064	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm51g01.r1 Stratagene fibroblast (B37	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	16.4
	443801	AW208942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
70	409060	AI815867	Hs.50130	neodin (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30098	ESTs	16.0
75	429663	M58874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	16.0
	417094	NM_005895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	V28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AI418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor I	15.5
20	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	15.4
	443674	AI081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW626686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418693	AI750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase	15.1
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288381	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	tumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432308	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AI699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phospholipase-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336695	ESTs	14.7
	403362			NM_001615:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUC1_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proti	14.5
75	410339	AI916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.146858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA158781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
	416836	D54745	Hs.80247	cholecystokinin	14.4
5	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
10	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeldt-Jakob)	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
15	433332	AI357347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	14.1
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
20	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	13.9
	418848	AI820961	Hs.193465	ESTs	13.9
25	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
	439518	W76326		gbzd60d04.r1 Soares_telal_heart_NbHH19W	13.9
	443967	AW284013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
30	447384	AI377221	Hs.40528	ESTs	13.9
	444880	AW118583	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
35	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
40	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139335	ATP-binding cassette, sub-family C (CFTR	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
50	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450315	WB4446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
55	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 5	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
60	410001	AB041036	Hs.57771	kallikrein 11	13.6
	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965*-Homo sapiens phosphoglucomula	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam1	13.6
65	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M68	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
70	445472	AB006831	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN IIII	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
75	447082	T85314	Hs.42644	thioredoxin-like	13.5
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypothi	13.3
80	433517	AW022133	Hs.189838	ESTs	13.3
	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226527	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fls, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
10	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.156880	ESTs	13.2
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68796	Hs.237731	ESTs	13.1
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fls, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI362575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
25	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fls, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fls, clone PL	12.9
30	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 Interacting protein 1; activi	12.8
35	417315	AJ080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW296451	Hs.24605	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	RS2795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
40	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
50	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI568801	Hs.71721	ESTs	12.6
55	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
60	427078	AI676082	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
65	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
70	432205	AI806583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965*:Homo sapiens phosphoglucomuta	12.4
75	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI459306	Hs.24908	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
80	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protein	12.2
	400880			NM_000611: Homo sapiens CD59 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW08762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odt (odd Oz/ten-m, Drosophila) homolog 1	12.1
15	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AI085198	Hs.164226	ESTs	12.0
	434874	NS2448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984625	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730045	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Mais (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheri	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	426981	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheri	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AI472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI038316		gb:cox48c08.x1 Soares_tota_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp5668213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	11.4
75	456804	AI421645	Hs.139851	caveolin 2	11.4
	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEF5_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AI473827	Hs.31793	ESTs	11.3

	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476~g 12737279 ref XP_012163.1	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
10	416913	AW934714		gb:RC1-DT0001-031299-011-e11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
15	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
20	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T86534	Hs.14372	ESTs	11.1
	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
25	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
	425289	AW139342	Hs.155530	Interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
30	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
	412622	AW664708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
35	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104696	KIAA1324 protein	10.9
45	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03878	Hs.158110	immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
50	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290269	ESTs, Weakly similar to I38022 hypotheti	10.9
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI623752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	10.8
55	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	H22953	Hs.137551	ESTs	10.8
	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
60	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
65	450206	AI796450	Hs.201600	ESTs	10.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	met transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
70	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.76400	KIAA0280 protein	10.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
75	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW975944	Hs.237398	ESTs	10.7
	419693	AA133749	Hs.301350	FXFD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
80	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (I	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:poly	10.7

	433923	AI823453	Hs.146625	ESTs	10.7
	418196	AI745649	Hs.26549	KIAA1708 protein	10.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
5	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	AI754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	cathepsin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	AI801098	Hs.151500	ESTs	10.6
	449685	AW286669	Hs.66095	ESTs	10.6
	441111	AI808867	Hs.126594	ESTs	10.6
	436671	AW137159	Hs.146151	ESTs	10.6
15	447974	R76886		gbyif54b03.s1 Soares placenta Nb2HP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-staic aci	10.6
	424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	AI694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284188	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	451900	AB023199	Hs.27207	KIAA0982 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037766	Hs.146085	KIAA1345 protein	10.5
35	402076			C5002020*gl 1082876 pir S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	AI380429	Hs.172445	ESTs	10.5
	443684	AI681307	Hs.55088	ESTs	10.5
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyclin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens prostatic mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-67	10.5
	416182	NM_004354	Hs.79069	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	AI033965	Hs.239926	start-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	AI909154		gb:CV-8T200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	408151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293798	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
	426581	AB040958	Hs.135890	KIAA1523 protein	10.3
75	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13653 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE081916	Hs.125849	chromosome 8 open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
	451593	AF151879	Hs.26706	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:U3-CT0214-291299-052-A12 CT0214 Homo	10.2
5	446553	AB021179	Hs.15299	HMB-Inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
15	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
25	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
30	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
35	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	10.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothe	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA053564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
55	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypothe	9.9
	441054	AA913591	Hs.126460	ESTs	9.9
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31584	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	senrin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yc35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451408	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypothe	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397888	Hs.179982	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
5	404571			NM_015902*:Homo sapiens progesteron induce	9.7
	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278826	Arg/Abt-Interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation Initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-tin	9.7
15	417171	BE613486	Hs.81412	tipin 1	9.7
	421709	AA155394	Hs.107056	CED-6 protein	9.7
	415156	XB4908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409180	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chl	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523939	Hs.165258	ESTs	9.6
	409752	AW963990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.125712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	9.5
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H46008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypothe	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AI636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulin 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
65	412446	AI768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	Intermediate filament protein syncollin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypothe	9.4
	441499	AW298235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923278	Hs.280905	ESTs, Weakly similar to protease [H.sapi]	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93795	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-Interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
80	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (tr	9.3
	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW530488	Hs.325820	protease, serine, 23	9.3

	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
5	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
	428465	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D86960	Hs.3510	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558			ENSP00000220478*:SECRETORANIN III.	9.2
15	428634	AA811845	Hs.106290	Ketch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450606	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
20	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
25	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (9.1
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
30	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
35	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
40	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
45	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
50	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [H.sapi	9.0
	405523			C8001409*:gij7441226[pln]S31212 collage	9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
55	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.9
60	414917	CD4863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA768268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
65	426158	NM_001982	Hs.199087	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	425490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
70	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502663	Hs.145037	ESTs	8.9
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
75	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostosins (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (senarin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
80	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97111.s1 NCL_CGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	A940675	Hs.20914	hypothetical protein FLJ23056	8.8
5	431705	A816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	necln 3; DKFZP56680846 protein	8.8
	444647	H14718	Hs.11506	Human clone Z3589 mRNA sequence	8.8
	444858	AJ199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN III	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, tota	8.8
15	424113	AJ743880	Hs.12876	ESTs	8.8
	459324	AW080953		gbxc28c12.x1 NCL_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypotheti	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALUA_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AJ929602	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA564489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	P1BF1 gene product	8.7
	430848	AW021726		gbx2f2e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypotheti	8.7
40	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	8.7
	427723	AJ355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45	447335	BE617685	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424783	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.108363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434054	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60	426907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AL077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

5	434747	AA837085	Hs.220585	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
	450813	A1739625	Hs.203376	ESTs	8.5
	413956	A1821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypothe	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
10	432620	AA777749	Hs.5978	LIM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 Interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	A1821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
	448474	A1792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
	421622	A8037748	Hs.106204	KIAA1327 protein	8.4
25	431160	AW971174	Hs.324330	ESTs	8.4
	449567	A1990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	VW domain binding protein 4 (formin bind	8.3
30	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425892	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431952	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	toll-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433815	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	A1799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450:Homo sapiens four and a half L	8.3
	436879	A1127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothe	8.3
	453121	A1968264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434O0921 (f	8.3
50	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (els domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	8.2
	432695	D63480	Hs.276634	KIAA0146 protein	8.2
	407300	AA102816		gb:zn43e07.s1 Stratagene HeLa cell s3 93	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN III	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypothe	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
65	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypothe	8.2
70	408108	A1580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	A1824719	Hs.328700	ESTs	8.2
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 598

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
5	411667	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	416913	163001_1 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	418866	179788_1 T65754 AA229857 AA229658
	418876	179960_1 AA740616 AA654854 AA229923
	419536	185688_1 AA603305 AA244095 AA244183
10	419544	185760_2 AI909154 AA526337 AA244193 AI909153
	423800	232161_1 AA331156 AA331157 AA331155
	426413	266650_1 AA377823 AW954494 AJ022688
	429163	300543_1 AA884766 AW974271 AA592975 AA447312
	430848	324621_1 AW021726 AA487752 AA488085
	431121	328275_1 AW971157 AA492575 AA492520
15	432189	342819_1 AA527941 AI810608 AI620190 AA635266
	432600	350959_1 AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	434415	385931_1 BE177494 AW276909 AA632849
	434579	38916_1 T55958 T57205 AF147346
20	439518	47334_1 W76326 AF086341 W72300
	443161	561305_1 AI038316 AI344631 AI261653
	447974	745643_1 R76886 AJ453674 R77049

TABLE 59C

25	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
30	NI_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NI_position
	400860	9757499	Minus	151830-152104,152649-152744
35	400880	9931121	Plus	29235-29336,36363-36580
	401197	9719705	Plus	176341-176452
	401424	8176894	Plus	24223-24428
	401519	6649315	Plus	157315-157950
	401558	7139678	Plus	103510-104090
40	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	402076	8117410	Plus	128316-128627
	402812	6010110	Plus	25026-25091,25844-25920
45	402855	9662953	Minus	59763-59909
	403047	3540153	Minus	59793-59968
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403149	9799833	Plus	25034-25185
	403362	8571772	Plus	64099-64260
50	404210	5006246	Plus	169926-170121
	404571	7249169	Minus	112450-112648
	404641	9796810	Minus	32247-32362
	404642	9796810	Plus	102999-103145
55	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos HuO3 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

65	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
70	R1:	Ratio of prostate tumor to normal adult body tissue			
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	426747	AA535210	Hs.171995	kalikrein 3, (prostate specific antigen	56.6
	419526	AI821895	Hs.193481	ESTs	56.2
75	420154	AI093155	Hs.95420	JM27 protein	44.0
	432441	AW292425	Hs.163484	ESTs	41.9
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
	431616	AA508552	Hs.195839	ESTs, Weakly similar to 138022 hypopheli	37.9
	400299	X07730	Hs.171995	kalikrein 3, (prostate specific antigen	36.0
80	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
	400298	AA032279	Hs.61635	stx transmembrane epithelial antigen of	30.0
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 lino-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TR-HY_HUMAN TRICH	27.9
	432101	AI918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_001172:Homo sapiens arginase, type II	24.5
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
15	407709	AA456135	Hs.23023	ESTs	20.0
	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
20	410929	HA7233	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	AI972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	425918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW450461	Hs.203965	ESTs	14.4
40	431548	AI834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	14.3
	430187	AI799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
50	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
55	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249368	Hs.98558	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	12.2
	443960	AI093577	Hs.255416	hypothetical protein FLJ21888	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	latexin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AI077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	11.9
70	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AI821085		gb:ns95a12.y5 NCL_GCAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	11.6
75	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218886	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	11.5
80	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AJ733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293572	ESTs, Weakly similar to ALUB_HUMAN IIII	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415263	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
15	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI699973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021955*:Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fs, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fs, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.5484	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CAMP-sialic aci	8.2
65	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BMO4	7.8
	453160	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fs, clone PL	7.6

	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
5	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AJ750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040856	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AJ918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278595	Homo sapiens prostein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI088489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homeo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AJ345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AJ077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
50	439492	AF086310	Hs.103159	ESTs	6.8
	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI732230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15787	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
60	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB039670	Hs.9728	ALEX1 protein	6.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA861697	Hs.120591	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystokinin	6.6
70	447033	AI357412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCI_OGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
75	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
80	421077	AK000061	Hs.101590	hypothetical protein	6.4
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76655	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	6.3
	453390	AA662496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively spliced	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	6.3
	433610	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AI922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
15	425465	L18964	Hs.1904	protein kinase C, iota	6.2
	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AI800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
20	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
25	437323	AA371145	Hs.194397	leptin receptor	6.1
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFpZ727C191 (fr	6.1
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
30	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFpZ434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AI652236	Hs.49376	hypothetical protein FLJ20844	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmegin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	405523			C8001409:gil7441226 pir J531212 collage	5.9
50	448807	AI571940	Hs.7549	ESTs	5.8
	404642			NM_021965:Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414528	AA148950	Hs.188836	ESTs	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE278738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063563	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AI739825	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AI364186		gb:qw34h07.x1 NC_CGAP_U14 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970976	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCL CGAP_Alv1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	AI241733	Hs.43871	ESTs	5.4
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AI459306	Hs.24908	ESTs	5.4
15	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
20	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (I	5.4
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
25	412677	AW029608	Hs.17384	ESTs	5.3
	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	AI829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 ferri	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	AI278802	Hs.25661	ESTs	5.3
	441102	AA973905		intermediate filament protein syncoilin	5.3
35	453387	AI990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	AI823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
	447574	AF162666	Hs.18895	tousled-like kinase 1	5.2
40	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	5.2
	429467	NM_004477	Hs.203772	FSHD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	toll-like receptor 5	5.2
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA889120	Hs.110637	homeo box A10	5.2
55	448944	AB014605	Hs.22589	atrophin-1 interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	448795	AI797713	Hs.156471	ESTs	5.1
	407300	AA102618	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.1
60	432340	AA534222		gb:nj21d02.s1 NCL CGAP_AA1 Homo sapiens	5.1
	448469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	5.1
	453293	AA382267	Hs.10863	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409643	AW450866	Hs.257359	ESTs	5.1
65	427723	AI355260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE483721	Hs.97101	putative G protein-coupled receptor	5.1
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068658	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
	433023	AW864793	Hs.87409	thrombospondin 1	5.0
80	433862	D86960	Hs.3610	KIAA0205 gene product	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	AI734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
15	417407	AA923278	Hs.290905	ESTs, Weakly similar to proleuse [H.sapi	4.9
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
20	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
25	424332	AA338919	Hs.101615	ESTs	4.9
	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245687	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	F-box and leucine-rich repeat protein 4	4.8
	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA453208	Hs.262960	RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*:SECRETORANIN III,	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.7
	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALUB_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403046			NM_005656*:Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	4.6
	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
80	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6

	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	448183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
5	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
	432093	H28383		gb:U52c03.r1 Soares breast 3NbHBst Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
10	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
15	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI532683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
20	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF069214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
25	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
30	414272	AI651603	Hs.46988	ESTs	4.5
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
35	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	4.5
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C150004766:gi12737279ref XP_012163.1	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
40	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	4.4
	433517	AW022133	Hs.189838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
45	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
50	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
55	448768	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
60	434022	R18374	Hs.117956	ESTs	4.4
	422365	AF035537	Hs.116521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
65	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
70	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
75	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb:wd73f12.x1 NCL_CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
80	420405	AA743396	Hs.189023	ESTs	4.3
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155694	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
5	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629666		ESTs, Weakly similar to S64054 hypothet	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
10	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulon 3	4.2
	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
15	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!!	4.2
	450546	AA010200	Hs.175551	ESTs	4.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
20	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
	447439	AA313555	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449885	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
25	450377	AB033091	Hs.74313	KIAA1265 protein	4.2
	419647	AA348947	Hs.91816	hypothetical protein	4.2
	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW969657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
30	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
35	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.1
	447752	M73700	Hs.105938	lactoferrin	4.1
	402855			NM_001839*:Homo sapiens calponin 3, acid	4.1
	443161	AJ038316		gb:ox48c08.x1 Soares_tota fetus_Nb2HF8_	4.1
	415827	H17462	Hs.23079	ESTs	4.1
40	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161690	ESTs	4.1
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AJ335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
45	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239499	KIAA0185 protein	4.1
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
50	410763	AF279145	Hs.8968	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
	423698	AA329798	Hs.1098	DKFZp434J1813 protein	4.1
	428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
55	425211	M18667	Hs.1887	progastricsin (papsinogen C)	4.0
	443273	AJ042063	Hs.132156	ESTs	4.0
	428055	AA420564	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AI457338	Hs.29894	ESTs	4.0
60	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441768	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
65	409706	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
	418594	AJ732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
70	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	4.0
	452387	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
75	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW277121	Hs.254881	ESTs	4.0
	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
80	400695			C11002514:gi11280151 ph E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (senbtrn)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.s	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
5	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGCS338	3.9
	431147	A1767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0982 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.9
	442320	A1287817	Hs.129636	ESTs	3.9
15	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
20	437916	BE565249	Hs.20999	hypothetical protein FLJ23142	3.9
	442242	AV547908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:aa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280699	ESTs	3.8
	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
35	443484	AI091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U83139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
50	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW105663	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
65	448207	AI475490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
	432606	NM_002104	Hs.3068	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.43418	ESTs	3.7
70	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
	408312	AF263613	Hs.44198	Intracellular membrane-associated catcli	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151048	hypothetical protein FLJ11193	3.7
	424882	AI379461	Hs.153635	far upstream element (FUSE) binding prot	3.7
75	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
80	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AW831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA: cDNA DKFZp566M0947 (I	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.7
	445941	AI267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochondrion)	3.6
10	412533	AA679863	Hs.69606	ESTs	3.6
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721.67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AA75858		gb:tc87d07.x1 NCL CGAP CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to)	3.6
15	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZp566B0846 protein	3.6
20	406815	AA833930	Hs.288036	IRNA isopenentenylpyrophosphate transferase	3.6
	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN IIII	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
25	433887	AW204232	Hs.279522	ESTs	3.6
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acidic)	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
30	435703	AW630133	Hs.83313	GK003 protein	3.6
	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothetical	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (AF1)	3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
35	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc finger	3.6
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypothetical	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944.1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55958		gb:yc35f05.r1 Stralagene fetal spleen (9)	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN 2	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:oc44f08.s1 NCL CGAP_GCB1 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro)	3.5
	419440	AB020889	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA523939	Hs.165258	ESTs	3.5
	410762	AF226053	Hs.68170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic subunit	3.5
55	420390	AA330047	Hs.191187	ESTs	3.5
	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
60	413950	AA249096	Hs.32793	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin)	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
70	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
75	432589	AL135725	Hs.131708	ESTs	3.5
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI824707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositide 3-phosphate-binding protein	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

	456497	AW987956	Hs.123648	ESTs, Weakly similar to AF108460.1 ublru	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
5	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
10	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AJ969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AJ215632	Hs.147487	ESTs	3.4
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.4
	434966	AA657494		gb:nt66104.s1 NCL_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902:Homo sapiens progesterin induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
20	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheti	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056:Plasma membrane calcium	3.4
25	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	443603	AJ855682	Hs.197698	ESTs	3.4
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437387	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
30	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.4
	430144	AJ732722	Hs.187694	ERGL protein; ERGLC-53-like protein	3.4
	415292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
35	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
40	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AJ058769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
45	442910	AJ365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
50	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
55	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79963	ESTs	3.4
	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDK2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
60	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
65	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AJ807320	Hs.227630	RE1-silencing transcription factor	3.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
70	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
75	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AJ064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263:HSPC213.	3.3
80	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_tetal_fetus_Nb2HF8_	3.3
	400880			NM_000611.Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H56195	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (tr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	3.3
	432363	AA534489		gb:mf76g11.s1 NCL_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE325276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AI077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulin 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chal	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	OGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.2
80	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI635386	Hs.142848	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450563	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
	408784	AW971350	Hs.63386	ESTs	3.2
15	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, Immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
20	426891	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128506	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
25	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08288	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE939767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA099249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII	3.1
	425071	NM_013989	Hs.154424	deiodinase, Iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.67159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gbzo65a02.r1 Stralagena pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
70	438979	AW976218	Hs.32565	ESTs	3.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29569	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.68474	ESTs	3.1
5	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc26a07.s1 NCL CGAP_Prl Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
	430280	AA361258	Hs.237868	Interleukin 7 receptor	3.0
15	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
	422788	AL117352	Hs.77196	Human DNA sequence from clone RPS-876B10	3.0
20	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805365	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	A1355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW898533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCL CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIR protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

80

TABLE 60B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number		
Accession: Genbank accession numbers		
Pkey	CAT Number	Accessions
5	411479	1247077_1
	411667	1253334_1
10	414372	143909_1
	414680	147525_1
	415989	156454_1
	416288	1585983_1
15	416882	162718_1
	416913	163001_1
	417379	167238_1
	418304	173658_2
	418647	177521_1
20	418866	179788_1
	419536	185688_1
	419544	185760_2
	423412	228001_1
25	423800	232161_1
	426226	262918_1
	426413	266650_1
	426503	268283_1
	426775	271683_1
30	426991	27415_1
	428342	290035_2
	429163	300543_1
35	429220	301384_1
	429258	301917_1
	430935	325772_1
	430968	326269_1
	431429	33313_1
40	432093	341283_1
	432125	341776_1
	432189	342819_1
	432340	345248_1
45	432363	345469_1
	432600	350959_1
	432810	354375_1
50	434579	38916_1
	434966	396504_1
	435023	398093_1
	437866	44433_2
55	438147	45074_1
	439092	468554_1
	439518	47334_1
	439904	479942_1
60	440840	50357_2
	441102	509604_1
	442562	54500_2
65	443161	561305_1
	445808	65133_1
	447082	707248_1
	448212	755099_1
70	449625	8113_1
	450580	83929_1
75	450582	83933_1
	452260	9074_1
	452598	92338_2
80	452815	93255_1
	453802	981589_1
	455100	1253334_1

457728 393853_1 AW974811 AA651634 AA650072

5 TABLE 60C

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400684	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9795668	Plus	45096-45229
404641	9795810	Minus	32247-32362
404642	9795810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

35 Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

45 Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*-HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW860709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	della (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (catle) glucose Induc	3.1	8.0
417407	AA923278	Hs.290906	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032859	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	6.1	6.1
437147	AL049564	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	3.3	5.9
	431548	A1834273	Hs.9711	novel protein	15.7	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
10	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5	5.5
	414516	AJ307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
15	451684	AF216751	Hs.26813	CDA14	3.9	5.4
	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
20	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
	444917	R68551	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
25	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
	433560	AJ925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
	421623	N40850	Hs.26625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AJ470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
30	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.35598	ESTs	5.4	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421853	AJ952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
35	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AJ685464		gbctt88f04.x1 NCI_OGAP_Pr28 Homo sapiens	9.1	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476:gij12737279[ref]XP_012163.1}	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
40	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	F5HD region gene 1	2.1	4.6
	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AJ676062	Hs.111902	ESTs	4.8	4.5
45	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
50	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
	428826	ALD46842	Hs.194019	atractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
55	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gbtzd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA577577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
60	443622	AJ911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AJ879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
65	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433687	AW204232	Hs.279522	ESTs	4.1	4.1
	436556	AJ364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443646	AJ085198	Hs.164226	ESTs	4.1	4.1
70	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
	433409	AJ278902	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KIX 18)	3.9	3.9
75	444755	AA431791	Hs.113823	CtpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9	3.9
80	423337	NM_004655	Hs.127337	axin 2 (conductin, axl)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
10	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AI263307	Hs.239884	H2B histone family, member L	9.2	3.8
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7	3.7
15	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AI571940	Hs.7549	ESTs	3.8	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
	451009	AA013140	Hs.115707	ESTs	4.1	3.6
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AI357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
25	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoi	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOK 4, clone HF.1	2.2	3.5
30	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AI918950	Hs.123642	EphA3	16.5	3.5
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78978	Hs.7314	KIAA0614 protein	2.1	3.5
35	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
40	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
45	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
50	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
55	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21058	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
	444489	AI151010	Hs.157774	ESTs	3.2	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
60	453078	AF053551	Hs.31584	metaxin 2	2.1	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCL_CGAP_Alv1 Homo saplens	2.1	3.1
	445840	AI277811	Hs.146291	ESTs	3.1	3.1
65	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
70	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
	420154	AK093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
75	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
80	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response S-8	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HU01 debrisqu	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 ferti	2.9	2.9
5	428500	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (I	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
15	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calcisarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-Interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
20	433865	N29862	Hs.44104	ESTs	2.8	2.8
	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW834714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654650	Hs.282906	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-Interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
35	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (senb1n)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191050	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
70	431474	AL133990	Hs.190642	ESTs	9.3	2.5
	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005655:Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protel	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_tetal_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
15	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
20	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
25	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
	426180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
40	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfor1)	4.1	2.3
	421069	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gi4507689[ref]NP_003298.1[tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	428277	AW452016	Hs.127863	ESTs, Weakly similar to SFRA_HUMAN SPUC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478*:SECRETORANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	toll-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 ferri	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGCI5548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGCA309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

5	422424	AI188431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770688		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
	404541			NM_021965*:Homo sapiens phosphoglucomuta	2.2	2.2
10	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008:gi 7303957 gb AAAF59000.1 (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
15	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kd	2.1	2.1
20	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
	452959	AI933416	Hs.189674	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251945	poly(A)-binding protein, cytoplasmic 14	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
35	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	Integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kd)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246973	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	409219	AA393383	Hs.133331	ESTs	2.1	2.0
	419988	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T96231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9186	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odc (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
	433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0
80						

TABLE 61B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150955 BE455475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 W04957 W63876 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581956 AA789002
15	424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA889300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290558 C15404
	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 C04967 C03045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW295554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T613
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
40	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
	401197	9719705	Plus	176341-176452
	401519	6649315	Plus	157315-157950
45	401558	7139678	Plus	103510-104090
	402802	3287156	Minus	53242-53432
	403047	3540153	Minus	59793-59968
	404641	9796810	Minus	32247-32362
	405685	4508129	Minus	37956-38097
50	406068	9114084	Plus	382-543

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
65	R1:	Ratio of prostate tumor to normal prostate tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
75	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	12.6
	401187			ENSP00000229263:HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
80	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449155	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE568568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	sfil (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.105768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTAD0151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
20	425174	D87450	Hs.154978	KIAA0261 protein	8.6
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	ectinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000543	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AI590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
	451957	AJ796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166458	programmed cell death 5	6.6
65	429490	AJ971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AJ350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AJ499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.263713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418196	AJ745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447955	AW292577	Hs.94445	ESTs	5.9

	449118	R67477	Hs.23103	Bcl1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	5.9
	431548	A1834273	Hs.9711	novel protein	5.8
5	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
10	435080	A1831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157845	Hs.48793	slatyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
15	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA905097	Hs.85050	phospholamban	5.7
	445467	A1239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
20	405672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
25	414516	A1307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
30	458079	A1796870	Hs.64277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KJAA0856 protein	5.4
	449907	AA004825	Hs.103281	ESTs	5.4
35	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	A1088691	Hs.208414	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	5.3
40	403851			C5002154*:g17299015[gb]AAAF54217.1[AE0	5.3
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
45	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
	407902	AL117474	Hs.41181	Homo sapiens mRNA: cDNA DKFZp727C191 (tr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
50	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
55	414212	AA136569	Hs.10848	KJAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
60	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GLD04 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
65	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	A1925195	Hs.130891	hypothetical protein MGC4400	5.0
	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
70	425397	J04088	Hs.156348	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
	453370	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
75	452323	W44358	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KJAA0010 gene product	4.8
80	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gbtt88f04.x1 NCL_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476*.gij12737279[ref]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123060	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46987	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:z85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	438446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA278530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW087805	Hs.172665	methylene tetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	4.2
	408554	AA838381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79888	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b57	4.2
	439518	W76326		gb:z85d04.r1 Soares_fetal_heart_NbH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA308105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AM58213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411868	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF069214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10589	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI384997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83383	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
40	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	CipX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abi subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122669	KIAA0264 protein	3.8
	403100			C2001027*gl 7296271 gb AA51582.1 (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW984806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.182245	ESTs	3.8
	432908	AI861896	Hs.304505	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	A1263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	A1566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	445554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	A1940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	A1571940	Hs.7549	ESTs	3.7
15	413403	AA129106	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	A1671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	Inhibitor of growth family, member 1-lik	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	A1361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	A1193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	A1077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	A1692181	Hs.49169	KIAA1634 protein	3.6
	433269	A1343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	A1357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	A1452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350:gi 6578126 gb AAAF17706.1 AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieti	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446418	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	A1918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M80721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb y12c04.r1 Soares Infant brain 1N1B H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0514 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	A1765082	Hs.48317	ESTs	3.5
	422673	N59027		gb yv59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
	401744			Target Exon	3.4
75	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

	432741	AI732358	Hs.185118	ESTs, Moderately similar to A37413 catb1	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
5	428466	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
10	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
15	431689	AA305688	Hs.267695	UDP-GalNAc4-epimerase beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
	403389			C3001393*:gij3327090[dbj]BAA31613.1[AB	3.3
	40749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
20	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
25	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
30	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
35	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6831	hypothetical protein FLJ20373	3.3
	450094	AJ174947	Hs.295789	Homo sapiens mRNA: cDNA DKFZp564D1164 (f	3.3
40	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AJ552236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
50	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
55	439047	AW979177		gb:EST391287 MAGE rasequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
60	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	AJ336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
65	433561	BE540937	Hs.20104	hypothetical protein FLJ000052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
70	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AJ381659	Hs.267086	ESTs	3.2
	424894	H83520	Hs.153678	reproduction 8	3.2
80	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 88	3.2
	410531	AW752953		gb:OVD-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metadn 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277552	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177654	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
	445840	AI277811	Hs.146291	ESTs	3.1
20	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp4341216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntadn 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
	403423			Target Exon	3.1
30	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
	422481	AL050163	Hs.117339	DNA-X-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB028015	Hs.54886	phospholipase C, epsilon 2	3.1
40	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE283466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
80	426448	R08054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochond	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411952	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AJ333439 AJ741845 AJ674468 R44190 R52535 R52617 AI220925 AJ979148 AJ744688 AW242437 AA618148
414680	147525_1	AI983837 AA399623 AI676204 AJ420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
415528	1539409_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
416128	157163_1	AA708749 AA644620 AA652769 AA242975 AA151074 T19890
416882	162718_1	R17236 R52580 F11642
422673	219674_1	AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
426448	267323_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AJ748815 AI763294 AI333114 AI277384 AJ088297 AI468477
430935	325772_1	AI824624 AW189606 AI631751 Z40749 AJ984673 AI671316 AA189024 AW235412 BE1784
430968	326269_1	N59027 AA314694 N53937 R08100
431304	331286_1	R06054 AA378789 AW956453
431676	336411_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
432125	341776_1	AW972830 AA527647 AA489820 AA570362
432363	345469_1	BE157283 BE157287 AA502438
437158	43392_5	AI685464 AW971336 AA513587 AA525142
437866	44433_2	AW972667 AA526539 AI057032 AW167842
439047	468139_1	AA534489 AW970240 AW970323
439518	47334_1	AW090198 AW173544 AW439860 AW007307 AI762577 W85516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
450508	836_1	AI801808 AW611634 AI393606 AW235356 AW000736 AW458599 AI582546 AA962057 AA523012 AW51
450580	83929_1	AA156781 AW239839 U52054 AA024953 AA778446 BE073977 AW444904 AW602574 BE164040 BE163972 BE163974 BE163992
452260	9074_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
453024	944876_28	AW979177 AA846994 AA829672
455473	1292917_1	W76326 AFD86341 W72300
456719	222707_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA095372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AJ671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718468 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984802 AW984800 AW984799 AW984825 AW984792 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-63628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39524-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

5

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75th percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75th percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

10

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

15

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal prostate tissue to prostate tumor tissue

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Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1958	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	A1738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	A1791314		gb:ae46g12y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AJ459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		Interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.256720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AJ280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936g13746443[gb]AAC63989.1 [AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523846	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N1B H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*:Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	A1218950	Hs.125461	hypothetical protein FLJ11539	4.1
5	425094	A1955956	Hs.21417	ESTs	4.1
	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	A1028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172:HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
15	449233	BE048401	Hs.196511	ESTs	3.9
	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	A1821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
20	409679	BE250521		ras homolog gene family, member A	3.8
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutaryl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:mp86b01.s1 NCL_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene	3.8
25	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
	443313	A1796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gilj6679124[ref]NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
30	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gilj12654691[gb]AAH01185.1 AAH0	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
35	436524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
40	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AJ222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
45	442097	AW015799	Hs.128474	ESTs	3.6
	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
50	400749			NM_003105*:Homo sapiens sortilin-related	3.6
	450295	AJ766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCL_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	429043	AJ824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AJ371978	Hs.128326	ESTs	3.4
60	445045	AJ652676	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KIAA1578 protein (Fragm	3.4
	445797	AJ253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	AJ625304	Hs.190312	ESTs	3.4
	442027	AJ652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gilj2695979[emb]CAA70854.1 (Y0	3.4
70	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AJ420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
75	418872	L44284	Hs.12915	ESTs	3.3
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypothi	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
80	458539	AJ733837	Hs.145661	ESTs	3.3
	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
5	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QVO-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
10	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:ym99h03.r1 Soares adult brain N2b5HB5	3.1
	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AI010063	Hs.343603	tin-cap (telothorin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
15	451686	AA059246	Hs.110293	ESTs	3.1
	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
20	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien	3.1
	402490			Target Exon	3.1
25	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
30	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
35	405422			ENSP00000216658*:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
40	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
45	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
	407275	AI364186		gb:xqw34h07.x1 NCL_CGAP_U14 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
50	449245	AI636539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058058	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
55	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp7611071 (fr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
60	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
65	419896	Z99382		gb:HSZ99362 DKFZpharmy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipooxygenase 3	2.9
	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
70	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
75	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCL_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:zt99b10.s1 Soares_testis_NHT Homo sap	2.8
	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
80	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALL6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433565	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:z53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.106362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gil7242973[jdb][BAA92547.1] (AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	Hs.201201	ESTs	2.7
	450044	R66444	Hs.51891	ESTs	2.7
20	403630			C3001708*:gil4758028[ref][NP_004360.1] co	2.7
	445514	AJ241280	Hs.148906	ESTs	2.7
	446362	AW612481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067952		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	Hs.199291	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcophilin	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hibr1)	2.7
	405678			CX001454:gil8393794[ref][NP_058681.1] myo	2.7
	432789	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R18046	Hs.5010	gb:yg21f11.r1 Soares infant brain 1NIB H	2.7
	402844			C1000118*:gil9951913[ref][NP_052832.1] pr	2.7
	456666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	441975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087887	Hs.42696	EST	2.7
	415642	U19878	Hs.338224	transmembrane protein with EGF-like and	2.7
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AJ792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AJ345985	Hs.127383	ESTs	2.6
	415054	AJ733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293896	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		wee1 (S. pombe) homolog	2.6
	426629	AJ203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30509	ESTs	2.6
	412281	AJ810054	Hs.141119	ESTs	2.6
65	434898	AW500458	Hs.28956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AJ215667	Hs.175044	ESTs	2.6
	438648	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW299506	Hs.232777	ESTs	2.6
	443650	AJ699330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AJ076262	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MR0-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AJ734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:xx57d07.s1 NCI_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	406003		Target Exon	2.6
	459584	AI910884	ESTs	2.6
	441597	AW135032	ESTs	2.6
5	411280	N50617	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	tumor necrosis factor receptor superfam	2.6
	445060	AA830811	ESTs	2.6
	436260	BE172762	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	hypothetical protein FLJ21120	2.6
10	401716		C16000902.gi403440.gb AAA73168.1 (M817	2.6
	416628	W03955	gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	ESTs, Weakly similar to I38022 hypotheti	2.6
	440702	AA904178	ESTs	2.6
	456310	AA225522	gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	ESTs	2.6
	455737	BE072248	gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	ESTs	2.6
	408432	AW195262	gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	ESTs	2.6
20	441053	AA913819	ESTs	2.6
	455505	AW970640	ESTs	2.6
	453491	AL040177	gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749	gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	HIV-1 Rev binding protein	2.6
25	444130	AI125263	ESTs	2.5
	422210	BE269319	steroid dehydrogenase-like	2.5
	424241	AW995948	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	AlE-75 binding protein protein	2.5
	400427	AB044934	histamine H4 receptor	2.5
30	410443	BE062906	KIAA1546 protein	2.5
	455210	AW866599	gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	CGI-203 protein	2.5
	441191	AI693930	ESTs	2.5
	413489	BE144228	gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	ESTs	2.5
	419354	M52839	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	ESTs	2.5
	450724	R55428	gb:yj79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	ESTs	2.5
	412671	AW977734	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146	gb:43111 Human retina cDNA randomly prim	2.5
45	404678		Target Exon	2.5
	408520	AA225063	ESTs	2.5
	411332	AW837212	gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	alkylglycerone phosphate synthase	2.5
	429906	AL080137	ESTs	2.5
50	433712	AF090887	Homo sapiens clone HQ0085	2.5
	438353	BE539951	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048462_1	AW176091 H24234
	408432	1058687_1	AW195262 R27868 AW811262
	409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AI221491 AA194239 D63046 AA193426 AA773243 AA193293
65	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW760178 BE163491 BE073763 BE073871
	411320	1238624_1	AW836646 AW836580 AW836610 AW836635 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411355	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
70	411829	1260309_1	AW865749 BE179419 BE179492
	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
75	415054	151827_1	AI733907 AA159708 AI732614
	415098	1522174_1	D59687 D59694 D59656 D59589
	415131	1523680_1	D61119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35694 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	419896	1888662_1	Z99362 Z99363
	420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538358 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599
			C02215 AI6525
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632553
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
	436190	41555_1	AK001059 AA633055
15	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
	447518	724787_1	T80061 AI382804
20	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
25	452351	91233_1	AA025647 R45716 AW763786
	453412	986264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866811 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072256 BE072211 BE072242
	455791	1355954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698
	455887	1380836_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
50	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
65	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469060	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
75	403649	8705159	Minus	27141-27247
	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
80	404678	9797204	Plus	115196-115448
	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

5	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079,102261-102443,102896-103202
	405564	2114222	Minus	16766-17344
	405678	4079670	Plus	151821-152027
	405735	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

15

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

25	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to normal adult body tissue		
30	Pkey	ExAccn	Unigene ID	Unigene Title
	420154	AI093155	Hs.95420	JM27 protein
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen
	419526	AI821895	Hs.193481	ESTs
	432441	AW292425	Hs.163484	ESTs
35	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti
	407202	N58172	Hs.109370	ESTs
	432101	AI918950	Hs.123642	EphA3
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen
	425075	AA506324	Hs.1852	acid phosphatase, prostate
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1
	410929	H47233	Hs.30643	ESTs
	400287	S39329	Hs.181350	kallikrein 2, prostatic
	445057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr
	415989	AI267700		ESTs
45	428336	AA503115	Hs.183752	microseminoprotein, beta-
	450693	AW450461	Hs.203965	ESTs
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of
	407168	R45175	Hs.117183	ESTs
50	408369	R38438	Hs.182575	solute carrier family 15 (H7?? transport
	454119	BE549773	Hs.40510	uncoupling protein 4
	428819	AL135623	Hs.193914	KIAA0575 gene product
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278
55	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti
	433444	AW975324	Hs.129816	ESTs
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL
60	401424			NM_001172:Homo sapiens arginase, type II
	432435	BE218886	Hs.282070	ESTs
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1
65	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U4 Homo sapiens
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma
	432473	AI202703	Hs.152414	ESTs
	410330	AW023830	Hs.159425	ESTs
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH
70	452792	AB037765	Hs.30652	KIAA1344 protein
	418848	AI820961	Hs.193465	ESTs
	400292	AA250737	Hs.72472	BMP-R18
	433647	AA603367	Hs.222294	ESTs
	453160	AI263307	Hs.239884	H2B histone family, member L
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624
	431474	AL133990	Hs.190642	CEGP1 protein
	429220	AW207206		ESTs
	428134	AA421773	Hs.161008	ESTs
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA
80	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu
	434792	AA649253	Hs.132458	ESTs
	433466	AA508353	Hs.105314	relaxin 1 (H1)
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr
	428398	AI249368	Hs.98558	ESTs

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.7130	copine IV	9.1
	453095	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450642	R39773	Hs.7130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.245773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434668	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146625	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	7.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
35	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739: Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fls, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA: cDNA DKFZp564B083 (fr	6.9
	415786	AW419198	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA158790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.22256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fls, clone PL	6.5
	429433	AA452699	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:rs95a12.y5 NCL_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
80	439569	AW602166	Hs.222399	CEGP1 protein	6.1
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257458	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUC1_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gbz32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132957	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
	438138	R98299	Hs.177502	ESTs	5.9
10	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Sta20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
	434485	AI623511	Hs.118567	ESTs	5.8
15	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gbzv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432956	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesteron induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gbxoc44f08.s1 NCL_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
	417511	AL049176	Hs.82223	chordin-like	5.6
30	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo	5.5
	426581	AB040958	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935982	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278695	Homo sapiens prostelin mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	446715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	M83941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc-5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419538	AA603305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
75	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
80	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (tr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
5	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.0
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100:gi 5852342 gb AAD54015.1 (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
10	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
15	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
20	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
25	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hact domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	4.7
30	452843	AI796769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
35	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
40	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
45	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
50	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
55	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
60	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
65	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
	418706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
75	442242	AV647908	Hs.80424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376:PREDE5 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapian	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

5	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
10	420111	AA255652		gb:zs21h11.1.r1 NC1_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001664:gil12698061 dbj BAB21849.1 (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
15	449603	AI655652	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
	420905	AA521307	Hs.186651	ESTs	4.2
20	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
	450597	AI701835	Hs.207077	ESTs	4.2
25	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
30	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
	458912	AI911066		ESTs	4.2
35	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
40	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AJ350199	Hs.269990	ESTs	4.1
45	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
50	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
55	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI761976	Hs.156080	ESTs	4.0
60	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
65	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
70	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partial	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
75	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
80	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	416288	H51299		gryp07c06.s1 Soares breast 3NbHBst Homo	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
5	435878	R08330	Hs.20152	ESTs	3.9
	446862	AV660697	Hs.282700	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403			Target Exon	3.9
10	448779	BE042877	Hs.177135	ESTs	3.9
	420533	AI809510	Hs.118971	ESTs	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	423453	AW450737	Hs.128791	CGI-09 protein	3.9
15	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	Hs.190325	ESTs	3.9
	421129	BE439899	Hs.89271	ESTs	3.9
	424332	AA338919	Hs.101615	ESTs	3.9
20	441766	R53790	Hs.23294	hypothetical protein FLJ14393	3.9
	447033	AI357412	Hs.157601	ESTs	3.9
	439306	BE220199		WD40 protein Clao1	3.8
	410352	AW969725	Hs.150444	KIAA0373 gene product	3.8
25	407951	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.8
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	458611	AI268407	Hs.211458	DC-specific transmembrane protein	3.8
30	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE617907	Hs.97635	ESTs	3.8
	438379	N23018	Hs.171391	C-terminal binding protein 2	3.8
	416009	Z43062		gb:HSC12E041 normalized Infant brain cDN	3.8
35	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	Hs.97266	protocadherin 18	3.8
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	Hs.191791	ESTs	3.8
	437718	AI927288	Hs.196779	ESTs	3.8
40	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	426981	AL044675	Hs.173081	KIAA0530 protein	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
45	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	3.7
50	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	423096	AA732684	Hs.278428	progesterin induced protein	3.7
	454037	AW998718		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420564	Hs.101760	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	453293	AA382267	Hs.10653	ESTs	3.7
	436671	AW137159	Hs.146151	ESTs	3.7
60	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	Hs.44743	KIAA1435 protein	3.7
	420092	AA814043	Hs.88045	ESTs	3.7
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	Hs.5722	hypothetical protein FLJ23316	3.7
65	419875	AA853410	Hs.93557	proenkephalin	3.7
	431231	AA653552	Hs.116532	ESTs	3.7
	418348	AI537167	Hs.96322	hypothetical protein FLJ23560	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
70	429183	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	Hs.292820	ESTs	3.7
	440947	AA910403		ESTs	3.7
	404561			trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	Hs.145225	ESTs	3.6
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	Hs.145037	ESTs	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
80	450630	AA010429	Hs.191939	ESTs	3.6
	411067	AI681006	Hs.71721	ESTs	3.6
	436326	BE085236		aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
10	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18954	Hs.1904	protein kinase C, iota	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C120005177:gi4758712[ref]NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
15	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fs, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
20	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCL CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
25	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769:BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA339300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23543	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.18928	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
65	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
70	438801	AA825871	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
80	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

5	418985	AJ042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AJ073424	Hs.5232	HSPC125 protein	3.3
	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AJ215632	Hs.147487	ESTs	3.3
	429227	AJ961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AJ248720	Hs.114390	ESTs	3.3
15	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
20	429318	AW881930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AJ291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
	423595	R82826	Hs.220702	ESTs	3.2
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AJ350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338*gl 7459502 pir J574665 outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	Hsapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.66731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	Integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429669	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262888	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypothei	3.1
75	423855	AA331761	Hs.254859	ESTs	3.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533	gb:Homo sapiens F-box protein Fb13b (FBL)	3.1
	416423	H54375	ESTs	3.1
	418037	AJ990212	ESTs	3.1
	419197	N48921	KIAA1615 protein	3.1
	420179	N74530	ESTs	3.1
	433610	AA806822	ESTs	3.1
	436295	N73895	gb:ra62d05.s1 Soares fetal liver spleen	3.1
	444800	AW119071	ESTs	3.1
10	418858	AW961605	hypothetical protein RG083M05.2	3.1
	446469	BE094848	homogenisate 1,2-dioxygenase (homogeni	3.1
	431992	NM_002742	protein kinase C, mu	3.1
	405510		ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Homo sapiens cDNA: FLJ22437 fls, clone H	3.1
15	410869	AW808361	gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	complement component 3a receptor 1	3.1
	425480	AB023198	KIAA0981 protein	3.1
	441492	AJ149998	ESTs	3.1
	447078	AW885727	ESTs	3.1
20	459324	AW080953	gb:cc28c12.x1 NCI_CGAP_Co18 Homo sapiens	3.1
	433852	AJ378329	ESTs	3.0
	448658	H71739	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	glycosyltransferase	3.0
	424690	BE538356	eukaryotic translation initiation factor	3.0
25	405264		NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	ESTs, Weakly similar to I38022 hypothe	3.0
	434497	AJ821803	ESTs	3.0
	420355	AW968263	ESTs	3.0
30	403481		Target Exon	3.0
	412988	BE046680	gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	transmembrane, prostate androgen induced	3.0
	416642	T96118	ESTs	3.0
	418948	AJ217097	gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	ESTs	3.0
	430459	BE178539	ESTs	3.0
	439182	AF086030	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	ESTs	3.0
	448686	AA158659	hypothetical protein FLJ14744	3.0
40	453455	AA063553	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	ESTs	3.0
	427302	AA400540	Homo sapiens cDNA FLJ11554 fls, clone HE	3.0
	437048	AA743240	ESTs	3.0
	450963	AI864668	ESTs	3.0
45	432336	NM_002759	protein kinase, interferon-inducible dou	3.0
	459535	AV654907	gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	hypothetical protein FLJ13197	3.0
50	420407	AA814732	lipopolysaccharide-specific response 5-li	3.0
	426743	AA383833	ESTs	3.0
	442326	H92962	hypothetical protein MGC14817	3.0
	449913	AA004696	ESTs	3.0
	454096	AW062757	gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	leptin receptor	3.0
	407137	T97307	gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087	ESTs	3.0
	429084	AJ001443	splicing factor 3b, subunit 1, 130kD	3.0
	418365	AW014345	ESTs	3.0
60	423784	AK000039	Homo sapiens cDNA FLJ14913 fls, clone PL	3.0
	435877	AA694142	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	hypothetical protein FLJ14600	3.0
	418819	AA228776	ESTs	3.0
	428634	AA811845	Kelch motif containing protein	3.0
65	431869	AA521136	ESTs	3.0
	435008	AF150262	ESTs	3.0
	448880	AW205507	ESTs, Highly similar to I38587 retroviru	3.0
	451391	AA017410	ESTs	3.0
	452959	AI933416	ESTs	3.0
70				

TABLE 64B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
410790	1221131_1	AW803357 AW803423 AW812233 R06814
410869	1225123_1	AW808361 AW808404 AW808385 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
411436	1245660_1	AW846433 AW846159 AW846377 AW846528

411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
412988	1342150_1	AW848905 AW848214
413081	1348563_1	BE046680 BE046738 BE044958
413525	1374635_1	BE064415 BE064430 BE064448
415989	156454_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
416009	1566379_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA356086
416288	1585983_1	Z43062 R13213 H14422
416882	162718_1	H51299 H44619 H46391 R86024 H51892 T72744
418259	173388_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
418866	179788_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
418948	180808_1	AA215404 AI990909 BE464132 AW271459 N74332 AI262061
419536	185688_1	T65754 AA229857 AA229658
420111	190755_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
420352	192979_1	AA603305 AA244095 AA244183
423412	228001_1	AA255652 AA280911 AW967920 AA262684
424200	236595_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
426413	266650_1	AF109300 AI299378 AI202654
426503	268283_1	AA337221 AA336756 AW966196
426991	27415_1	AA377823 AW954494 AI022688
428002	285602_1	AA380153 AA380233 AW963529
428342	290035_2	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
429163	300543_1	AA418703 AA418711 BE071915 BE071920 BE071912
429220	301384_1	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
430535	319643_1	AI092404 AI085630 AA731340
432600	350959_1	AA884766 AW974271 AA592975 AA447312
432765	353907_1	AW207206 AW341473 AA448195 AI951341
433523	368873_1	AW968485 AW968670 AA480922 BE350425
434763	392847_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
436295	41733_1	AJ003429 AJ003367 AA564825
436326	41795_2	H29982 AW655333 AW149901 AI572917 AA598500 AI688466 AI336390 AW864390 AW864320
437866	44433_2	AA648618 AW974389 H51771
439092	468554_1	N73895 AJ001872
439306	47088_1	BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281
440840	50357_2	AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706
440947	506904_1	AW270601 AW873282
442481	543588_1	AA156781 AW293839 U52054 AA024963 AA778448 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
445432	63943_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D02016 AI536733
448044	747196_1	AA812489 AW874142 AI47188
449343	80517_2	AA830149 AW978407 M85983 AW503637
449570	81018_1	BE220199 W01813 AF088118 N70760 BE221405
449625	8113_1	AW629665 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207
450317	831956_1	AA921877
450580	83929_1	AA910403 AI815593 W58361 AW162520 AI816550
450582	83933_1	N99828 BE079873 AI110738 AF074645
450687	84327_1	AV653771 BE089370
452462	918580_1	AI458682 H24240 R14537 R18426 AW867082
453682	977454_1	AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053
454037	996287_1	AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467
454171	1049240_1	H00789 R76925 AW1828
454457	1207274_1	AA001793 AA001871
454860	1237732_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW295554 AA323193 AA235370 AW779760
454968	1247029_1	NM8674 AJ375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
455276	1272541_1	AI692689 R14223 R18395
455646	1348567_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816858 AW816889 AW816940
455710	1352368_1	AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
457374	328758_1	AA164518 AA730973 W00417 W65303
458912	823104_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
		AA495800 AA495737 AA010736 AA654716 AA640726
		BE173515 BE173560 AI902860
		T79703 T96307 AL079725
		AW998716 AW022148 N68020
		AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
		AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
		AW753456 AW753036 AW854868 AW854882
		AW835767 AW835537 BE160187
		AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
		BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
		BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
		BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
		AA493662 AW897396 BE154814
		AJ911066 AI933734 AI680888 AJ003599

TABLE 64C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
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5	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9965004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8246547	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85th percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

35	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to prostate tumor tissue		
	Pkey	ExAccn	Unigene ID	Unigene Title
	428134	AA421773	Hs.161008	ESTs
	446336	AW815036	Hs.151251	ESTs
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K
	400533			ENSP00000209376:-PRE65 protein (Fragmen
	418310	AA814100	Hs.86693	ESTs
	404592			NM_022739*:Homo sapiens E3 ubiquitin lig
45	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo
	400080			Eos Control
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c
	438231	AW594539	Hs.155689	ESTs
50	418387	R18085		gb:yg16b12.r1 Soares Infant brain 1N1B H
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen
	449249	T62285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe
	404967			Target Exon
55	430535	AW969485		gb:EST380561 MAGE resequences, MAGJ Homo
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222
	412988	BE046680		gb:tn42h03.x1 NCL_CGAP_RDF2 Homo sapiens
	400440	X83957	Hs.83870	nebulin
60	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo
	400086			Eos Control
	440911	AA090536	Hs.143562	ESTs
	425312	AA354940	Hs.145958	ESTs
65	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence
	419015	T79262	Hs.14463	ESTs
	453789	AA628517	Hs.118502	ESTs
	424940	AA985308	Hs.283902	ESTs
	403667			Target Exon
70	429014	AI800518	Hs.118158	ESTs
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte
	419999	AI760942	Hs.191754	ESTs
	405348			C7001664:gi12698061 dbj BAB21849.1 (AB
	404003			Target Exon
75	453200	AA033832	Hs.212433	ESTs
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi
	432319	AW510770	Hs.126366	ESTs
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi
	443361	AI792628	Hs.133273	ESTs
80	411518	AW850248		gb:IL3-CT0219-291099-021-E07 CT0219 Homo
	439079	AF085937	Hs.38348	ESTs
	422081	AW136820	Hs.196011	ESTs
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked
	423529	T87318	Hs.120411	ESTs

	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothel	5.3
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
15	446495	D60923	Hs.153460	ESTs	5.2
	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
20	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gii4758712[ref]NP_004659.1] al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0188-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:CV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stratagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
70	441620	R59595	Hs.26875	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_008825		transmembrane protein (53kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
80	430124	AW204994	Hs.253450	ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-060-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AJ350199	Hs.269990	ESTs	4.1
	442400	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AJ741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
5	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AJ761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QVO-DT0020-090200-106-g05 DT0020 Homo	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
10	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	441568	AJ733322	Hs.127176	ESTs	4.0
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
15	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA935527	Hs.293507	hypothetical protein FLJ23403	3.9
	453387	AJ990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	454806	AW872430	Hs.273743	ESTs	3.9
20	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC-9658, mRNA, comp	3.9
	447530	AW192053	Hs.248855	ESTs, Moderately similar to JCS238 galac	3.9
	407834	AW084991	Hs.26100	ESTs	3.9
25	400398	AF137396	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*:gij9790241[ref]NP_062628.1 S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthene dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AJ141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.8
	440450	AJ333129	Hs.156147	ESTs	3.8
	437587	AJ591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized Infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NC1_CGAP_P12 Homo saplens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QVO-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 JH	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AJ637649	Hs.196105	ESTs	3.8
	443635	AJ080230	Hs.134214	ESTs	3.7
	428200	AJ039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AJ470874	Hs.343799	ESTs	3.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AJ359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, 3' terminal portion	3.7
	447458	AJ741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AJ203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophthalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455087	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AJ671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
5	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AJ732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517:g[4758712]a[NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144533	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769:BG153Q3.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AJ39732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	407344	AJ038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
50	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AJ042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA069050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AJ291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypotheti	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501:g[129092]p[P23270]OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D78435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243598	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AJ203933	Hs.97142	ESTs	3.2
	447892	AJ435848	Hs.172978	ESTs	3.2
	457138	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW837417	Hs.293561	ESTs	3.1
	429559	AA454993	Hs.136343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AI754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
15	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	448765	R15337	Hs.21958	Homo sapiens mRNA: cDNA DKFZp547D086 (fr	3.1
25	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
30	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AI939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_hear_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140: Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-Ilk	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AI381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

55 TABLE 65B

Pkey:		Unique Eos probeset identifier number
CAT number:		Gene cluster number
Accession:		Genbank accession numbers
60	Pkey	CAT Number
	408304	1050848_1
		AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515
		AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288
		AW810263 AW810325 AW810443 AW8
65	409189	110687_1
		AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 NB4829 AA084752 AA076512
		AA085119 AA085208 AA085045
	410559	1208283_1
	410790	1221131_1
	410869	1225123_1
70		AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
		AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
		AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1
	411518	1248692_1
	411552	1249255_1
75	412701	1322288_1
	412988	1342150_1
	413081	1348583_1
	413525	1374635_1
80	416009	1566379_1
	416422	1593811_1
	418059	171879_1
	418387	174731_1
	418948	180808_1
		AW754192 W00554 AW857797 AW754203 AW754197 AW754193
		AW803357 AW803423 AW812233 R06814
		AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934
		AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739
		AW808704 AW808558 AW808714 AW808420 AW8
		AW846433 AW846159 AW846377 AW846528
		AW850246 AW850251 AW850302
		AW851255 AW851432 AW850955
		AW984757 AW984797 AW984734 AW984745
		BE046680 BE046738 BE044958
		BE064415 BE064430 BE064448
		BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
		Z43062 R13213 H14422
		H60457 H68709 H73528 H54335 R87154
		AA211586 F35799 AA211641 F29720 AW937387 AW937408
		R18085 AA219028 R17712 Z44345
		AI217097 AW886090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 A1372685 AA349501 A1372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 A1792312 A1792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 A1815593 W58361 AW162520 A1816550
	442481	543588_1	N9828 BE079873 A110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	A1692689 R14223 R18395
	450582	83933_1	A139732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 A1902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
30	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW86079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
35	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
	455772	1363114_1	W28799 BE086078
40	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	A1820973 A1734077 A1820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

TABLE 65C

Pkey: Unique number corresponding to an Eos probe set
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	NL_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
	403305	8099945	Plus	114632-114805
65	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	105655-106050
	403433	9719611	Minus	72225-72437
	403481	8965004	Plus	93496-93633
	403510	7652047	Plus	61866-62027
70	403667	6850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
	404592	9943965	Minus	39067-39225
75	404848	8248647	Minus	23955-24034,25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
	405321	3419846	Minus	44654-45210
80	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85th percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number				
ExAccn:	Exemplar Accession number, Genbank accession number				
UnigeneID:	Unigene number				
Unigene Title:	Unigene gene title				
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue				
Pkey	ExAccn	Unigene ID	Unigene Title	R1	
410929	H47233	Hs.30643	ESTs	21.1	
450693	AW450461	Hs.203965	ESTs	16.7	
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedin)	14.2	
432473	A1202703	Hs.152414	ESTs	11.3	
446336	AW815036	Hs.151251	ESTs	10.9	
407275	A1364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	10.7	
428134	AA421773	Hs.161008	ESTs	10.2	
400297	A1127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8	
433468	AA508353	Hs.105314	relaxin 1 (H1)	9.5	
415293	R49462	Hs.106541	ESTs	9.1	
458072	A1890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8	
428927	AA441837	Hs.90250	ESTs	8.6	
420345	AW295230	Hs.25231	ESTs	8.5	
453387	A1990741	Hs.252809	ESTs	8.2	
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7	
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	7.5	
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4	
400080			Eos Control	7.4	
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4	
404592			NM_022739: Homo sapiens E3 ubiquitin lig	7.3	
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3	
438231	AW594539	Hs.155689	ESTs	7.3	
410330	AW023630	Hs.159425	ESTs	7.2	
449300	A1656959	Hs.346514	ESTs	7.1	
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0	
426384	A1472078	Hs.303862	hypothetical protein FLJ13189 (FLJ13189)	6.8	
454171	AW854832		gb:QV2-CT0261-201099-011-R05 CT0261 Homo	6.6	
408197	AA282282	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6	
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 domain)	6.6	
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5	
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5	
424433	H04607	Hs.9218	ESTs	6.5	
442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	6.4	
425312	AA354940	Hs.145958	ESTs	6.4	
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4	
440911	AA909536	Hs.143562	ESTs	6.4	
400533			ENSP00000209376: PRED65 protein (Fragmen	6.2	
418310	AA814100	Hs.86693	ESTs	6.2	
403667			Target Exon	6.1	
436396	A1683487	Hs.152213	wingless-type MMTV integration site fami	6.1	
404003			Target Exon	5.9	
424853	BE459737	Hs.132967	Human EST clone 122887 mariner transpos	5.9	
438138	R98299	Hs.177502	ESTs	5.9	
424940	AA985308	Hs.283902	ESTs	5.8	
434485	A1623511	Hs.118567	ESTs	5.8	
453200	AA033832	Hs.212433	ESTs	5.7	
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7	
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6	
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6	
443361	A1792628	Hs.133273	ESTs	5.6	
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5	
439079	AF085937	Hs.38348	ESTs	5.5	
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5	
436578	A1091435	Hs.134859	ESTs	5.5	
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp58J1922 (f	5.4	
421853	A1952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4	
435072	AW592176	Hs.116932	ESTs	5.4	
435375	A1733610	Hs.187832	ESTs	5.4	
444609	AW571659	Hs.278081	ESTs	5.4	
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4	
433087	A1720686	Hs.152520	ESTs	5.3	
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GC81 Homo sapiens	5.3	
437257	AW511443	Hs.258110	ESTs	5.3	
441916	AA993571	Hs.129075	ESTs	5.3	
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3	
452531	AA429462	Hs.293946	ESTs, Weakly similar to t38022 hypotheti	5.3	

	423101	M83941	Hs.123642	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:U3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-like	5.1
15	445238	AA883971	Hs.187506	ESTs	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
20	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
25	450497	H64159	Hs.15328	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213585	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
30	450317	AI692689		gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8
	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
40	405348			C7001664.gij12698061[dbj]BAB21849.1 (AB	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI871141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI093155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255552		gb:zs21h11.r1 NCL_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409706	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
65	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MFO-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434380	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.169059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW529517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothel	4.0
5	435136	R27299	Hs.10172	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurolypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
15	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	412988	BE046680		gb:hn42h03.x1 NCI_CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
20	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
30	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PMA-BN0067-250300-002-f11 BN0067 Homo	3.7
40	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	436345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
55	422899	O16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
	430098	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
65	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3523	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
70	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C12000517::g 4758712 ref NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 NCI_CGAP_Ew1 Homo sapiens	3.5
80	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

5	430865	AJ073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (I	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
10	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AJ760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
15	408480	AJ350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
20	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
25	456995	T89832	Hs.170278	ESTs	3.4
	405610			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AJ457449	Hs.192817	ESTs	3.4
30	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	433628	AJ821784	Hs.188578	ESTs	3.4
	436703	AW880814	Hs.146381	RNA binding motif protein, X chromosome	3.4
35	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AJ126288	Hs.192232	ESTs	3.4
	459646	AW883958	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
40	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	448108	AW300021	Hs.170685	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
45	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AJ989963	Hs.197505	ESTs	3.3
	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
50	418985	AJ042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-006 BT0532 Homo	3.3
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
55	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
60	453973	AJ291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AJ821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AJ123555	Hs.81796	ESTs	3.2
65	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AJ808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
70	402145			Target Exon	3.2
	448131	AJ675054	Hs.200481	ESTs	3.2
	422352	AA766296	Hs.89200	ESTs	3.2
	432825	AJ243596	Hs.94830	ESTs, Moderately similar to T03094 A-kln	3.2
	447183	AJ554733	Hs.173182	ESTs	3.2
75	447597	AJ886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
	434408	AJ031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.2
80	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 ty	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AJ538323	Hs.52620	Integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AJ458682		gb:tk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1	
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	433444	AW975324	Hs.129816	ESTs	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
	415861	Z43123	Hs.144513	ESTs	3.1
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.1
10	432527	AW975028	Hs.102754	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	417958	AA767382	Hs.193417	ESTs	3.1
15	407425	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	405548			Target Exon	3.1
	423595	R82826	Hs.220702	ESTs	3.1
	412533	AA679853	Hs.69606	ESTs	3.1
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.1
25	405264			NM_030813*:Homo sapiens suppressor of po	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-104 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
30	435021	AA922192	Hs.54709	ESTs	3.0
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087		ESTs	3.0
	432319	AW510770	Hs.128386	ESTs	3.0
	453713	R20640	Hs.79133	cadherin 8, type 2	3.0
35	445784	AI253155	Hs.146065	ESTs	3.0
	416642	T98118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:xd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
40	404995			ENSP00000251890*:Monocytic leukemia zinc	3.0
	444794	AI419991	Hs.145225	ESTs	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	420133	AA426117	Hs.155543	ESTs	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CMQ-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338	ESTs	3.0
50	449745	AI688593		gb:yt38a05.x5 Soares breast 3NbHBst Homo	3.0
	426412	AA428240	Hs.126083	ESTs	3.0
	428200	AI039624	Hs.98388	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
55	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 66B

60	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
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65	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW803760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8 AW846433 AW846159 AW846377 AW846528 AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 Z43062 R13213 H14422 AI217097 AW886090 W38035 W38792 AA232835 AW936043 AA255652 AA280911 AW967920 AA262684 BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R35280 AA337221 AA338756 AW966196 AW954525 AI372685 AA349501 AI372687 H10564 AA418703 AA418711 BE071915 BE071920 BE071912
70	411436	1245660_1	
	411479	1247077_1	
75	412988	1342150_1	
	413081	1348563_1	
	413525	1374635_1	
	416009	1566379_1	
	418948	180808_1	
	420111	190755_1	
80	420352	192979_1	
	424200	236595_1	
	424994	245786_1	
	428002	285602_1	

428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AJ377728 AW293682 AI928140 AA731438
430535	319643_1	AI092404 AI085530 AA731340
432765	353907_1	AW968485 AW968670 AA480922 BE350425
433523	368873_1	AJ003429 AJ003357 AA564825
434763	392847_1	H29882 AW665533 AW149901 AJ572917 AA598500 AI686466 AJ336390 AW864390 AW864320
436295	41733_1	AA546618 AW974389 H51771
439092	468554_1	N73895 AJ001872
439306	47088_1	AA830149 AW978407 M85983 AW503637
440947	505904_1	BE220199 W01813 AF086118 N70760 BE221405
442481	543568_1	AA910403 AI815593 W58361 AW162520 AI816550
445432	63943_1	N99828 BE079873 AI110738 AF074545
448044	747196_1	AV653771 BE089370
449570	81018_1	AI456682 H24240 R14537 R18426 AW867082
449745	814534_1	AA001793 AA001871
450317	831956_1	AJ688593 AJ820774 R86205 H39971 H22177 H26241
450580	83929_1	AI692689 R14223 R18395
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
		AA164518 AA730973 W00417 W65303
450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
452462	918580_1	BE173515 BE173560 AI902860
453682	977454_1	T79703 T96307 AL079725
454037	996287_1	AW998716 AW022148 N68020
454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454457	1207274_1	AW753456 AW753036 AW854868 AW854862
454665	1228599_1	AW812868 AW812748 AW812747 AW812884 AW812763 AW812722
454860	1237732_1	AW835767 AW835537 BE160187
454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW846698 AW849034 AW849033
455087	1252050_1	AW854538 AW854418 AW854412
455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
457374	328758_1	AA493662 AW897396 BE154814
458912	823104_1	AI911066 AI933734 AI680888 AJ003599

TABLE 66C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113088-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61886-62027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	8943965	Minus	39067-39225
404848	8248647	Minus	23965-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	445057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R18	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R18	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	RA5175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA881697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428852	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete ods	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249388	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	Insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAc	10.2
75	408000	L11690	Hs.198689	bulous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odx (odd Ozter-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothei	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKF2p434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_005769	Hs.3844	UM domain only 4	9.3
5	411887	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
10	432101	AI918950	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
15	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AI076405	Hs.29381	solute carrier family 26 (sulfate transp	8.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	8.5
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.5
20	416182	NM_004354	Hs.79069	cyclin G2	8.5
	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0666 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	7.3
	432586	AA568548		ESTs	7.3
45	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
60	450377	AB033091		KIAA1265 protein	6.6
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (iso	6.6
	415111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AA20611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW518204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI287652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AJ297436	Hs.20168	prostate stem cell antigen	6.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	stx transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP56680846 protein	5.8
5	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	5.7
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothel	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens prostein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
	425211	M18667	Hs.1867	progastricin (pepsinogen C)	5.4
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sln3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-8 protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
30	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
	404532			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262478	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79135	LIV-1 protein, estrogen regulated	5.1
35	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptotagmin 2	5.0
	403046			NM_005656:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-tyrosine/alpha-aminoadipate aminotra	5.0
	450164	AI239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.126629	ESTs	4.9
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
50	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGH-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111258	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.5
75	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
5	435706	W31254	Hs.7045	GL004 protein	4.3
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypothet	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
10	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23128	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
15	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430698	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
20	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
25	432363	AA534489		gb:nf76g11.s1 NCL CGAP_Co3 Homo sapiens	4.1
	447574	AF162666	Hs.18895	lousied-like kinase 1	4.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
30	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gb:zp99b10.s1 Striatogene muscle 937209 H	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
35	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.282070	ESTs	3.9
45	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
50	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417057	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
55	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432675	AI791855		ESTs	3.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
60	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
65	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
70	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
	416655	AW968613	Hs.79428	BCL2adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
75	417051	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	axin 2 (conductin, axi)	3.7
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.7
80	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pro-B-cell leukemia transcription factor	3.6

	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
	422424	AJ186431	Hs.296638	prostate differentiation factor	3.6
5	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
	412520	AA442324	Hs.795	H2A histone family, member O	3.6
10	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
15	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
	428055	AA420564	Hs.101760	ESTs	3.5
20	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
	443884	N20617	Hs.194397	leptin receptor	3.4
30	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:y853h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	AI026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
45	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	435873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
	433891	AA613792		gb:mo97h03.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
60	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
65	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
70	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476*:gil12737279[ref]XP_012163.1	3.2
75	419517	AF052107	Hs.90797	Homo sapiens clone 23820 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
80	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AJ923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73508	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
15	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31060	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267588	Hs.268012	fatty acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.128791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.1
	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
45	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429638	AI916662	Hs.211577	kineclin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H56220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE268822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10869	ESTs, Weakly similar to TD0050 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78106	phosphodiesterase 8B	2.9
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420061	AW024937	Hs.29410	ESTs	2.9
80	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI532278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

5	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
	445880	AI811807	Hs.108846	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferr	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	2.9
15	423551	AA327598	Hs.89633	ESTs	2.9
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
20	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (tr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
25	418166	AI754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
30	425320	U29344	Hs.83190	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
40	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
45	448913	AA194422	Hs.22564	myosin VI	2.7
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434829	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
55	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
65	400301	X03635	Hs.1657	estrogen receptor 1	2.7
	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
70	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
	432388	X15218	Hs.2969	v-aki avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
75	409650	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
80	420818	AW969635	Hs.33032	ESTs, Weakly similar to T207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

	440695	AW088353	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	nlban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
5	426110	NM_002913	Hs.165563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*-HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
15	408157	AA047685	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulon 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
20	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
30	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6814	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
40	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor I	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
50	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA Z310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AJ041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
55	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AI373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557488	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
60	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
65	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
70	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
75	450628	AW382884	Hs.204715	ESTs	2.5
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
80	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418849	AJ096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
	414556	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
10	427050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.5
	443837	AI984625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
15	435021	AA922192	Hs.73962	ESTs	2.5
	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaelp, yeas	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
20	449458	AI805078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.181444	hypothetical protein	2.5
	424369	R87622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433586	T85301	Hs.194397	gbryd78d06.s1 Soares fetal liver spleen	2.5
	436682	AA354489	Hs.222103	EBP50-PDZ Interactor of 64 kD	2.5
	427515	T79526	Hs.179516	Integral type I protein	2.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

35	Pkey	CAT Number	Accession
	415989	10194_1	BC013389 BC017398 AJ023543 AA191424 AE167700 AJ469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AJ720344 BF541715 AA355086 AA172236
40	429220	15103_7	AW341473 AA448195 AW207206 AJ951341 AA969259
	412446	63467_1	BC021735 AJ669212 AL120184 AJ769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AJ632824 BF512340 BF952021 BF960776 BF943437 BF942847 AJ768015 F09778 F04816 F02721 AA102645 AJ633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
45	434304	7392_1	BC022980 BF224081 BG149908 AW672842 BE670687 AJ702161 AW341832 BE222503 N71836 AJ026061 AW953116 AW083132 AJ979261 AV725377 AJ423298 AJ640707 AW675518 AJ032611 AJ818044 AJ299508 AJ911386 AJ270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
	449625	249224_1	BI918168 AW779760 N48674 AJ375997 AA235370 BG699146 AJ913631 AJ498402 AJ016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AJ203107 R35004 F07491 R25094 R35360
50	453160	6028_5	BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AJ263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AJ143991 AA084581 AA033610 AV742510 AV735788 R08336
	420218	191547_1	AW958037 R42557 AJ337047 AA948360 AJ638005 AA459950 AJ624915 AJ638047 AJ467856 AJ521826 AA860305 AJ932315 AW003092 AW271758 AW779380 AA609879 AJ634791 AJ93770 AJ555211 Z41145 AJ627952 AA303734 BE349457 AW196765 AA256527 BE089727
55	437124	59408_1	AL050013 BG939500 AW969191 AA769925 AJ377973 AJ625545 AA811365 AA521114 N24705 AJ379579 AA424899 AJ684671 AA829715 AJ453010 N35401 AA677452 AA504340 AJ209149 AA883574 AJ379062 AJ084455 AJ280147 AA644327 BF432508 N27873 N47364 N34880 AJ147024 T86860 AJ219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AJ292318 AA829886 N95742 AJ218758 H25588 N36822 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AJ262504 AJ452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AJ016509 AW563972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422
60	432586	6633_1	BC022881 AU150944 BG750783 AW754175 AW857737 AJ911659 AJ050036 AA554053 AJ826259 AA568548
	438869	52134_1	AF075009 R63109 R63068
	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 AJ679751 AJ873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AJ857643 AJ768485 AW512118 AA479302 AW770384 AW072470 AJ041696 AJ049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AJ693720 AA743364 AJ915793 N48185 AJ573107 AA043474 AJ351615 AJ969490 AJ910763 R50866 AJ699181 N73808 H08164
65	436063	5483_1	AK000028 AA494483 AJ298674 AA720773 AV761529 AJ884670 AJ938202 AW294235 D61652 BF881184 AV711384 N27154 AJ926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
70	428342	6712_1	AK056315 AJ015524 AA724079 BI713619 AJ377728 AW293682 AJ928140 AJ092404 AJ085630 AA731340 BM469629 AW968804 AA426558 AA769094 BF446026 AW118719 AJ332765 AW500888 AW576556 AJ859571 AW499664 AW614573 AW829495 AW505314 W74704 AJ356361 AJ923640 AW070509 AJ521500 AL042095 AA609309 AA761319 AJ381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AJ392620 Z40708 AJ985564 AW263513 AA913892 AJ693486 AW263502 AJ0806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166
75	424036	6226_1	NM_033445 BC001193 AJ885781 BF794032 AA476620 AA810905 AA810905 AJ291244 AJ885097 AJ359708 AJ35629 H97396 AJ344589 AA300377 AA457566 AW771833 BE465621 AJ364068 AJ364452 AJ648505 AJ918342 AJ928670 AA886580 AL531029 AA886344 AJ166419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427
	450203	19009_1	AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AJ819354 AW974068 AJ393635 AJ580846 AJ024796 AW020098 BI491127 AJ336444 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
80	451762	10408_5	AB032997 AJ141678 AW978722 BE467119 AJ761408 BF727385 AW237035 AJ934521 BF436248 AJ479688 Z40632 AA832081 AW295901 BF057835 BE465977 AJ621269 BE465983 BF765369 N74056 AJ718796 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
	432363	1234917_1	

5	422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 BI792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI368013 AI867923 BG911906 D81142 C15616 AI438697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T4078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
10	417379	1610005_1	AA196390 AA507837 AA196468
	407819	7392_2	AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
15	419733	7612_3	AK027321 W63576 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA845232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706684 BE706539 BE153177 BF084925 AI133779 AW961788 AA658693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE10736 BF687723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
	432675	1237917_1	AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610
	447620	687223_1	AI973051 AI400921 AI796154 AW241817 AW290951
	409151	4123_1	NM_004892 AF047442 BE275338 BF724863 BI917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
20	409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI056920 AA481861 BF763597 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF11012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
25	433891	647290_1	AW182329 AA613792 T06304 AW858385
	414922	1563_2	BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE326188 AI952820 AI581363 AA557165 AI695677 AL562079 AI700926 AI470561 BF063058 AW196387 AI132984 BI064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW664827
30	414222	18695_1	BC021085 AL527872 AL526296 AL557087 BI255090 AU143499 AI560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI420449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI385522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AW013929 AI826274 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 AW328268 AI244888 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AT06105
35	426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
40	434194	62680_1	AF119847 AA437261 AA436987 AI132965
	432908	452541_1	AF150424 AI881896 AA570057 AV738855
	412652	18858_2	AI801777 BE677762 AW008210 AW009441 BE350394 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780
45	437179	12239_1	AA889119 AI537472 Z39730 AI866953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
50	437179	12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977604 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R55480 AI400988 R54266 R31422
55	418166	18858_1	AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AI133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE845790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 AA811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE845916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97846 R39899 AA375242 BF109388 AI860939 AI680060 AW953899 BF971488 AI972337 AW953841 AA372437 AI216748 H11384 R38484 AA249043 AA249732
60	431416	120918_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974
	447881	44623_1	AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI872039 T28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 BI697926 BF594165 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA698444 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
65	407192	2200202_1	AA602964 AA609200
	434747	117643_1	AW976537 AI033582 AA837085 AA745261 AA648395
	410297	2990_1	BC013939 BI494690 BI491211 AI928393 AA843540 BG938644 AU185628 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928769 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N84382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA651791 BI474307 BI911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI962893 AI989299 Z42328 BF029504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AA276488 AA992453 AA342821 AA648303 AI349354 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827169 BI494872 AW021094 BI494871 AA905500 AA460923 BI492041 AW028965 AI824611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 A93579 AI362553 D60006 N29572 AI916833 N75273 AI418710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70560 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI855262 R55325 AI468927 R34681 H96211 Z39807 BF954386
70	424339	50559_1	NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF080526 F12128 AL566773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833

445636	8561_5	BF339388 AJ345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE857593 AA090310 AA090672
419175	35068_1	AB018322 BC012480 B1524873 AW665554 A1934469 A1479916 BF096179 BF096162 BF096132 AA744972 A1951988 A1858339 BE076331 AA886998 A1570585 A1916688 A1678811 A1693109 A1308135 AA659046 AA961084 A1018062 H80618 BE221942 R52609 A1915164 AA365626 Z44671 B1052776 BF882486 BG286184 A1589558 A931663 AA534979 A1275392 A1273455 R52553 AA829920 H80652 AA360728 F10618 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 A1334004 BF057179 A1857450 A1341191 A1434143 A1917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 A1580157 A1364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 A1203159 N49403 F02090 A1187299 A1609644 Z40516 AW952314
441128	20932_1	BC014072 BE328850 A1356567 A148171 A1022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 A1005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 A1473237 BF033706 N90525 AW973623 A1359627 BG674574 BE903322 A1041403 Z49148
405789	0_0	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 A1884867 BE858461 A1885227 A1935218 BE645596 A1922406 AA778161 BF345973 AW195853 A1687121 A1336147 A1091364 A1769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 A1358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 A1935916 AA912295 BG910887 AL568301 A1567278 B1522445 B1754384 BG819375 BF835950 AA323718 AA860955 A1089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 B1913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 B1519896
400263	18977_1	Z11692 X51466 NM_001951 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 BM016525 A1560409 AL562866 A1909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF869862 BG998348 B1011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BM016990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF898506 A1038390 BM044934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG674499 BG774174 B1015084

TABLE 67C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-165995, 166189-166314, 166408-16656
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	A1420227	Hs.149358	Trp-p8 transient receptor potential cati	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	A1821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	A1694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
	400292	AA250737	Hs.72472	BMP-R1B	31.4
5	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
10	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	AI733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
15	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
20	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	foliate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
25	437052	AA861697	Hs.120591	ESTs	22.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
30	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW957646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	418078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448519	AW175665	Hs.278595	Homo sapiens protein mRNA, complete cds	14.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
55	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bulous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.155110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415283	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
80	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	11.1
	440529	AW207540	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_008769	Hs.3844	LIM domain only 4	10.6
5	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
	445100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
10	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91682	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
20	443180	R15875	Hs.258576	claudin 12	9.5
	406964	M21305		FGENES predicted novel secreted protein	9.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
25	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegln	9.3
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
30	437124	AA554458		KIAA0666 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
35	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AI655499	Hs.161712	ESTs	8.8
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.7
40	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isof	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger)	8.7
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425455	L18964	Hs.1904	protein kinase C, iota	8.5
45	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP564I052 protein	8.4
	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420611	Hs.153934	ESTs	8.3
50	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
55	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
60	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	7.7
65	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
	451952	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
70	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.6
	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	441866	BE464341	Hs.21201	necln 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18687	Hs.1867	progastricin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-receptl	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0818 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheli	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	lactenin protein	6.3
35	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20885	sln3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.6019	DnaI (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
	458440	AJ095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyl	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AJ694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AJ497778	Hs.20509	HBV pX associated protein-8	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AJ378329	Hs.128629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GL004 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AJ916662	Hs.211577	kinecin 1 (kinesin receptor)	5.5
75	403046			NM_005656:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90780	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88566	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
	417318	AW953937	Hs.240845	ESTs	5.3
5	429467	NM_004477	Hs.203772	F5HD region gene 1	5.3
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
15	450832	AW970602	Hs.105421	ESTs	5.1
	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
20	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R56784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (mainlylsn,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032997		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489		gb:mf76g11.s1 NCLCGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.295039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (I	4.7
50	447574	AF162666	Hs.18895	tousled-like kinase 1	4.7
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gb:zp99b10.s1 Stralagene muscde 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	4.7
	441224	AU076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.137398	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154978	KIAA0261 protein	4.7
65	420380	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.7
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWI/SNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
75	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	4.5
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.28482	ESTs	4.5
	417061	AI875944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
5	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:poly	4.4
	417958	AA767382	Hs.193417	ESTs	4.4
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
20	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
30	432875	AI791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AJ248720	Hs.114390	ESTs	4.2
	410297	AA148710		harnican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW280951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AJ355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calcarsin-1	4.1
	407192	AA609200		gb:af12a02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (lg),	4.1
	427479	BE410092	Hs.178471	KIAA0788 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108842	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47168	HT021	4.0
	446791	AJ632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	tepin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476"gi 12737279 ref XP_012163.1	4.0
75	407846	AA426202	Hs.40403	Chp/p300-interacting transactivator, wtl	4.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubtinuclein 1	3.9
	429163	AA884766		gb:zm20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
5	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AI249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
15	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.69622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AI186431	Hs.256638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypofest	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429686	AB716113	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Sequey (s	3.7
	432579	AF043244	Hs.278439	nuclear protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AI861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	AI806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*-HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulin 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dy4-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
55	405387			NM_022170*-Homo sapiens Williams-Beuren	3.7
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-aki avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	scute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lactalbumin prolina rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
75	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
80	403752			NM_002753*-Homo sapiens mitogen-activate	3.6
	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gb:nc97h03.s1 NCI_CGAP_Py2 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434872	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104338	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3795	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoaCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwov and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14632 fis, clone OV	3.4
55	452295	BE378936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
70	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_016569	Hs.267182	TBX3-Iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to I36022 hypotheti	3.3
	436278	BE395290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone Z3733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418168	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2

5	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275: Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	3.2
	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	3.2
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 fem	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371: Homo sapiens hydroxysteroid (1	3.2
15	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
20	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimertizat	3.2
	437179	AA393508		serologically defined colon cancer anti	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
25	450548	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638: Homo sapiens hypothetical prot	3.2
30	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
35	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
40	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-coop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
45	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161085	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
50	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105954	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436289	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
55	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437295	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
60	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
65	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
70	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
75	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSURE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
80	434974	AA78711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_005979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279338	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445596	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	3.0
	408298	AJ745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
15	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma emptyfilled sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
20	447881	BE620888		GCN1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447953	AJ452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AJ584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AJ129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	AJ675881	Hs.86538	ESTs	2.9
	433009	AA761688		gb:z24c08.s1 NCI_CGAP_GCB1 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15438	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.83758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AJ200281	Hs.123910	ESTs, Highly similar to B34087 hypotheti	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	nlban protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749865		ESTs, Weakly similar to I38022 hypotheti	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AI015709	Hs.172089	Homo sapiens mRNA: cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	AJ373544	Hs.331328	Intermediate filament protein syncollin	2.8
	433312	AJ241331	Hs.131765	ESTs, Moderately similar to I38937 DNVR	2.8
	431604	AF175265	Hs.264180	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AJ984625	Hs.9884	spindle pole body protein	2.8
75	418198	AJ745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
80	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AJ557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74824	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467084	Hs.5740	ESTs	2.8
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
5	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.86969	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
15	440080	AW051597		ESTs	2.8
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447696	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA508476	Hs.10500	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
25	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217615	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gbnt78105.x5 NCL_CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045650	Hs.63125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rii-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T48395 hypotheti	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000061	Hs.101590	hypothetical protein	2.7
60	418359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.263594	intron of trichorhinophthalangeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411950	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806184	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.156184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ Interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
15	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, ei	2.7
	423476	AL035633		Human DNA sequence from clone RP5-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
	404913			NM_024408*:Homo sapiens Notch (Drosophi	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443668	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, Intermediate polype	2.6
35	407887	AA579568	Hs.41072	serine (or cysteine) proteinase inhibito	2.6
	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subun	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004922	Hs.81954	SEC24 (S. cerevisiae) related gene famil	2.6
50	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated ethanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283478	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
75	458948	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
80	442338	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29708	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
5	457638	AJ792670	Hs.144406	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14850	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AJ419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthet	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AJ878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypotheti	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425892	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W06656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fls, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCH5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 688

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
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			AW953668 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AJ857450 AI341191 AJ34143 AI917449 AW517207 AA255424 AW008334 AA847572 AA949211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW852314
5	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884667 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812395 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818618 AI935916 AA912295 BG910887 AI568301 AI557278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AI567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AI581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896 BC014072 BE328850 AI356567 AI48171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127651 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322 AI041403 Z49148
10	441128	20932_1	AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AI563737 BG029705 W52882 AI439658 BE551237 AA283724 BF109530 AI457096 AI085992 BE467736 AA693467 AI697593 AI887863 AI167419 AW901880 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AI18634 T31586 AA436630 AI365472 AA706191 AI422304 AI204899 AI041169 AA211402 AW827081 AA788593 T32736 AI767935 AA747914 T03534 AW959843 AL119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767113 AA658826 AI821926 AI791191 AA635129 AA564492 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF888666 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
15	406789 410099	0_0 16732_1	BG256892 H10532 N46614 R52610 AW977698 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672156 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298 BF339388 AI345516 BG391657 BE708957 BG026034 BE261703 H55716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672 NZ7807 AA256634 BE276324 AF263308 BF951698 T66089 F11783 F11784 H29379 R19493 H18042 AL133995 AW134660 AI299437 AA057405 AA917450 AI002692 T09262 R43839 H29290 T65008 H78357 AI221207 AI659856 AA913591 AI220302 NM_000786 U23942 BI601050 BG771947 BG773455 BI561558 BI460206 BG714348 BM126447 AU129411 AU129401 AL119303 AV724389 AU093323 AU127089 BG701614 BM150364 D55553 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 AI217668 AA399409 BE182318 BM128040 AI693998 AW615411 AW070426 AI124550 AW778736 AA477781 AW263013 AA59619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 BI916393 BM470755 BI333211 AA095636 BI256415 U47727 BG773392 N58531 AA264540 BG878564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H47580 R48858 T91611 H42019 BI869421 BG502073 BG425943 W37290 W13163 BE004451 BF208311 BI048717 N78122 AA226597 AI252534 AI963821 AA657925 AA935436 AW975068 BC000222 AL136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI227161 BG820180 AA54463 AA255885 N31549 AA326504 BC019924 BG257230 BI092368 BI869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF686779 AI755222 AA452772 AW241170 AU155655 F28259 T16319 AA362506 N64153 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 AI922439 BE270975 AI119339 BF956085 AI565178 AL554305 AL573240 AL572917 AI129627 AL546640 BE392285 AI092843 AI371057 BE302410 AI608763 AW674261 AI750057 AI052649 N47822 AL516249 AI589903 BG258439 AI123662 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 AI061112 AI783806 AL559622 AA070466 BF229936 N58159 H00288 N32598 H80279 AL581253 AW571884 AI361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 BI262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA362527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 BI085686 AA564566 AI221630 D52045 C14510 AA029390 W60153 H98743 AI682641 H28485 AA723093 AI081730 AA841309 AA687083 BI224818 AW204722 AI309186 AI215122 AI200785 BE467373 BM352502 AI304400 AI193071 AI742483 AW003408 AI400201 AI658740 AW665173 AI215120 AI147599 AI803429 AI076110 AI754349 AW205103 AI262491 AI808243 AI281007 AI051273 AI004801 AW768918 AW103289 AI47637 AI264446 AI699509 BE704420 AA989278 AA918256 AA830958 AA989425 AA911929 AA262598 BE740563 BE727592 BE761003 BG030940 BE258750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94863 N69544 AA181762 D20132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R66252 AA936029 AI813809 AA933607 AA129695 AA548261 AA714393 AA775006 AA653439 AA938308 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489683 D52138 D51696 D55942 D52740 AI000118 AL516304 AL534259 N54940 AL579194 AI669399 AI342925 BE939201 AA633000 BI222963 AI619676 AW180306 BF035010 AW087897 AI864969 T57243 R48211 AA113880 R26594 C14467 C14444 BI195459 BE896346 BE270780 AL568073 BG389833 BE891549 BI223147 AW381001 AA484864 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304 AI380443 AI240179 AA977516 AA864543 AW079380 AW294316 AI913755 AI884320 AI685770 H25135 AI972654 AI538592 AI174783 R12271 R83569 AI274757 AI559500 AW022192 AW970134 AA516420 AA543007 BG057526 BI001430 AJ498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656
20	432745 400263	112643_1 18977_1	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF888666 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
25			
30	411605	10026_3	
35	445636	8561_5	
40	420223 423476 441054 429925	191648_1 32437_1 2641490_1 33135_1	
45	434976 440191	121716_1 MH790_2	
50			
55			
60			
65	440409 44610 446091 431843	588375_1 2145292_1 515091_1 445334_1	
70	400262	18977_1	
75			
80			

TABLE 68C

Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
5	403047	3540153	Minus	59793-59968
	401424	8176894	Plus	24223-24428
	401451	6634068	Minus	119926-121272
	401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
10	404632	9796668	Plus	45096-45229
	403046	3540153	Minus	55707-55859, 56369-56511
	404922	7341893	Plus	13248-13428
	401519	6649315	Plus	157315-157950
15	401197	9719705	Plus	176341-176452
	401856	8018106	Plus	73126-73623
	405387	6587915	Minus	3769-3833, 5708-5895
	403752	7678857	Plus	33704-33828
20	404210	5006246	Plus	169926-170121
	401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
	406214	7342036	Plus	86320-86523
	403532	8076842	Minus	81750-81901
	400860	9757499	Minus	151830-152104, 152649-152744
	404913	7341740	Plus	97717-97976

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Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

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Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

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TABLE 69A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

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Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AU077196	Hs.82885	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624: Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931: Homo sapiens NADPH oxidase 4 (2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW996651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.145858	protocadherin 10	1.65
432673	AB028859	Hs.278605	Onaj (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*: CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301887	Hs.76224	EGF-containing fibulin-like extracellular	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448574	W31178	Hs.154140	ovary-specific acidic protein	1.47
407051	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	AJ824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AJ750878	Hs.87409	thrombospondin 1	1.89
	426535	AJ077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase Insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein [Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb:Y656g12s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AJ821409	Hs.304471	EST	1.45
40	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
45	406506			Target Exon	1.97
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22968	Intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptotagmin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407862	BE548267	Hs.337886	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	448727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414785	AJ246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiopoietin-2	1.91
	406627	T64904	Hs.163780	ESTs	1.78
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfamily	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF056085	Hs.198612	G protein-coupled receptor 61	1.65
	407704	BE316072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractual ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

5	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.74
	444409	AJ792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1369	decay accelerating factor for complement	1.74
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AJ380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfamily	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AJ834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW294102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AJ535997	Hs.30089	ESTs	2.39
20	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AJ346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219891	Hs.73625	RAB6 interacting, kinesin-like (rabkines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.76514	nucleoside phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
30	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AJ878857	Hs.109706	hematological and neurological expressed	1.65
	408669	AJ493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs;similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
45	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
50	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
55	449722	BE280074	Hs.23960	cyclin B1	1.76
	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242687	Hs.118651	hematopoietically expressed homeobox	2.15
	406954	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AJ701916	Hs.202509	ESTs	2.27
60	408989	AW381668	Hs.49500	KIAA0746 protein	1.43
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
65	407975	X89428	Hs.41716	endothelial cell-specific molecule 1	2.82
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	mulimerin	2.72
	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	2.25
70	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AJ056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AJ597655	Hs.49265	ESTs	3.08
75	422424	AJ186431	Hs.296638	prostate differentiation factor	2.96
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

779

5	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	AI193115	Hs.16611	tumor protein D52-like 1	2.27
10	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pycnodysostosis)	2.38
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	2.39
15	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427580	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
30	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	telranectin (plasminogen-binding protein	2.67
35	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXVD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
40	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.88
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
45	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425622	AW360847	Hs.16578	ESTs	3.01
50	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
55	414840	R27319	Hs.23823	hair/enhancer-of-split related with YRP	3.14
	424651	AI493206		ESTs	3.17
	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
60	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin (OSF-2os)	3.24
	447384	AI377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like	3.25
	447023	AA356764	Hs.17109	Integral membrane protein 2A	3.25
65	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gbc:Human H19 RNA gene, complete cds.	3.26
	410132	NM_003480	Hs.300948	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
70	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI091195	Hs.65029	growth arrest-specific 1	3.35
	451529	AI917901	Hs.208641	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
75	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
80	407938	AA905097	Hs.85050	phospholamban	3.48
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	Integrin, alpha 8	3.52
	404277			NM_019111*:Homo sapiens major histocompa	3.54

5	407815	AW373850	Hs.183850	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (porsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194579	WNT1 inducible signaling pathway protein	3.89
15	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
20	449925	AK342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.295049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW939251	Hs.25547	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.34
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78055	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
45	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235835	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	catponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
60	412636	1438_1
65		M77830 NM_004415 AF139065 BC681115 BG740377 BI712984 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925828 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE705863 BF985642 BE001923 BF833510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873879 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159648 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705957 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156821 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AA39101 AA451923 AI304326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI488588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77661 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF889173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

5
454042 30254_1
10
440820 3091_1
15
424651 46029_5

BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012
BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442
BI058659 BE813665 W95048 W25458 AW177788 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090
BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653
BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487
AJ420458 AI018523 AA708666 BF949633 AL119553 BF945960 AI081305 AA041432 AI821013 AI684910 AI654847 AW874199 AI206120
AW241428 RA3035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BI040435 BF931589 BI600000 AV722350
W27787 H45331 BI549761 R53955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199
AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI365468 N64350 AA779107 AW025969 R49056
AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202561 AA788851 AI494436 BF856114 H22570
AW964381 BG007409 BM314056 AA465642 T30661 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267360 N64249
W67500 F07962 AA322394 BI489987 BE644965 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325
AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302
N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV648384 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383
AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121
R56280
BG435302 BM083687 AA904035 AA488889 W76175 AA781874 H28767 AA910081 AA837086 AI521825 BG986378 AI478562 AA743152 AA746092
H88863 BG986375 AA635644 AM93206 AA669979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495

TABLE 70C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
25 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404277	1834458	Minus	91665-91946

30

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

35 Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymatrix/Eos Hu30 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 Pkey: Unique Eos probeset Identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 75th percentile of ewing sarcoma to 85th percentile of body map

Pkey	ExAccn	UnigeneID	Unigene Title	R1
104659	AW969769	Hs.105201	ESTs	70.3
101447	M21305		gb:Human alpha satellite and satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	46.6
110278	AF061573	Hs.19492	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008593	Hs.91622	neuronal pentadactyl receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U28690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	38.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	35.5
121362	AF050147	Hs.97932	chondromodulin I precursor	34.7
131291	NM_004350	Hs.170019	runt-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidyseri	28.7
122651	AW975398	Hs.293836	ESTs	28.0
100299	D49493	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
123619	AA602964		gbmo97c02.s1 NCLCGAP_P12 Homo sapiens	26.1
124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyl	23.1
116301	AW969706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	21.3
131313	R96290	Hs.75874	ribosomal protein L44	20.8
116790	AW161357		microtubule-associated protein tau	18.7
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1694	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW282315	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126799	AW753865	Hs.74376	olfactomedin related ER localized protei	16.3
105298	BE387790	Hs.26369	hypothetical protein FLJ20287	15.5
107160	AA314490	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40665	Hs.31564	ESTs	13.8
	106498	AJ221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;catyntarin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
10	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
15	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6816	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104968	AJ249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033084	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
25	123049	BE047680	Hs.211869	clckopl (Xenopus laevis) homolog 2	10.6
	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein Interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
30	110730	N67655	Hs.26411	ESTs	10.3
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAPI_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AJ204600	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-lin	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown [H.saple	8.8
55	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0458 protein	8.6
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109843	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AI347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AI823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66815	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133083	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h05.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp78111912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
80	119082	AF252297	Hs.91546	cytochrome P450 reductase metabolizing pr	7.7
	125400	AL110151	Hs.128797	DKFZP564D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

	105143	AI368835	Hs.24808	ESTs, Weakly similar to I38022 hypothe	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (7.6
	118036	AJ471852	Hs.195008	Homo sapiens cDNA FLJ11723 fis, clone HE	7.6
	131170	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	7.5
5	104548	R39398	Hs.91559	ESTs	7.5
	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
10	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893940	Hs.59698	ESTs	7.1
15	105127	AA045648	Hs.301957	nudix (nucleoside diphosphate linked mol	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gbnc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
20	128132	AA225632		gbnc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 fem1	7.0
	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	108213	N45018	Hs.8769	hypothetical protein DKFZp761J17121	6.9
25	118013	AI674126	Hs.94031	ESTs	6.9
	120147	AI917116		hemoglobin, beta	6.8
	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20824	6.8
	120325	AA195851		AP-2 beta transcription factor	6.8
30	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
	127664	AA806164	Hs.116502	ESTs	6.7
	109778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
35	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
40	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI869372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
45	134719	AA852885	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
50	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078845	Hs.431	murine leukemia viral (bml-1) oncogene h	6.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA: cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
55	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
60	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-53015	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypothe	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
65	109841	H01052		gb:bj32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AI088691	Hs.208414	Homo sapiens mRNA: cDNA DKFZp564D0472 (f	5.8
	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
70	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668831	Hs.159971	KIAA0379 protein	5.8
	128300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
75	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	5.7
80	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gbxyz8h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
5	126165	AJ741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AJ243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
	106668	R49390	Hs.254129	KIAA1678	5.4
10	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
	131185	BE280074	Hs.23960	cyclin B1	5.4
15	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
20	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N17807		gbxyz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferr	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/arginine rich (6.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41387	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	5.2
30	120830	AI568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	103318	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054728	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107659	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	116814	H50834	Hs.77899	gbxyz8a10.s1 Soares fetal liver spleen	5.0
50	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971148	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	109768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AJ476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AJ005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	125769	AA083456		gbzcn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gbxyz77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AJ022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AJ475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	XD2404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

5	113974	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bindl	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
10	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AJ571940	Hs.7549	ESTs	4.5
15	101031	J05070	Hs.161738	matrix metalloproteinase 9 (gelatinase B	4.5
	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
20	106489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
25	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
	102250	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127498	AI031650		ESTs	4.4
30	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61839	Hs.103822	ESTs	4.4
35	120922	AA481003	Hs.97128	ESTs	4.3
	115167	AA749209	Hs.43728	hypothetical protein	4.3
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
40	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
45	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106248	AL036917	Hs.288821	KIAA1638 protein	4.3
	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
50	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
	105073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AJ473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
55	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
	106012	AI240665		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130832	AW838006	Hs.20082	zinc finger protein 3 (AB-51)	4.2
60	125960	AJ754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
65	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73964	EphA4	4.2
	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
70	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypotheti	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
	119271	AJ061118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
75	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153748	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	ODC28 protein kinase 2	4.1
80	129948	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid)	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovirus	4.0
	127153	A1732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
10	100031			AFFX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
	128559	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo)	4.0
	126965	AA70523	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	4.0
15	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S3390 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
20	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
25	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_	4.0
	126522	W31912	Hs.21168	gb:zc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
30	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105808	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
35	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	AI668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
40	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	3.9
45	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
50	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	105476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
55	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19008	Hs.184780	ESTs	3.8
	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.8
60	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
65	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA295874	Hs.77494	deoxyguanosine kinase	3.8
	127262	AA828125		gb:xd71a09.s1 NCL_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UL-H-BI3-ala-a-12-0-ULs1 NCL_CGAP_Su	3.7
70	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87306	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
75	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
80	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	A1300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypothe	3.6
	125174	W51835	Hs.231082	EST	3.6
	104799	AA029703		gb:z895h08.s1 Soares_fetal_heart_NbH19W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X16868	Hs.333497	cytochrome P450, subfamily IID (debrisoq	3.6
20	124367	AI883183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypothe	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI494372	Hs.98958	hypothetical protein FLJ23058	3.5
	126996	BE181065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:yh16c10.r1 Soares Infant brain 1N18 H	3.5
	117265	AA451856		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protel	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128848	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	Insulin receptor substrate 2	3.5
	111223	AA652773	Hs.334838	KIAA1866 protein	3.5
60	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94563		gb:H.sapiens db/accbp gene exon 1 & 2.	3.5
	101088	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114098	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
80	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (tr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C188 protein	3.4
5	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	apoptosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypothel	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037756	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.186209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZP564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothel	3.3
	125693	H23989	Hs.169743	Homo sapiens clone Z5121 neuronal octet	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gb:ym37a05.r1 Soares Infant brain 1N1B H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA826974	Hs.32646	hypothetical protein FLJ21901	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54988	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404081		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv65f11.s1 Soares_tetal_tetus_Nb2HF8_	3.3
	123284	AA488988	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GC81 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129519	AA209534	Hs.284243	tetraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.286141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113826	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
5	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein I3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109566	H09103	Hs.30897	EST	3.2
15	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN IIII	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
30	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
35	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
45	134984	AI803516	Hs.272891	hippocampin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease H1, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
60	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809872	Hs.123304	ESTs	3.1
	114250	AI914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
75	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
80	123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.768	ESTs	3.1
	117297	AW779829		gb:hn88a05.x1 NCI_CGAP_Kd111 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88357	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
15	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA604021	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW182758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	126219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133956	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26966	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated protea	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485081	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
35	129928	AI338993	Hs.134535	ESTs	3.0
	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sept	3.0
	122219	AA436002	Hs.183161	ESTs	3.0
40	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
45	126902	AA036637	Hs.107052	ESTs	3.0
	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-II	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H58818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	105735	R77698	Hs.337778	ESTs	3.0
	126528	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AA99220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE266986	Hs.11896	hypothetical protein FLJ12089	3.0
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032984	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110fH4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	126887	H20832		gb:ym48d03.s1 Soares Infant brain 1N1B H	3.0
70	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

	108451	13766_27	AA079195 AA084955 AA126308 AA084956
	107908	46987_1	AF087999 N29296 AI928858 AA846757 N20229 AA026894 D80634 AW388923 AW388802 AW388957 AW571771 AW388839
5	123619	371681_1	AI686662 AW389079 AA502099 AW134567 AW517843 AI682674 AI474874 AA374167
	131495	142008_1	AA602964 AA609200
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			AI566634 AW971760 AA211796 AA430089
10	101445	1650_5	M21259
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	117265	10421_1	AA451966 NM_016370 AB036693 AL139228 R58124 AI634847 AI119333 W07356 AI334284 H29050 AI192685 AA652438
			AW172843 W19794 N21460 AI743852 AW130622 AA991348 AI204553 AA992664 N80848 AA699329 AI824676 R26624 R49653
	117297	647718_1	AW779829 N22494 AI248120
15	108859	137143_1	AL121500 AW291763 AI732432 AA129708 AA133309 AI733750 AI225224
	125165	1852047_1	W45350 W45406
	116790	19864_1	AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F06653 AI936671
20			AA476718 AW772454 AI807703 R44253 AA976667 AI985186 AI650254 H38942 R84829 AA018724 AA001000 H85934 AA019126
			H85609 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477
			AI857475 AW249771 AW162661 H38943 AA018628 R65885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221
			D53851 H85610 AI749674 F21582 AA323145 AA019127 AA687444 T08745 AI699293 H29532 AA214029 AA223656 NM_016834
			X14474 R19697 H09695 R17455 R13812 R19056 AI681231 AI590200 R37671 AA861828 AI990023 AI935669 AW005821 AA324581
			H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507
			T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045
25	103038	15024_1	AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267638 H83186 AA469909 N85396 AA001348 BE535736 AA081745
			BE566245 AA082436 H72525 H77575 N49786 W80565 H87846 BE569085 W04339 R99127 T55938 BE279271 AW960304 T29812
			AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955
			AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H58460 N31428 BE255916 H03265 AI857576 AA776920
			AA910644 AA459522 AA293140 AW514667 R75953 AW662396 AA662522 AI865147 AI423153 AW262230 AA584410 AA583187
30			AW024595 AW069734 AI828996 AA282997 AA876046 AW613002 AA527373 AW972459 AI831360 AA621337 AA100926 AA772418
			AA594628 AI033892 W85096 AI034317 AA398727 AI085031 N95510 AI459432 AI041437 AA932124 AA627684 AA935829
			AI004827 AI423513 AI094597 H42079 R54703 AI630359 AA617681 AA978045 AA643280 W44561 AI991988 AI537692 AI090262
			AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880
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35			AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AI494211
			AW059601 AW865710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789
			AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520
			H72923 H03266 BE261919 AA769633 AA480310 AA507454 AA910586 AI203723 W104725 W25611 W25071 T89980 H03513
			T77589 R99156 W95095 R97470 AA702275 T77551 AA911952 H82958 N83673 AA283672
40	126086	1606216_1	H75681 H70975
	126098	1629789_1	M79088 N88221
	125464	168460_1	N71807 AA203399
	126127	1205826_1	N95428 W24040 AW751368 H81987
	125558	1703083_1	R59305 R19748
	126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752
45			AA076512 AA085119 AA085208 AA085045
	118644	81501_1	AA443241 R23784 R67255 R00047 AI457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864
			AI953638 R31669 AW765278 R82398 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605
			AA327133 AI080590 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732
50			R78932 AA368675 R18760 R26523 H40161 W93671 R99823 R77958 H61601 R98785 R09738 H78317 H53537 H81056 T53780
			H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H68993 T48748 AI702300 R30775 H68996 AI014957 AA369082
			AF075351 AI110886 AI742050 AW954245 AI768458 C19062 AI393674 C18911 C18029 AA708613 AI168432 R67389 AI168453
			H00188 R21233 H03055 R53822 AA367558 R75872 W04151 AI220869 AI090290 AA368730 R94434 H81153 H70950 AA367783
			H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070
			R80360 H78318 H40199 R33887 R02529 H94918 R00900 T80729 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615
55			H60972 R98784 W66323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957082 R82759 C19002 H01715
	127262	231725_1	AA828125 AA834883 AA330555
	127315	37938_1	AF116622 AI114507 AA640834 AA377999
	103898	187213_3	AA248884
	126769	119008_1	AA083456 AA127028 AA084934 AA120972 AA085317
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	126080	1540039_1	F12310 T66402 H07202
	104590	44964_1	AW373062 T55652 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607
			AW898616 AA709126 AW898628 AW898644 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA587230 T62522
65			BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984
			AI922204 N98343 BE174213 AA845571 AI813854 AI214518 AI635252 AI139455 AI707807 AI680805 AW884528 AI024768
			AI004723 AW087420 AI565133 N94964 AI268939 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019
			AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337871 T62499 AA890205
			AI640908 H75956 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072
			AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
70	127496	340470_1	AI031650 AA860882 AI458212 AA524453
	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA84358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359
			BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
			H20832 Z40184
75	126887	1572189_1	AA225632 AI820970 AI820952 AA226472 AI732140 AI732059 AA226307 AA225500
	128132	177108_1	AA205976 AA205930
	126967	169750_1	AA195651 AW235123
	120325	166688_1	AW970420 AW973132 AA811736 AW301029 BE207945 AW449936 AI376801 AA039581 AA424444 AA810925 AA749267 BE205843
	112511	17406_2	AI360184 BE205945 AI761796 AI185049 R94606 AI343947 AI565814 AI341735 AI749190 AW269588 AI393145 AI520080
80			AW003752 AI750035 AI624837 AI797658 AA679066 N87182 AI937537 AW003753 R72610 R72724 AA757401 AA553744 AA460166
			AA535727 AW304422 R68273 AW027615 C01651 AI090327 AI538258 AW003744 AA938372 AW051486 AA505513 BE466452
			AA931719 AI174548 AW182752 T84662 R11149 AI767627 BE218556 BE217988 BE222697 AI782382 BE299559 AA987212
			AI767136 AI268928 AA090761 AA329290 AI700593 AA460766 BE222710 BE550651 R11148 AI979278 AW235819 AW874095
			AW196492

106012	95214_1	AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 A095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 A1803329 R27528 R36203 A1809932 A1808765 R78948 AA411449 AA976929 A1378760 A1378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02680 H12839 N58781 AA742532 A1360919 H03502 BE208298 R58588 A1350463 R31935 AW069127 AA411821 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
5	127705 966283_2 127728 3398_5 129012 22280_4	AJ003322 AJ003324 AW404061 R09654 T67160 N50566 N53259 R81936 D78695 D78806 D78780 C17009 AA004406 AA122102 R70625 AA148932 H59583 H81148 H80378 H49863 H21182 H46534 H51478 H20702 H46515 H40200 H50046 H23647 H50439 H18383 H21846 H23849 H40182 R21924 H01290 H01283 H42464 W31947 W39660 AA046219 H03539 H01741 R22008 AA043911 AA156838 D78832 R36616 R66039 A492481 AA088608 R69918 R35334 H80281 N58483 A1075154 A1086754 AA595787 H81051 H01187 A1057251 T96992 H59584 T47016 R31800 H13647 H01193 N74660 AA156601 H03455 R66040 R81937 R92416 H89486 R36617 R65795 A1088338 A1373324 H66992 R96235 A1494132 R16678 AA088178 AA705356 AA962143 AA148933 R09231 A1160937 R70525 T46980 A1200046 H02301 AA367587 R35968 T97106 D78703 N78072 D78668 D63268 R28197 AA085579 R63766 R92415 W00998 R80765 R67875 R27583 R09343 H13646 R27682 T89007
10	106498 245223_1	AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 A1341345 AW298800 AA724961 AA931158 A1741227 A1806660 A1982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 A492961 A1361526 F04002 AA452141 T23551 A1472655 A1193667 A1341984 N92658 T32870 R52664 N50428 AW089291 A1934175 A1423737 D60665 AA226198 AA226513 AA383773
15	120934 177521_1 115197 42408_1	R18656 AW958014 AA262288 AW968002 X93079 AJ002788 R51324 A1381600 D80031 AW500520 AW593740 F09382 AA810597 AA262174 AA810595 AA810596
20	129706 81501_1	AAA43241 R23784 R67255 R00047 A457612 R63254 R28645 R27616 H01310 R78329 R76046 R76055 AA369734 N57914 H94864 A1953638 R31669 AW769278 R82398 AA131925 R21776 R79031 A129553 N70340 A1276116 AA709381 N63734 A1342605 AA327133 A1805980 AA005377 AW611718 T86946 AA369083 R67250 H00240 R32578 W86279 R80248 R23734 H00977 R21732 R78932 AA368675 R16780 R26523 H40161 W93671 R99823 R77956 H61601 R98785 R09738 H78317 H53537 H81056 T53700 H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 A1702300 R30775 H68996 A1014957 AA369082 AF075351 A1110886 A1742050 AW954245 A1768458 C19062 A1393674 C18911 C18029 AA708613 A1168432 R67389 A1168453 H00188 R21233 H03055 R53822 AA367558 R76872 W04151 A1220869 A1090290 AA368730 R94434 H81153 H70950 AA367783 H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070 R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615 H50972 R98784 W86323 R09737 C17492 D78811 R67494 D78775 AA368244 H12650 D79043 AW957062 R82759 C19002 H01715 W28614 W27435 A1983043 AA364395 AW572472 AW190386 A129278 A1913081 AW473549 AA830713 A1982871 A1638647 A1828466 AW572486 N52583 N89687 AW075567 A1571047 A1887479 A1559469 A1685802 AA805256 A1458777 AA974369 A1866929 A1866032 A1823925 A1823566 AW198135 A1287510 A1565910 AA765775 A1866019 A1263697 A1355825 R42668 AA894603
30	131019 223488_3	AW105585 A1824555 AW339175 D20479 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039080 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A191631 A1498402 T61382 A1016320 N45526 T61415 AA331486
35	131170 8113_1	AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630168 AL041326 AA780690 L40517 U21556 A1093182 AW062487 AA833387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780049 AL043931 BE149744 AW963292 BE439669 BE091737 BE091657 AA484004 A1673095 AA599106 AW601545 A1538739 A1538730 A1521786 AW366369 AW021010 AA362576 A1289927 AA382592
40	123470 8785_29	AA608733 T74884 AA620552 U42359 N57493 H01052
45	123532 genbank_AA608733 125032 genbank_T74884 123808 genbank_AA620552 102398 entrez_U42359 118129 genbank_N57493 109841 genbank_H01052 118922 220560_1	AW206193 AW137594 A1953685 A1919143 A1242371 AW007698 AW025681 A1954289 R40438 AW070384 A1679653 A1679081 A1623213 A1652310 A1631411 A1565384 A1566734 AA149597 A1538172 A1040831 A1770021 A1914287 AA279311 W73001 A1493117 A1693374 A1802007 A1990645 N29752 R94559 AA806475 AA806828 R90998 R94558 AW300112 W24097 AW003016 N91920 T47910 AA029703 T91015
50	113119 genbank_T47910 104799 genbank_AA029703 113560 genbank_T91015 129794 39565_1	AF093097 A1869509 T27070 AA326718 AA024743 W23922 AA479593 A1765668 W23908 U92986 AA081632 N50578 AA065245 AW365046 AW365014 AA961091 AA150231 H53426 AA234651 N50522 T79343 T87399 N91858 H41179 AW009453 AA024744 T27069 A1346379 H88431 AA152289 R45373 AA477432 A1745607 A1807602 H41152 AA065244 A1242569 A1091032 A1251849 F03857 H88369 A1174488 A1002696 H53427 T87293 N91869 W35270 AA453723 AA453705 AW071829 A1393866 AW071807 W23592 A1342074 D31168 AA833756 A1991896 AA447791 A1864125 AW377239 AA295365 A1687570 R34076 F07607 AA521310 AW499865 R94584 R21283
55	124250 314220_1 101447 entrez_M21305 117357 genbank_N24829 103392 entrez_X94563 135029 H58818_at 105225 genbank_AA211777 121292 genbank_AA401807 105909 82840_1	AA350258 H68126 M21305 N24829 X94563 H58818 AA211777 AA401807 AA195191 AA190578 A1632307 AA195227 AA743633 A1823408 A1832203 A1653114 AA205307 AW021913 A1687980 A1674198 A1675563 A1417935 AA707350 AA135157 A1434721 A1515036 A1038305 R52643 AA780141 AW207645 D19691 A1474370 AA401739 N22905 N70378
60	100237 entrez_D30715 114988 genbank_AA251089 123423 genbank_AA598484	D30715 AA251089 AA598484
65		
70		
75		

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title

Seq ID No:		Seq ID number correlation for those sequences in Table 73			Seq ID No	
Pkey*	ExAccn	UnigenelD	Unigene Title			
5	103080	AU077231	Hs.82932	cydin D1 (PRAD1: parathyroid adenomas	Seq ID No B1 & B2	
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi	Seq ID No B3 & B4	
	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	Seq ID No B5 & B6	
	447761	AF061573	Hs.19492	protocadherin 8	Seq ID No B7 & B8	
	428183	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	Seq ID No B9 & B10	
10	439221	AA737106	Hs.32250	ESTs, Moderately similar to 178885 serin	Seq ID No B11 & B12	
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri	Seq ID No B13, B14, & B15	
	104659	AW969769	Hs.105201	ESTs	Seq ID No B16	
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	Seq ID No B17 & B18	
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	Seq ID No B19 & B20	
15	100299	D49493	Hs.2171	growth differentiation factor 10	Seq ID No B21 & B22	
	116301	AW969706	Hs.293332	ESTs	Seq ID No B23 & B24	
	106533	AL134708	Hs.145998	ESTs	Seq ID No B25-B27	
	131313	R96290	Hs.75874	ribosomal protein L44	Seq ID No B28 & B29	
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	Seq ID No B30 & B31	
20	113003	AW292315	Hs.7215	ESTs	Seq ID No B32	
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	Seq ID No B33 & B34	
	102745	AW753865	Hs.74376	olfactomedin related ER localized protel	Seq ID No B35-B40	
	123308	C14187	Hs.157208	ESTs	Seq ID No B41 & B42	
	120147	AI917116	Hs.211869	hemoglobin, beta	Seq ID No B43	
25	123049	BE047680	Hs.211869	dicckopf (Xenopus laevis) homolog 2	Seq ID No B44 & B45	
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	Seq ID No B46 & B47	
	105301	AW352357	Hs.7457	MAGE1 protein	Seq ID No B48 & B49	
	128478	AA708205	Hs.100343	ESTs	Seq ID No B50-B53	
	106111	AW875398	Hs.6451	PRO0659 protein	Seq ID No B54 & B55	
30	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	Seq ID No B56 & B57	
	120830	AI568170	Hs.96886	ESTs	Seq ID No B58 & B59	
	127664	AA806164	Hs.116502	ESTs	Seq ID No B60	
	102725	AB026187	Hs.159156	protocadherin 11	Seq ID No B61 & B62	
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	Seq ID No B63 & B64	
35	130637	AA356764	Hs.17109	integral membrane protein 2A	Seq ID No B65 & B66	
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	Seq ID No B67 & B68	
	128797	NM_002975	Hs.105927	stem cell growth factor, lymphocyte secr	Seq ID No B69 & B70	
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	Seq ID No B71 & B72	
	125770	AA143045	Hs.81665	v-kil Hardy-Zuckerman 4 feline sarcoma v	Seq ID No B73 & B74	
40	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	Seq ID No B75 & B76	
	420462	AF050147	Hs.97932	chondromodulin I precursor	Seq ID No B77 & B78	
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	Seq ID No B79 & B80	
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	Seq ID No B81 & B82	
	416836	D54745	Hs.80247	cholecystokinin	Seq ID No B83 & B84	
Table 72B						
Pkey:		Unique Eos probeset identifier number				
CAT number:		Gene cluster number				
Accession:		Genbank accession numbers				
50	Pkey	CAT Number	Accession			
	131307	3138_1	NM_000025 X72861 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134			
	131313	93372_1	R96290 H02411 C18327 AA367588 AA367557 HB9632 C17954 AA568850 AI752983 AA699451 H04260 AI128118 AW193364 N94503			
			AA029995 T40538 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226			
			AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R65618 H73711 R58545 D79189 AW265710			
55			R77684 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R87000 AA156623 AA368336 H63662			
	116301	52669_2	AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW968997 AA040053 AI807206 AW663917 AA454645			
			AA489238 BE241958 AA743491			
			AU077231 AA852219 M74092 X59798 M64349 NM_001758 AA226806 M73554 BE409154 AA160096 BE384352 AA160820 BE382880			
			BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW387101 AW367093 U47703 AI347077			
60			W05266 AI824103 AI49061 AA642944 AI042556 AA906539 W60380 AI571777 AL135581 AA112340 N75459 AA592929 AI085348 AI278890			
			AA126942 AI023701 AI873252 AA156319 AI190622 W60289 AI274886 R81309 AA100801 AA227161 AI568929 AA160603 AI074344 AI344561			
			AI150778 AA852218 AA158286 N20142 AA622148 AA864225 AA576357 AW182124 T89175 AI758455 AA780573 N17157 R81200 AI659596			
			AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620604 AI298125 BE075272 N40078 BE075109 BE080779			
			AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H66084			
65			AI146884 BE075154 AW992247 AI186526 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H93284 AA227101 AA631077			
			AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141			
			BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329			
			BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W46412 AW771113 AI700678 AA502628 AA133137 BE274186			
			BE396090 BE813371 BE012645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW169156 H24970			
70			AW298822 AW080962 AI073747 W24123 AA577596 H21716 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347			
			AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T92084 AI689037 AI624162			
			W49709 AW514883 AA100676 AI366087 AA089474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333594 AI289794			
			AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI065890 AI660881 AI366117 AA403090 AI272818			
			AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079968 AI752231 AA076431 AA113245			
75			AI168564 AA918965 AI066484 AI123599 AI921518 W94586 AA535600 AA064623 AA962503 AI924926 AW131206			
			AW275281 AI280632 T29597 W48728 AW954336 W38317 W94768 AI084717 W46567 AI245645 AW302501 N72201 AW510563 AW079132			
			AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526			
			AA487486 R92970 AA334071 AI080448 AA083257 C05786 N99099 R42969 AA887065 AA662686 AA533833 AA662304 H51748 BE539444			
			AI382164 AI814595 BE537043 AI168307 BE408335 AA453606 R89428 AA936527 AA936890 AW369618 AW284602 R18074 AI474189			
80			AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086652 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692			

132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW838107 AW838106 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE000988 AA131806 BE180577 AW838269 AL039831 A1754380 C06051 AA131737 AW838239 A1767455 AA801314 AA810312 AW383190 AA379252 AW838282 AA484027 AA423413 A1685064 BE328307 A1241857 AW838281 AW838284 A1571267 A1814928 AA828367 A1476306 A1270180 AA622362 A1076497 A1635519 A1444994 A1194028 A1669159 A1928131 AA448853 A1350143 AW079289 AW467807 AA480442 AA522935 BE180570 AW360087 AW380109 A1081015 A1690818 A1589485 A1698510 AA642019 AA714366 A1580430 AA985527 A1740475 C21398 AA257993 A1302393 A1689018 AW770194 AW753750 A1079164 BE550338 AA559851 T16108 A1864822 A1932827 AA045095 AA045062 A1954225 AA768569 AA709308 AW958363 N35020 AB026187 NM_014522 U79247 F13304 AA224524 F10902 R39431 AW753865 F07644 F11280 F06355 F08138 U79299 F07459 F08750 F12419 F12842 F06488 F08585 F13403 F05921 F05512 F11683 F05416 F12841 F12810 F05418 F12850 R24551 F06276 H11803 H10237 H11542 H22894 R59563 H19351 H16722 F11237 F08507 H23123 R61595 F07796 F06201 F12289 F07107 T78113 F08734 F13344 F05760 F11784 F08780 F05835 R20588 F07739 F11497 R17410 H17414 R20440 T66090 R25292 T66236 T78766 T79908 R25286 R60071 C14761 AW905192 AA331914 AW965291 H09000 F05212 F08313 F05825 H06399 H15135 H11378 R66424 R61541 AA235405 A1205041 R59564 H23124 H18638 R37359 A1571275 R41780 T66174 T66159 R54102 W07657 H10794 R52337 R42890 H14354 R40962 T17391 H12068 R56797 R51000 R60011 R37617 R39434 H29286 T16403 H09129 R49114 H15161 H11729 R39160 H10468 H24454 H11432 R54433 H08768 H24042 H09511 H17281 H15292 R37849 A1991965 R52815 R42850 T17390 T16438 T17388 T16285 R48963 R50782 R44247 R46729 R59558 R40696 R43575 R44420 T17403 R37754 R46537 R51039 R40513 T23785 F10433 T16350 H10191 R43688 T23543 H08591 R44351 R37575 R49508 F04379 F04056 F05067 F02010 F09158 F10038 F08900 F02559 F09914 F09434 F05034 H17415 F02644 H10650 F10451 H14589 F10444 T16440 R44517 R46643 F03993 F10443 F02170 F09343 F10414 F04794 F11122 F04997 F03894 AW005932 F02767 F10941 F01777 R45260 F03386 R45261 T65009 F10990 R08942 F01673 H23253 F04533 F02082 F10669 F03689 H09568 R40763 H06400 R05098 N06570 A1082296 A1198226 T23763 AA814486 AW015823 A1886272 H08514 AA515969 F10049 A1984267 A1886279 AA558516 F02071 A1783843 A1804884 F01468 AA730438 AF035301 R38389 R41440 R59468 R14437 T89036 R43580 H10821 R52850 R56722 R14559 T09299 H10467 R25829 F13546 R56786 R51151 D82657 T32952 T66257 H05659 F12430 T74326 H08489 R34430 R13083 H23364 R21134 T77098 AW557157 H24150 H11403 R52338 F12830 T77173 T74281 T77663 T74738 H10649 H12067 R20092 T74735 R54530 R17552 R59557 R54529 H17280 T75171 H14694 T74975 H15291 R18574 R54157 R13446 H15221 R35120 R35031 R21277 R19632 R35820 R05099 R13923 R36771 R26485 R33061 R20100 H24426 H09184 H15958 R19253 H15196 H09510 R36032 R19691 H14402 H14885 T17068 AF252297 N27888 F13415 R34552 R14377 AA323962 AW611514 AW614097 AW195487 A1026040 A1097663 AA012834 AW969885 AA988198 R49069 AW873673 R37774 F08840 AA484668 AW873664 AA170805 AA170825 AA585275 AA585280 AA012833 U94320 NM_006174 U66275 AA143045 AW271802 A1017093 AA450183 W93694 A1885044 A1890068 AW264522 AW073559 A1355325 A1051302 A1567686 A1143554 A1457891 AW468784 A1567693 AW884460 A1244892 AA401298 AW244098 A122938 N24824 AA552932 AA873164 A1308810 N26098 H18152 N20798 AW263947 A1696267 AA449422 AW877967 A1917116 AA633698 A1580389 Z39483 AW292315 A1090408 AW517041 A1928695 A1092060 A4716741 N98235 T23629 AW969769 AA484137 A1291362 N64753 AL137374 AA007153 BE046923 D59990 C16166 D59991 D60194 AA648108 N76160 D61027 D60630 U29690 AF272890 AA078166 AA010748 R23839 H59572 R23383 A1625747 AA011176 AW665324 H02174 H59573 A157931 H12502 R66851 AA702310 AA748431 AA749352 C01127 A1003679 T93352 AW352357 AA852419 T80568 AA332610 AW149659 AA341609 AA809550 A183690 AA730875 T31719 AW965536 A1A779709 T05461 AA584806 A142536 A1553857 D53384 D53747 D54101 D55112 AW071935 A1082447 A1290911 AW168872 A1199743 A1091646 A1246702 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AA730357 AI128690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087
 AA773947 AA469192 AI199289 AI127085 H89232 N30719 AI028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061
 N59622 AI360825 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407
 AA736720 AA664587 AA648572 AA503406 AA508123 AA503140 H45638 N75812 AA730938 D60548 AA483039 AA507705 AA480448
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 AA428252 AA769212 AA312778 AA810901 AA461315 AI969286 AI953668 AW296248 AI291422 AA704747 Z44718 BE541235 AW608806
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 D54745 AU077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571
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 AF050147 NM_007015 AB006000 AB005999 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194
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 AW136179 AA327834 BE327350 BE327366
 AW959726 AA424028 AI266636 AI271571 AA423988 AI266634 AA702780 AA452037 AI424856 AA742931 AA483361
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Table 73: Sequences

Seq ID NO: B1 DNA sequence
Nucleic Acid Accession #: NM_053056.1
Coding sequence: 210..1097

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	TCCCCAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCGG	CCGCGCGTAC	CCCAGTGCCA	ACCTCCTCAA	CGACCCGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAATGT	GTGCAGAAAG	360
15	AGGTCTCTGC	GTCCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCGAGGAAC	420
	AGAAAGTGA	GGAGGAGGTC	TTCCCGCTGG	CCATGAACCTA	CCTGGACCGC	TTCTGTGCG	480
	TGGAGCCCGT	GAAGAAAGAGC	CGCCCTGCAGC	TGCTGGGGGC	CACCTTGATG	TTCTGTGCGT	540
	CTAAGATGAA	GGAGACCATC	CCCTGACGG	CGGAGAAGCT	GTGCATCTAC	ACCGACAACCT	600
	CCATCCGCCC	CGAGGAGCTG	CTGCAATGG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTGG	660
20	ACCTGGCCGC	AATGACCCCG	CACGATTTC	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
	CGGAGGAGAA	GAAGAGAGATC	ATCCGCAAC	ACGCGCAGAG	CTTCTGTGCC	CTCTGTGCCA	780
	CAGATGTGAA	GTTTATTTC	AATCCGCCCT	CCATGCTGGC	AGCGGGGAGC	GTGGTGGCCG	840
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	GCTTCTCTC	CAGAGTGATC	AAGTGTGACC	CAGACTGCCT	CGGGCCCTGC	CAGGAGCAGA	960
25	TGGAAGCCCT	GCTGGAGTCA	AGCCTGCGCC	AGGCCAGCA	GAACATGGAC	CCCAAGGCCG	1020
	CCGAGGAGGA	GGAGAGGAG	GAGGAGGAGG	TGGACCTGGC	TTGCACACCC	ACCGACGTGC	1080
	GGGACGTGGA	CATCTGAGGG	CGCCAGGCAG	GCGGGCGCCA	CGCCACCCG	CAGCGAGGGC	1140
	GGAGCCGGCC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGGAGCATTT	TGATACCGAA	1200
	AGGGAAGCT	TCACTCTCCT	TGTTGTGGT	TGTTTTTCC	TTTGTCTCTT	CCCCCTTCCA	1260
30	TCTCTGACTT	AAGCAAAAGA	AAAAGATTAC	CCAAAACTG	TCTTTAAAAG	AGAGAGAGAG	1320
	AAAAAAAGAA	TAGTATTTC	ATAACCTGA	GCGGTGGGG	AGGAGGGTTG	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TGTTTTTAT	ATTAATGTAC	TTGTTTCTCT	1440
	GTGTGAAGAA	TAGGCATTAA	CACAAAGSAG	GCGTCTCGGG	AGAGGATTAG	GTTCATCTCT	1500
	TTACGTGTTT	AAAAAAAGC	ATAAAAAACAT	TTTAAAAACA	TAGAAAAATT	CAGCAAAACCA	1560
35	TTTTTAAAGT	AGAAGAGGGT	TTTAGGTAGA	AAAACATATT	CTTGTGCTTT	TCCTGATAAA	1620
	GCACAGCTGT	AGTGGGGTTC	TAGGCATCTC	TGTACTTTGC	TTGCTCATAT	GCATGTAGTC	1680
	ACTTTATAAG	TCAITGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAAAC	TCTTCACTTT	1740
	ATTCTAGGCT	GAAGTCACTT	CTTGGTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCTTT	1800
	TGCGCCCTGT	ACCACCACCC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
40	TGCGGCACCA	GCCAGCGTAG	CAGGGTCGGG	AAAGGCCACC	TGTCCCACCT	CTACGATACG	1920
	CTACTATAAA	GAGAGAGACA	AATAGTGACA	TAATATATT	TATTTTATA	CTCTTCTTAT	1980
	TTTTGTAGTG	ACCTGTATT	GAGATGCTGG	TTTTCTACCC	AACGGCCCTG	CAGCCAGCTC	2040
	ACGTCCAGGT	TCAACCCACA	GCTACTTGGT	TTGTGTTCTT	CTTCATATTC	TAAAACCAAT	2100
	CCATTTCCAA	GCACTTTCAG	TCCAATAGGT	GTAGGAAATA	GCGCTGTTTT	TGTTGTGTGT	2160
45	GCAGGAGGGG	CAGTTTTCTA	ATGGAATGGT	TTGGGAATAT	CCATGTACTT	GTTTGCAGAG	2220
	AGGACTTTGA	GGCAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGCCAG	TCAAGAGGAA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCCT	2340
	TTCTTTTCT	TTAAAGAGT	TGAAGTTTAG	GAATCCTTTG	GTGCCAACTG	GTGTTTGAAG	2400
	GTAGGAGACT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGGTTAT	CTTAGATGTT	2460
50	TCACACCCGA	AGGTTTTTAA	ACACTAAAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
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	TTAAACACAC	AGATACACAC	ACACACACAC	ACACACACAC	AAACCTTCTG	CCCTTGTATG	2640
	TACAGATTTA	ATACAGTTTA	TTTTTAAAGA	TAGATCCTTT	TATAGGTGAG	AAAAAAACAA	2700
	TCTGGAAGAA	AAAAACCA	CAAGACATT	GATTACGCC	GTTTGGCGTT	TCCAGAGTCT	2760
55	ATCTGATTGG	ACAGGCATGG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTGCGTTCC	2820
	GATGAATTCT	TATCCCTCTG	CCCTTCTCTT	AAAAAACTTA	GTGACAAAT	AGACAATTTG	2880
	CACATCTTGG	CTATGTAAAT	CTTGTAAATT	TTATTTAGGA	AGTGTGAAG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGGAGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGCTC	3000
	CCGAGGGGAA	GGGGCGGTGC	CCACACCGGG	GACAGGCGCG	AGCTCCATTT	TCTTATTGCG	3060
60	CTGCTACCGT	TGACTTCCAG	GCACGGTTTG	GAATATTCA	CATGCTTCT	GTGTATCTCT	3120
	TTACATTGT	TTGCTGCTAT	TGGAGGATCA	GTTTTTTGT	TTACAATGTC	ATATACTGCC	3180
	ATGTACTAGT	TTTAGTTTTC	TCTTAGAACA	TTGTATTACA	GATGCCTTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATTC	CAAAAAGGTT	3300
	GCTGTTTTCAC	AATACCTCAT	GCTTCACTTA	GCCATGTTGG	ACCCAGCGGG	CAGGTTCTGC	3360
65	CTGCTTTGGC	GGGCAGACAC	GCGGGCGCGA	TCCACACAG	GCTGGCGGGG	GCGGGCCCGG	3420
	AGGCCGCGTG	CGTGAGAAAC	GCGCCGGTGT	CCCCAGAGAC	CAGGCTGTGT	CCCTCTTCTC	3480
	TTCCCTGGCG	CTGTGATGCT	GGGCACCTCA	TCTGATCGGG	GGCGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATTCTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTTAA	CGTGCCACCA	CGGGTTTGT	CCTGTAGGAC	TCTCATTTCCG	3660
70	GATGATTGGA	ATAGCTTCTG	GAATTGTTC	AAGTTTGGG	TATGTTAAT	CTGTTATGTA	3720
	CTAGTGTCT	GTTTGTATT	GTTTTGTAA	TTACACCATA	ATGCTAATTT	AAAGAGACTC	3780
	CAATCTCAA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCGG	GTACCTAGC	AAGCTGCCGA	3840
	ACCAAAAGAA	TTTGACCCCC	GCTGCGGGCC	CAGTGGTTG	GGGCCCTGCC	CTGGCAGGGT	3900
	CATCCTGTGC	TGGGAGGCCA	TCTGGGGCAC	AGGCCACCCC	CGCCCCACCC	CTCCAGAACCA	3960
75	CGGCTCACGC	TTACCTCAAC	CATCCTGGCT	GCGCGGCTG	TCTGAACCC	GCGGGGGCCT	4020
	TGAGGGAAGC	TTTGTCTGTG	GTGATGGGGC	AAGGGCACAA	GTCCCTGGAT	TTGTGTGTAT	4080
	CGAGAGGCCA	AAGGCTGGTG	GCAAGTGCAC	GGGGCACAGC	GGAGTCTGTC	CTGTGAOCCG	4140
	CAAGTCTGAG	GGTCTGGGG	GCGGGCGGCT	GGGTCTGTGC	ATTTCTGGTT	GCACCGCGGC	4200
80	GCTTCCGAGC	ACCAACATGT	AACCGGCATG	TTTCCAGCAG	AAGACAAAAA	GACAAACATG	4260
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Seq ID NO: B2 Protein sequence
Protein Accession #: NP_444284.1

1 11 21 31 41 51
797

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 5 ATWMLVECEE QKCEBEVPL AMNYLDRPLS LEPVKSRLO LLGATONFVA SKMKETIPLT 120
 AEKLCIYTDN STRPEELLQM ELLLVNKLWN NLAAMTPHDF IEHPLSKMPE ABEKQIIRK 180
 HAQTFVALCA TDVRFISNPP SMVAAGSVVA AVQGLNLRSP NFPLSYRLT RPLSRVIKCD 240
 PDCLRAQCEQ IEALLESSLR QAQONMDPKA AEEEEEEEEE VDLACTPTDV RDVDI

Seq ID NO: B3 DNA sequence
 Nucleic Acid Accession #: XM_044166
 Coding sequence: 1..1576

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 15 CTTTGTGTTT GCCATGCTTA GTCTAGTGGT ATCTGGAATA ATGGAAGAA ATGGGGGCTT 60
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 CAGGCGCGGC GAGGACGGGG GAGGTGGGGG GGGCGGCGCC CCGGCGCAGC CGACAGCCCC 240
 CCGGCGAGCG CGCCGCGCGC CGCGCGCGCG GGGCGCCCCG GCGCGCCCGA CGACGGCCCC 300
 20 CGCAGCGCAG ACGCCCGAGC CCCCCACCGC CCCCAAGGGG GCGAGCGAGC CCAAGCTCTG 360
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 TCCGCTGCCC ACCTCGAGC ACGTGGCCGA GATCGTGGG AGGCAAGGCT GCAAGATTAA 480
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 GTTCATGTGT ACAGGGCGAG GGGAGGACGT GGCCACAGCC CGGCGGGAAT TCATCTCAGC 600
 25 AGCGAGCAC TTCTCCATGA TCCGTGCTTC CCGCAACAAG TCAGGCGCGC CCTTGGTGT 660
 GGCCTCTGCT CTGCGCGGCC AGGTGACCAT CCGTGTGGG GTGCGCTACC GCGTGGTGGG 720
 GCTGTGTGTG GGCCTCAAGG GGGCAACCAT CAAGCGCATC CAGCAGCAAA CCAACACATA 780
 CATTATCACA CCAAGCGGTG ACCGCGACCC CGTGTTCGAG ATCAGCGGTG CCCCAGGCAA 840
 CGTGGAGCGT GCGCGCGAGG AGATCGAGAC GCACATCGCG GTGCGCACTG GCAAGATCCT 900
 30 CGAGTACAAC AATGAAAAAG ACTTCTGGC GGGGAGCCCC GACGCGACAA TOGATAGCCG 960
 CTACTCCGAC GCCTGGCGGG TGCAACAGCC CGGCTGCAAG CCGCTCTCCA CCTTCCGGCA 1020
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 AGTGACTGCC GCGCTGTGTC CCGCGGACCA CAACCTGTTC TGATGGAGT GTGCAGTACG 1500
 40 CATCTCGAG AGGACGGAAC CAGAGTGTTC CGTCTGCCAC ATCAGAGCCA CGCAAGCCAT 1560
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 50 CTACCAAGCC AGCTTTGGGG ACACCATCCT TCTGGGAGA AGTAGGGGGA GGAATATTGG 2160
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 AATACTGGGG TAAAGGGTCA AAGCCCCACC TTCATCACTA TGGGCATTAT ATTTAGGGAG 2340
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 55 ATTTAAGAGT ACAGGAAAGG GCGTGAAGCA GAGGAGAGGA CTGGTGGAGG GAAGAGCTCG 2460
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 65 GGAAGGAGGT CACAGCCAAAG AAAAATGCCC TGTGAAGACT TCCCTCTTTC CCGCTATGCT 3060
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 AGAAACAAA AATAGCAAAA AAAAAAAA AAAGCAGTTC TTTATAATT AATATTCTAT 3420
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Seq ID NO: B4 Protein sequence
 Protein Accession #: XP_044166.2

1 11 21 31 41 51
 75 FCFAMPSLVV SGIMERNNGF GELGCFGGSA KDRGLLEDER ALQLALDQLC LLGLGEPPAP 60
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 80 ALYKEAELRL KGSNTTECV PVPTSEHVAE IVRGQCKIK ALRAKTNTYI KTFVRGEEPV 180
 FMVTGRREDV ATARRIEISA AEHPSMIRAS RNKSGAAGV APALPGQVTI RVRVPYRVVG 240
 LVVGPKGATI KRIQQQTNTY IITPSRRDRP VPEITGAPGN VERARBEIET HIAVRTGKIL 300
 EYNNENDFLA GSPDAALDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360
 GEQGGDFGYG GYLFPYGVGV KQDVYYGVAE TSPPLWAGQE NATPTSVLPF SASSSSSSSA 420

KARAGPPGAH RSPATSAGPB LAGLPRRPPG EPLQGPSKLG GGGLRSPGGG RDCMVCPESE 480
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5 Seq ID NO: B5 DNA sequence
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209..1363

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    ATAATCTATA ACAACCAAAC CAATCAAAAT GAATTCACCA TTATTTTCCC AGGTGGAATA 240
    TCATTGAGTC CACTCTAATT TCTCAGAGAA GAATGCCAG CTCTGGGCTT TTGAAAATGA 300
15  TGATTGTGAT CTGCCCCTTG CCATGATATT TACCTTAGCT CTGTCTTATG GAGCTGTGAT 360
    CATCTCTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420
    GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTGTCAT 480
    CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540
    GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT 600
20  GGTTCCTCAT GTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660
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    GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGATGC 780
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    TACCACTCTC CTCTTGGTGC TGCAGTATTT TGGTCCACTT TGTTTATAT TTATTGCTA 900
25  CTTCAAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGACAAGA TGAGAGACAA 960
    TAAGTACAGG TCCAGTGAAA CAAAAAGAAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
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    ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGAAC AAAAATCTTC AGAGAGACTT 1200
30  GCAGTTCTTC TTCAACTTTT GTGATTTCGG GTCTCGGGAT GATGATTATG AAACAATAGC 1260
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    GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
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    TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
40  TAGTGTGTTA CAATAGTAAC AGTATGCAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
    GAAGTCATTG TGAAGTGGTT TGAGGTTTCT GTTTTGGT GTTTTGTGTT TGTTTTGT 1920
    TTTTTCACC TTAAGGGAGG CTTTCATTTC CTCCGACTG ATTGTCACTT AAATCAAAAT 1980
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    GTTAATGTGC CTAATTTTCA GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTGAGG 2580
    AAACATATAT TTAAGAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640
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Seq ID NO: B6 Protein sequence
Protein Accession #: NP_000900.1

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    CVSITVSIPS LVLLAVERHQ LIINPRGWRP NNRHAYVGLA VIWVLAVASS LPFLYQVMT 180
65  DEFPQNVTLA AYKDKYVCFD QPPSDSHRLS YTTLLLVLYQ FGFLCFIFIC YFKYIYRLKR 240
    RNNMMDKMRD NKYRSSETKR INIMLLSIVV AFVNCWLPIT IFNTVFDWNL QIATCNENL 300
    LFLLCILHAM ISTCVNIFY GFLENKFPQRD LQFFNFCDP RSRDDYETI AMSTMHTDVS 360
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70 Seq ID NO: B7 DNA sequence
Nucleic Acid Accession #: NM_002590.2
Coding sequence: 204..3416

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    TTCCGAGAGC CTGAGACTGA CGCCCGACCT GGAAACACAGA GAAGACTTCC TTAGCCTTTC 180
80  GGATCGCACT TGAAGCTGGA GGCATGAGTC CTGTGAGGCG TTGGGGCAGC COCTGCCTTT 240
    TCCCTTGCA GCTCTTCAGC CTCTGCTGGG TGCTCTCAGT GGCCGAGAGC AAAACAGTCC 300
    GATACAGCAC CTTGAGGAG GATGCCCGCG GACAGTCAT CGGACCCCTG CGCAGGACC 360
    TGCAATGAA AGTATCGGGT GACACAAGCT TCCGCTGAT GAAGCAATTC AACAGCTCTC 420
    TGCTCCGGGT CGCGAAGGC GACGGGCAGC TGACCGTCGG GAGCGCCGCG CTGACCCGCG 480
    AGCGGCTGTG TGGCCAGGCC CCGCAGTGG TGCTGGCCTT CGATGTGGTC AGCTTCTCGC 540

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5 AGGAGCAGTT CCGGCTGGTG CACGTGGAGG TAGAGGTGAG GGACGTCAAC GACCACGCGC 600
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 10 CCGAGGAGGG ACCTAACGGC GACGTGGTGT TCGCATTTGG GCGCCGACCC CCGCCGAGG 1080
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Seq ID NO: B8 Protein sequence
 Protein Accession #: NP_002581.2

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 70 HSPAPPQVAG AEVELAEDAP VGLLLLDLDA ADPDEGFNGD VVFAFGARTP PEARRLFRLD 300
 PRSGRLTLAG FVDYERQDTY ELDVRAQDEG PGFRAATCKV IVRIIRDVNDN APDIAITPLA 360
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 AFAIGRRTGE ILLTGDLSE PPGRVPRALL VISDGGRPPL TTTATVSPV TAGGGRGPA 720
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 FNTISGREAE KPSGKDSGKG DSDFNDSDD ISGDALKKDL INHMQSGLWA CTAECKILGH 960
 SDRCWSPSCS GPNAPSPHP PAQMSTFCKS TSLPRDPLRR DNYQAQLPK TVGLQSVYEK 1020
 VLHRDYDRTV TLLSPRPGR LFDLQBIGVP LVQSPPGRYL SPKKGANENV

Seq ID NO: B9 DNA sequence
Nucleic Acid Accession #: AL121939.12
Coding sequence: 185..1426

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GCTCAGGCTG GCTGAGAGGC TCCCAGCTGC AGCGTCCCGG CCGGCCTCCT CGGAGGCTCT 120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAGCCTG GCAGGACAAA ATTAGAAGAT 180
10     CAAAATGGAA AATATGCTGC TTGGTTGAT ATTTTTCACC CTGGGTGGA CCCTCATTGA 240
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15     AGTTCAGAT TTGGTTCCTG AGCCGACTCA AATATCACC ACAAGGGGAG TATCTGTTAG 540
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45     GCTACATTTT TAGGACAAAG AATTCTGTAA TCTTTTCAA GAAAGAGTCT TTTTCTCCTT 2340
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Seq ID NO: B10 Protein sequence
Protein Accession #: CAC35071.1

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KRQVYGTDSR F8ILDKRFLL NFFPSTAVKL STGCSGILIS PQHVLTAHCH VHDGKDYVK 180
SKDLRVLGK MRNKGSGKRR RGSRRSRREA SGGDQREGTR EHLRERAKGG RRRKKSGRGQ 240
60     RIASGRPSQP WTRVKNTHIP KGWARGGMD ATLDDYDALL ELKRAHKKKY MELGISPTIK 300
KMPGGMIPHS GPDNDRADQL VYRPFCSVSE SLDLLYQYCD AEGSGTSGSV YLRLLKDPDKK 360
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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002035.1
Coding sequence: 108..1106

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CCAAGCCCTC CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
75     GGAAGTGAT TGCTATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGCAAGAA 300
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80     ATTACCTGGG CAGCGTGTAC CCCAGCGGG CCGTGTACAC CACCATGAAG GAGCGCGGG 600
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CTTACTCTGC ATCCAAGTT GCCATAAGGG GATTGGCAGA AGCTTTGAG ATGGAGGTGA 720
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CCGAGAGAAA CAGAACAAAG CCTTTGGAGA CTCGACTTAT TTCAGAGACC ACATCTGTGT 840
GCAACCAGA ACAGGTGGCC AACCAAATG TTAAGATGTC CATACAAGGA AATTTCACAA 900

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GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960
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 20 TTAGCATCTA CTGTGTTTTT CCATCTCTTC CTTTCCAATT TTGCTTATAC TGCTGTAAATA 2040
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25 Seq ID NO: B12 Protein sequence
 Protein Accession #: NP_002026.1

30 1 11 21 31 41 51
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 CAGMAVSGKF EDLEVTFFER LMSINYLGVS YPSRAVITTM KERRVGRIVP VSSQAGQLGL 180
 PGFTAYSASK PAIRGLAEAL QMEVKPYNVY ITVAYPPDIT TPGFABENRT KPLETRLISE 240
 35 TTSVCKPEQV AKQIVKDAIQ GNFNSSLGSD GYMLSALTG MAPVTSITEG LQQVVTMGLF 300
 RTIALPYLGS PDSIVRRQPM QREKSENADK TA

Seq ID NO: B13 DNA sequence
 Nucleic Acid Accession #: CAT Cluster

40 1 11 21 31 41 51
 CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTAA TTTTAAAAAT 60
 CGGCAAAATA TTGGTGCTT TCCCGAAATT TGGTCCCGGG CTCCTTATA GGATAATTGG 120
 45 TTGGGATTGG TTAAGTCCAA TTATTAAATG CTGCGGTTTC AAATTCAGG CTGGAAGGAC 180
 CACCCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAATAAT 240
 CCAGGCATTG GTTTGACATA TTTCCAGAGC TCAATCTGCG AGTGTTCAC ATGCACATAC 300
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 TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
 50 AAGAACACAT AAGATGCCTT CTTCATCAA ATGCACTTGC TTGTGAATTA ATGGACTTGT 480
 AAATGAACA ATGCAATCAG TCTTTTATAA TGCACTGTTC AATTGAGAT TCAAGTATT 540
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55 Seq ID NO: B14 DNA sequence
 Nucleic Acid Accession #: XM_086767.1
 Coding sequence: 276..611

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 65 ACCTCTTAGG ACCACTGTGT TTTTGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240
 ATTTTOTTCT CAGTATAATT GTTCCAGATA AAACATGAT GGATGGCTCG TTTTCATTTA 300
 AATTATTAAA TCAGCTTGGG ATGATTGAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT 360
 TTTATAAAT TCAAGAAGTC AAGATTCTTG CTCATTTTAA TAATGACTTT GTAAATATT 420
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 70 AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCCACA CTTTGCAGGT 540
 ATAAATTTGT ACTTAAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600
 AGAACACATA AGATGCCTTC TTCCATCAAA TGCACTGTCT TGTGAATTA TGGACTTGTA 660
 AATGAACCAA TGCAATCAGT CTTTATAAT GCACGTGTCA ATTTGAGATT CAAGTATTTC 720
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 AACATTCC

75 Seq ID NO: B15 Protein sequence
 Protein Accession #: XP_086767.1

80 1 11 21 31 41 51
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 LQCTCTYIKI QRLLMLSLTY PERPPLCRYN IVLKDRREV LNPNTCTPKN T

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

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      ATGCACAATG GTACATATGC ACAAAATGGA ATTATATCAA CAAATATACA AAATACCCAA 240
      AATAAAATAT TTACAGGTTT AAAAAATATA ACATTGATTC CTCTATCCCA TTAAACCATT 300
10     GGAGTGGAGA AAGGAGGAAA GACCCATTG CTATTAGAA TCCTTTTAA AACAGTTT 360
      TAAAACATAG AATTAGTTCT AGGAGACAAT TTTTGATGTT TTTGAGGGT TTAACATTCT 420
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      CTGCCAAAC CTGTCTCTCA AGACATGCCT GACTTTTCAG AAAGCTAATT ATGGAAATGG 540
      AGTTTCTGTT TTGGGTTATC TTTGTTACTA TTTTCAATA ACCAGCAACT CCTATATTA 600
15     CACTGAGATA CTTTATATAA ATAACTGGG CGAAACCTGA AGTTCACAAT GAGCCTGCTA 660
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      TTCCCTGATA TTCTGTATAG ACCTACCACT ATCAGATCCT CCATATTCAA TAAGATTAT 780
      CCTGGAAGCA ATGAAAATGT TAAATATTAC TTTGCTAGAG TTTCTCTCC TTTATTAGA 840
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20     CCTTCAGACC CATGCCG

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Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM_022898.1

Coding sequence: 268..2739

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30     AAACACCAAC CCGGGCAGAG GAGGAGGTGC GCGGGCGCGG CCGGGCGCGG CAGCGGCGGC 180
      AGCGGCGCGG CGCGGCTCG GACCCCTCC CCCGCTCCC CCATCAGTG CAGCTCTCCG 240
      GGGGATGCCA GAATAGATGC CGGGGCAATG TCCCGCCGCA AACAGGGCAA CCCGAGCAC 300
      TTGTCCGAGA GGGAGCTCAT CACCCAGAG GCTGACCATG TGGAGGCGCG CATCTCGAA 360
      GAAGAGGAGG GTCTGGAGAT AGAGGAGCCA AGTGGCTCG GGTGATGGT GGTGGGCCCC 420
35     GACCTGACC TGCTCACTG TGGCCAGTGT CAAATGAAC TCCCTTGGG GGCATCCTG 480
      GTTTTATAG AGCACAAAAG GAAGCAGTGT GCGGCGAGCT TGGTGGCTG CTATGACAAG 540
      GCCCTGGACA AGGACAGGCC GCCACCTCC TCAGCTCCG AGCTCAGGAA AGTGTCCGAG 600
      CCGGTGGAGA TCGGATCCA AGTCAACCCC GACGAAGATG ACCACCTGCT CTCACCCACG 660
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40     TGCACAACAT GCAAGCAGCC CTTCAACAGC GCGTGGTTC TGCTGCAGCA CGCGCAGAAC 780
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5 GAGATGTAGC ACTCATGTGC TCCCGAGTCA AGCGGCCCTTT TCTGTGTGA TTTCCGCTTT 3480
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Seq ID NO: B18 Protein sequence
 Protein Accession #: NP_075049.1

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 AGACCTTCAC TACATGGGCG AAGTTCTCCA TTGACCTCA GTACCTGGT GCCAGCTGCT 660
 ACCCAGAAGG CATAATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGCT ACTTCCCCAG 720
 CTTCAACCAAC AGCCTCATCT AGCGTCACCT CTGCTCCGCC CAACCCACTG GCCACAGGAC 780
 CCTGGGTGT GTGCACCATG TCCCAGACCC AGCCTGACCT GGACCACTG TACTCTCGCG 840
 CACGCGCTCC TCCTCCTTAT TCTGGCTGTG CAGGAGACCT CTACCAAGAC CCTTCTGGGT 900
 TCCTGTCAAG AGCCACCACT TCCACCTCTT CCTCTCTGGC CTACCCACCA CCTCTCTCTC 960
 ATCCATCCCC CAAGCCAGCC AGCGACCCAG GTCTCTTCCC AATGATCCCA GACTATCCTG 1020
 GATTCCTTCC ATCTCAGTGC CAGAGAGACC TACATGTTAC AGCTGGCCCA GACCGTAAGC 1080
 CCTTTCCTCG CCACCTGGAC ACCCTGCGGG TGCCCTCTCC ACTCACTCCA CTCTCTACAA 1140
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 ATTTGAGATA AGAATGTACA TAAATGTACC GGAGCTGATT TGTGTTGTCA TTAGCTCTTA 2880
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Seq ID NO: B20 Protein sequence
 Protein Accession #: NP_000390.2

1 11 21 31 41 51
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 LQGVTSFST TASSSVTSAS FNPLATGPIG VCTMSQTQPD LDHLYSPPPP PFPYSGCAGD 180
 LYQDPSAPLS AATTSTSSSL AYPPPPSYPS PKPATDPGLF PMIPDYPGFF PSQCQRDLHG 240
 TAGPDRKPPF CPLDILRVPP PLTPLSTIRN FTLGGPSAGV TGPGASGGSE GPRLPGSSSA 300
 AAAAAAAYY NPHHLLPLRI LRPRKYFNRP SKTPVHERFY PCPAEGCDRR PSRSDBLTRH 360
 IRIHTGHKPF QCRICMRNPS RSDHLTTHIR THTGKPPFAC DYCGRKPARS DERKRHTKIH 420
 LRQKERKSSA PSASVPAPST ASCSGGVQPG GTLCSSNSSS LGGGPLAPCS SRTTRP

Seq ID NO: B21 DNA sequence
 Nucleic Acid Accession #: NM_004962.2
 Coding sequence: 457..1893

1 11 21 31 41 51

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 GGCTGACAGG GGGACAGGGA TCTCCAGCGG CACCTGGGG ACGGCGCGCG CACGTTGGGC 660
 CCGAGCGCCC AGGACATGGT CGCTGTCCAC ATGCACAGGC TCTATGAGAA GTACAGCCGG 720
 CAGGGCGCGC GCGCGGAGG GGGCAACAG GTCCGCGAGT TCAGGCGCAG GCTGGAAGTG 780
 GTGACACAGA AGGCGGTGTA TTTCTTCAAC CTGACTTCCA TGCAAGACTC GGAAATGATC 840
 15 CTTACGGCCA CTTTCCACTT CTACTCAGAG CGCCCTCGGT GGCCCTGAGC GCTCGAGGTG 900
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 20 ATGTCAGAG CGCGCGCGCG GGATGGGAG CTGCTCCTCT CGGCCAGCT GGAATTCGAG 1140
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 GCCCAGCAGA GCTGCTTCTT CGGAGCCTTC TGCAACCAAG ACTGTGGTGT CAGCTGCAGA 1980
 35 CACAGACGAC AGCTCATGGG CAACATCACT GGGGCCAGA GAGAGCTGTC CGCCAGTGCA 2040
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 40 TAAATGCTCA GTTCAGAACCA CTTTGGGCCA CATAGTGATT TTGAAAACA GGATAATCGT 2340
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 CATGTAGCCA ATATTGTTTT CTTTCTTATA ATATATATAT TTTATTTTAA AACACAAAA 2460
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 CATGCATATT GAAATAACAC ATATAGTAAC GTGGGAATAC TAAATAATAA CCAAGATTTT 2580
 45 ATATTTTTGT AAATTATACT TTCTATACCT TAGATTGTGT ATGTTATGTG TTTTATGGA 2640
 AAGCTAATAA ATTAAGGTA CAGTGGTATC TTGA

Seq ID NO: B22 Protein sequence
 Protein Accession #: NP_004953.1

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 GDAATLQPS AQDMVAVHMH RLYEKYSROG ARPGGENTVR SFRARLEVVD QKAVYFFNLT 120
 55 SMQDSAMILT ATFHYPYSEPP RWPRALEVLC KPRAKNASGR PLPLGPFTQ HLLFRSLSQN 180
 TATQGLLRGA MALAPPPRGL WQAKDISPIV KAARRDGELL LSAQLDSEER DPGVPRPSPY 240
 APYILVYAND LAISEPNSVA VTLQRYDPFP AGDPEPRAP NNSADPRVR AQAATGFLQD 300
 NELPLQDERP PRAHAQHFKH HQLWPSFPRA LKPRPGRKDR RKRQGEVPM ASQVLDPDEK 360
 TMQKARRQW DEPRVCSRRY LKVPFADIGW NEWIISPKSF DAYYCAGACE FPMFKIVRPS 420
 60 NHATIQSIVR AVGIIPGIPE PCCVPDKMNS LGVLFLEENR NVVLKVYPM SVDTACR

Seq ID NO: B23 DNA sequence
 Nucleic Acid Accession #: AK026322.1

65 1 11 21 31 41 51
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 ACATATCCTT GCTTCTTCCC ATATTAGTA AAGTTTAGTT GGATGCTGGA TTGTTTAAAT 180
 70 TTAGCATTTT GGAGTGACTG CTTTGGCACT TGCCCTTAAA AGTATTGGAC TTCGTTTGA 240
 TAGTTGAATT ACTTGCAAT CAGCTTGATC ATTCTGAGAC TTGTTTTTAA CTTTGTGCGA 300
 AAAGGCTATG CTACTTCAAG TATAATAAAA CCTAGTTTAA GTTTTATCCT ATAACAAAGG 360
 CATGTGTTCA ATTGGAATGT CTCCAACCTT GTGTGAACCT TGAAAAATGT TCAGCTCCCA 420
 ATTTGCGAGT AATTTTTTTT GTTCAGCCTT GCGAGTCTAT CCTACTCAAG TGTGGCTCTG 480
 75 TATCCAACAA CAGTCTTGGA GATCTCATGA AGATTTCGTA AACTTTTGCT CTGCAGGATA 540
 CCTTCTTTTG TGGTTATGTG CCGTGAAGAC TCCAGCCTCC GTGTCTTCAA TTCAGTGAAG 600
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 TACTATACCA CCGTGCAGCC AATGTGTGAG AATGGTGGTT TCATACATTT TCTCCAATTC 780
 80 TTTCTTGTTA CAGGAGCCTC CATTACTTTT CAAACAGTAA TGCAATTGCA GTTGCTCTC 840
 CTTTCTTCTA TTATGTGTTT ATCTGTGCA GTTTGAGCCA AGAGAGGGCA CGGAGAAGTA 900
 CAATGACTAG AGAGCACTTC TGTGAGGCT CATTATTGTA CCGCTACCCC AGTGCTTTAT 960
 GAATGTGTGC TGCAGATGTC ATACAGCATC ACAGCTTCTT CTCTAATTTA TGAGCCATAA 1020
 TTTTTTTTTT TGTATTTTAA TTGTATTACC TGCTTGGTGT CAAGAGGATG ATGAGGAGGA 1080
 CTACTATAGG ATAAATTTGT TTTTATAGAG CAATTTCTCA TGGGTACGA GGGATAGTAC 1140

TCCATTTTCC TCACTGATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200
TATGGAATCC TTTATGCTTT TTCTCAGGCT GCTTCTGTTA CATGAAATAA AGCCAGAGTT 1260
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5 Seq ID NO: B24 DNA sequence
Nucleic Acid Accession #: cat cluster

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CTTTOCCACT CTGATGATTT GTGCTCTTAT TTTTCTCTAGA TTTACCTCAT CTAGGGCATA 180
TTCTTTTCCC TCCTCTCTCT TACCTTTCTCT GGTCTGTATC CCTCTGTACT CAGTTCCCTCT 240
15 AAATTATTGG ACTACAACT AATATACTAG AAAAGCATAC ACTTATTTTA TTTGAATGCA 300
GAAATGCTAT CTATCAGTAT ATATACATAA GAATGTATAT TACAGTATAT CTATATATAC 360
TTAACAACGT AACTTTTCAGT ATTCCCAGT TAGCGTACCT AACTCTCCTG TGGGTATATG 420
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20 GAGTGTATGT ACAAATAATG AAAATTTTAT GAAAAATGAAC ATGTTTTTAT GATGTTATTT 660
CTAGTTTATA AGAATGTGAT GACTGCTTTG CTTCATTTAT GTACGTTCCC ATTATATTCT 720
TGCTGTCAAT CAATCAAAA TTTATATCAG ATTAGGATAA ACTAAGCCAT TTTATGTATT 780
TTATTTTAAA CCTTATTTTG GCAGAGTAAT TCCTTAGAAT TGGAAAGCT GTTACTTTGA 840
25 AATTACCAAT TTATTACAAA ACATAGAAAT GTATTGTAGC TACAAGACA ACCAAGCATT 900
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TGATTTTTTT ACTGGCTCTA TTGCTTTAAA ATAATAAGA GATTATATGAT TCCTTTGTATA 1020
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30 AATTGTGAGC AGTAAGATTA CTGATGTAAT ATGTATGTTG GACTGAAGTA TTTCTTTATA 1200
AACATTTCTAT TTGATTTTAA GCAAAATGTA TGTAAAGCA TGTTTTACA TCAGTAAAGT 1260
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TAACAATCAT ATTTGTCATT GTTGTGTTCT GCAAAACAAA ATGTTTATGG CTTTCATGTA 1380
GGCTTAAGAT TGTAGGCAAA AATGGACTGA GTTCAGSACC CTTCAAGCAG TAGGCATTCA 1440
35 GTTACAGAGC AGTTGGTACT TTGTAACCCA GACTTACAGT TTAATAATAT CAAGTTAGCT 1500
GATGTTTCAT TATAATAAAA ATACTATTTT GCTTAAGAGT TGTATTACAA ATATTTGTGC 1560
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GCATGTGTTA TTTTAAATAA TGAATAGAG AACATAATAC GTAATGTTCA GTATAACAGC 1680
TGAGTTAAAA CATCTGCCAG GATTAACATC AGTGGGTTTT TGCCAATGCA TAGAGGCATT 1740
40 TTTCTCTAAG TATGATGGCT AATGATAACT ATTCTTTGTT ACACATTCAA GTCACTCCCA 1800
TACAAGTAAC TATGGGTGTA TATGTTTCAC TCCAAAGGGT GTATTAACTC TGAATGCTAA 1860
TCATGAAGAC TTAAGTTAGG ACAACACTTC AAACCAGGAA GTGTGAAGCT ATTTA

Seq ID NO: B25 DNA sequence
Nucleic Acid Accession #: FGENSESH predicted
Coding sequence: 1..1144

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GGCATGAGAC TGTCCCTGGC GCGCGCGGCT CGGGAACGCC CGGCGTCTC CTCCCTGCTG 180
CCCTGCGGCT GCTTGCAGCC GGCTGACCCC GAGGGGGCAG GGCTGCTGTT CCGCGCGGCT 240
GGAGGAGCGG GCGCGCGCAG CGCGGGAAGT GCGCGCGGCG GCGCGCGGCG GGTGGGTGTC 300
55 CCGGGGCTGC TAGTAGGTTT AGCCGGCGTT GGGGGCGACC CTAGCCTAAG CAGCCTGCGG 360
CGCGGGGCGG CCTTTGCTT CAAGTACGGC GAAAGCGGGA GCGGGGCTC GGTGGCGGAG 420
AGCAGCGGCG GCGAGCAGAG CCGCGACGAC GACAGCGAGC GTGCGTGGCA GCTCGTGCTG 480
CGGGCGGAG TAGCGGACCC GCGGGCTTCC CCGGGAGCGG GAGGTGTTGG CGGGAAGGCA 540
GCCGAGGGCT GCTCCATGTC CCACCTCCAC GCGGGGCCA GCGTCCCCC GGGGGGCTG 600
60 GCGGCGGCGG GCGGCGGGGG TAGCAGCAGC GGTAGCAGTG CCGGCGGTGG CGGTAGCGGT 660
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65 GAGGAGATGC GCGGCTAGT CGCCTACCTC AACCAAGGCC AGGCCATCTC GGTGCGCTCC 960
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CCTT

70 Seq ID NO: B26 Protein sequence
Protein Accession #: FGENSESH predicted

1 11 21 31 41 51
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AGAAALCLKYG ESASRGSAE SSGGEQSPDD DSDGRCELVL RAGVADPRAS PGAGGGGAKA 180
AEGCSNAHLH GGASVPPGGL GGGCGGSSSS GSSGGGGGSG SGGGSSSSSS SSSSKSKSQ 240
80 KALRLNINAR ERRRMHDLND ALDELRAVIP YAHSPSVRL SKIATLLAK NYILMQAQL 300
EEMRLVAYL NQQQAISAAS LPSSAAAAA AALHPALGA YEQAAGYPFS AGLPPAASCP 360
BKALFNSV8 SSLCKQCTEK P

Seq ID NO: B27 DNA sequence
Nucleic Acid Accession #: cat cluster

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Seq ID NO: B28 DNA sequence
Nucleic Acid Accession #: NM_002581.2
Coding sequence: 368..5251

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CAAGAGTGGG GAGAGTGGAG CACACACCTT GAGGAGGAAA GCGAGAAAGA AAAGAAAAAA 240
GCAAGTGAAG GGGGGCTCGC CCAAGAAGGG TGAAGAAGCG AAGAAAGTCG AGGCGCGGAG 300
GCTCCCAAG CTGGCAGCTC CGGTTGGCGG TGCAAGGGCGG AAGGGGGGGG CGGGGGGAAC 360
GTGAGACATG CGGCTCTGGA GTTGGGTGCT GCACCTGGGG CTGCTGAGCG CCGCGCTGGG 420
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GGGCCCCCGC GCCGGCCCCG CCACTTGCGC CACCCGCGGC CCGCGGCCGC CGCGCTCGC 540
CGCGCGCGCG GCCCGCGCGG GCGGTGCTTG GGAAGCCGTG CCGTCTCCCC GCGCGCGGCA 600
GCAGCGGGAG GCGAGGGGCG CCAACGAGGA GCCGAGCCCG CCGAGCCCGG CGCTCTATTT 660
CAGCGGGCGA GCGAGCGAGC TGCGAGTCCT CCGGGCGGAC CTCGAGCTGC CCGGGGAGCG 720
45     GTTCACGCTG CAAGTGTGGC TGCGAGCGGA GGGGGGCCAG AGGTCTCCGG CAGTGATCAC 780
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50     CACCTCTGGG GAACAAGTGG GTGGCATATT CAGCCCACTG ACCCAGAGT GCAAAAGTCT 1080
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55     CCCCAGGAGT GCGGAGCACA GCCCCAAGT GGAATTCAGC AATGCCACG GCTTTCTGCT 1320
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60     GATTGGGGAT GAGAACTGTG ACCCCGAGTG CAACCAACG CTGAAGAGAG CAGCACAAGG GGGTGTGTGA 1680
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CATGGAGTGC AACTATGAAC GGTTCAACTT TGATGGTGGA GAGTGTGTG ACCCTGAAAT 1800
CACCAATGTC ACTCAGACTT GCTTTGACCC CGACTCTCCA CACAGAGCCT ACTTGGATGT 1860
TAATGAGTTC AAGAACATTC TTAATTTGGA TGGATCAACA CATCTCAATA TTTTCTTTGC 1920
65     AAAATCCTCA GAGGAGGAGT TGGCAGGAGT AGCAACTTGG CCATGGGACA AGGAGGCCCT 1980
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CACCATGATC CATGAGATTG GTCACAGCCT GGGCCTCTAT CAGTCTTCC GAGGCATCTC 2100
AGAAATCCAG TCCTGCACTG ACCCTGTCAT GGAGACAGAG CCCTCTCTCG AGACTGGAGA 2160
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70     AAATGACACC TGTGGCTTTC ATAGCTTCTT CAACACTCCT TACAACACT TCATGAGCTA 2280
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75     CCTGGTGCGA TATGCTTCCA ACGCTTCTTC CCCAATGCCC TGCAGCCCAT CAGGACACTG 2580
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TCAAGGCTGC TACCTGAGCC TGGAGTTCTT CTACCCCTTG GTCCCTGAGT CTCTGACCAT 2760
80     TTGGGTGACC TTTGTCTCCA CTGACTGGGA CTCTAGTGGG GCTGTCAATG ACATCAAACT 2820
GTTGGCTGTC AGTGGGAAGA ACATCTCCCT GGGTCTCTAG AATGTCTTCT GTGATGTCCC 2880
ACTGACCATC AGACTCTGGG ACGTGGGCGA GGAGGTGTAT GGCATCCAAA TCTACACGCT 2940
GGATGAGCAC CTGGAGATCG ATGCTGCCAT GTTGACCTCC ACTGCAGACA CCCCACCTCT 3000
TCTACAGTGT AAGCCCTTGA AGTATAAGGT GGTCCGGGAC OCTCTCTCC AGATGGATGT 3060
GGCCTCCATC CTACATCTCA ATAGGAAATT CGTAGACATG GATCTAAATC TTGGCAGTGT 3120

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5 GTACCAGTAT TGGGTCATAA CTATTTTCAGG AACTGAAAGAG AGTGAGCCAT CACCTGCTGT 3180
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 TAGGATCAAG TGTGAAGACA GTGATGCTTC CCAGGAGACT GGGAGCAATG TCATTCAATG 4740
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 30 CTCGTTCCA AACGAGCTCA ACAGCAACT CAACTGCGAG TGCCCTGATG GCTATGCCAT 4860
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 35 TGACGGTGGG GATTGCTGCA CCTCCACAGT GAAGACCAAA AAGGTCAACC CATTCCTAT 5160
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 40 CCTCTCCACA CAGGGATACC TTAGCACCCA ACCGGTCTGC CTTTAATTTT ACCCAGGAAG 5400
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Seq ID NO: B29 Protein sequence
 Protein Accession #: NP_002572.1

45 1 11 21 31 41 51
 MRLMSVVLHL GLLSAALGCG LAERPRRARR DPRAGRPRP AAGPATCATR GPRPPRLAAA 60
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 50 LQVWLRAEGG QRSFAVITGL YDKCSYISRD RGWVVGINTI SDQDNKDFRY FFSKTKDRAR 180
 QVTTINAHRS YLPQGVVYLA ATYDQGMKXL YVNGAQVATS GEQVGGIFSP LTQKCKVLM 240
 GGSALAHNRY GYIEHPSLWK VARTQREILS DMETHGAHTA LPQLLLQENW DNVKHAWSM 300
 KDGSSPKVEF SNAHGFLIDT SLEPPLCGQT LCDNTEVIAS YNQLSSFRQP KVVRYRVVNL 360
 55 YEDDHKNPTV TREQVDFQHH QLAFAFKQYN ISWELDLVLE SNSSLRRRLI LANCDISKIG 420
 DENCDPECNH TLTGHDGGDC RHLRHPAPVK QHNGVCDMD CNYERPNFDG GECCDPEITN 480
 VTQCTFPDPS PHRAYLDVNE LKNILKLDGS THLNIPPAKS SEELAGVAT WPDWKEALMH 540
 LGQVLNPSF YQMPGHHTM IHEIGHSLGL YHVFRGISEI QSCSDPCMET EPSFETGDL 600
 NDTNPAPKHK SCGDGPGQND TCGFHSFPNT FYNFMVSAD DDCTDSFTPN QVARMHCYLD 660
 60 LVYQGWQPSR KPAPVALAPQ VLHGTDSVT LEWFPPIIDGH FFERELGSAC HLCLEGRILV 720
 QYASNASPM PCSPSGHWSR REAEGHPDVE QPCKSSVRTW SPNSAVNPHT VPPACPEPQG 780
 CYLELEFLYP LVPESLTIWV TFWSTWDSS GAVNDIKLLA VSGKNISLGP QNVFCDVPLT 840
 IRLMDVGEEV YGIQIYTLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVR DPPLQMDVAS 900
 ILHLNRKFPV MDLNLGSSVYQ YWVITISGTE ESEPSFAVTY IHGRGYCGDG IIQKDGQEGC 960
 65 DDMNKINGDG CSLFCRQEVN FNCIDEPBRC YFHDGDGVE EPEQKTSIKD CGVYTPQGFL 1020
 DQWASNASVS HQDQCCPGWV IIGQPAASQV CRTKVIDLSE GISQHWYPC TISYFYSQLA 1080
 QTTFWLRYAF SQPMVAAYVI VHLVTDGTYI GDQKQETISV QLLDTKDQSH DLGLHVLSCR 1140
 NNPLIIPVVH DLSQPPYHSQ AVERVSFSSPL VAISGVALRS FDNFDPVTL SQRGETYSP 1200
 ADQSCVHFAC EKTDCPELAV ENASLNCSSS DRYHGAQCTV SCRTGYVLQI RRDELIKSQ 1260
 70 TGPSVTVTCT EGRWNKQVAC EPVDCSIFDH HQVYAASPS CEGTTFGSQC SPQCRHFAQL 1320
 KGNNSLLTCM EDGLHSPFEA LCELMCLAPP FVFNADLQTA RCRENKHVKG SPCKYCKMPG 1380
 YHVPSSSRKS KRAFKTQCT QDGSWQEGAC VVFTCDPPPP KPHGLYQCTN GPQPNSECR 1440
 KCEDSDASQG LGSNVHCRK DGTWNGSPHV CQEMQGCQSV FNELNSNLKL QCPDGYAIGS 1500
 ECATSCLDHN SESIILPMNV TVRDIPHMLN PTRVERVVCT AGLKWPYHPA LIHCVKGCEP 1560
 75 FMGDNYCDAI NNRAFCNYDG GDCCTSTVKT KKVTPPFMSC DLQGDCACRD PQAQHSRSD 1620
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Seq ID NO: B30 DNA sequence
 Nucleic Acid Accession #: NM_032808.1
 Coding sequence: 61..1008

80 1 11 21 31 41 51
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 ATGTTGTCATG AGCTGCTCCG GCTGCAGGAG ATCCAGCTCG TGGGCGGGCA GCTGGCGGTG 120

	1	11	21	31	41	51	
65	GAAAGGCTAT	CGGTAACAAC	TGACCTGCCA	CAAAGTTAGA	AGAAAGGATT	GATTCAAGAA	60
	AGACATAATA	ATGGATTATTAG	ATGCTCAGAGA	TATTATTAAAC	AAGACACCTG	CAACAGAGAA	120
	TAATACTGCT	GCCACTCGGA	ATCTCGATTT	CCGATCTCGG	GATGACTATA	AAAGCAGTGT	180
	AGATGACTTA	CAGTATTTC	TGATTGGGCT	TCATACATTT	TGAAGTCTTC	TTGGCTTTAT	240
70	GGGGAACCTA	CTTATTTTAA	TGGCTCTCAT	GAAAAGGGT	AATCAGAAGA	TACGGTAAAA	300
	CTTCTCAT	GCGAACTCGG	CCTTTCTGGA	TATCTTGTTT	GTCGTGTTT	GCTCACCTTT	360
	CACACTGAGC	TCGTGCTGCG	TGGATCAGTG	GATGTTTGCG	AAAGTCATGT	GCCATATTAT	420
	GCGTTTCTT	CAATGTGTGT	TGAGTTTGGT	TTCAACTTTA	ATTTTAATAT	CAATTGCCAT	480
	TGTCAGGAT	CATATGATAA	AACATCCCAT	ATCTAAATAT	TTAACAGCAA	ACCATGGCTA	540
75	CTTTCTGATA	GCTACTGTCT	GGACATCAGG	TTTGGCCATC	TGTTCTCCCC	TTCCAGTGT	600
	TCACAGTCTT	GTGGAAAGCT	AAGAAACATT	TGGTTCAGCA	TTGCTGAGCA	CGAGGTATTT	660
	ATGTTGTGAG	TCATGGCCAT	CTGATTCATA	CAGAAATTGCC	TTTACTATCT	TTTATTGGCT	720
	AGTTCAGTAT	ATTCTGCCCT	TAGTTTGTCT	TACTGTAACT	CATACAAGTT	TGTCGAGAAG	780
	TATAAGCTGT	GGATTGTCCA	ACRAAGAAAA	CAGACTTGAA	GAAATAGAGA	TGCTCAACTT	840
80	AACCTCTCAT	CCATCCAAAA	AGGTGGGCC	TCAGGTGAAA	CTTCTGGCA	GCCATAAATG	900
	GAGTTATCTA	TTCAATCAAA	AACACAGAA	AAGATATAGC	AAGAAGACAG	GATCTGTGTT	960
	ACCTGTCCCA	GAAAGACCTT	CTCAAGAGAA	CCACTCCAGA	ATAACTCCAG	AAATCTTTGG	1020
	CTCTGTAAAG	AGTCAGCTCT	CTTCACTCCAG	TAAAGTTCATA	CCAGGGGGTCC	CGACTTGCTT	1080
	TGAGATAAAA	CTTGAAGAAA	ATTCCAGATG	TCATGAATTG	AGAGTAAAAA	TTCTGTGATT	1140

5 AAGAATAAAA AAGAGATCTC GAAGTGTGTT CTACAGACTG ACCATACTGA TATTAGTATT 1200
 TCGTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAATCT 1260
 TATTTCAAAT AGGCATTTC AAGTGGTGTA TTGCATTGTT CATTGTGTGG GCATGATGTC 1320
 CTGTGTCTT AATCCAATTC TATATGGGTT TCTTAATAAT GGGATTAAG CTGATTAGT 1380
 GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence
 Protein Accession #: NP_006165.1

10 1 11 21 31 41 51
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 QCVSVLSTL ILISIAIVRY HMIKHPISNN LTANHGYPLI ATVWTLGFAL CSPLPVFHSN 180
 15 VELQBTGSA LLSRYLVCE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240
 GLSNKENRLE ENEMINLTIL PSKKSQPVVK LSGSHKWSYS PIKGRHRRYS KKTACVLPA 300
 ERPSQENHSR ILPENFGSVR SQLSSSSKFI PGVPTCFEIK PEENSVDHEL RVKRSVTRIK 360
 KRSRSVYFRL TILILVFAVS WMPLHLFHV TDFNDNLISN RHPKLVCYC HLLGMMSCCL 420
 NPILYGFLLNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence
 Nucleic Acid Accession #: NM_014279.1
 Coding sequence: 286..1689

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 30 GGGACACGAG CCAGGCGCGG CCGCGCGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
 TCCGCGTCCA CGCAGCGCGC GGC CGGCGCAG CACCCAGGGC CCTGCATGCC AGTTCGTTGG 300
 AGGTGCGAGC GAGACATGCA CCCGCGCGCG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
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 AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTGGCCCC ACAGCAGACC 480
 35 ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
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 AAGATGGAGA ACCAATGAA AGGACTGGAG TCCAGTTCA AACAGGTGGA GGAGAGTCAT 660
 AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAGCGA AAATGGATGA ACTTAGGCCT 720
 TTGATACCTG TGTGGAAGA GTACAAGGCC GATGCCAAT TGGTATTGCA GTTTAAGAG 780
 40 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATTGG CGCCTATGAC 840
 TACGATGAAC TTCAGAGCAG AGTGCTCAAT CTTGAAGAAA GGCTCCGTGC ATGCTATGCA 900
 AAACCTAGCT GCGGGAAGTT GACGCGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC 960
 TCGAGGTTG GATCCTGGAT GACAGACCCCT CTGCGCCCTG AAGCGGATAA CCGGGTGTGG 1020
 TACATGACG GCTATCAGAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGACTTTC 1080
 45 ATGAACACCG ACAATTTTAC CTCCACCGST CTCCCCACCC CTGCTGCGG CAGCGGGCAG 1140
 GTGGTCTACA ACGGTTCTAT CTACTTCAAC AAGTTCGAGA GCCACATCAT CATCAGGTTT 1200
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCGG TTACAACAAC 1260
 ATGTACCACT ACGCTGGGG TGGCCACTCG GACATCGACC TCATGGTGA CGAGAGCGGG 1320
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 50 CCGGTGTCCT TGCAGACCTT GCAGACCTGG AACACGAGCT ACCCAAGCG CAGCGCGGG 1440
 GAGGCTTCA TCATCTGCGG CAGCGGTGAC GTCAACCAAG GCTACTCAGG GGTATCCAAG 1500
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 55 GAGTTGTAGC TCCCTCTTCC TGGAAAGCAA GGGCCCAAGT CCTCACCAC AAGGGAATCC 1740
 TGTGAAATCT GTGCCAAAA GATACCAATA ACTATAACAA TACGATCTTT GAAAAATCAT 1800
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 60 GGCAATGACT GTTGCCAGT TCTCACCGG GAAAAACCA CTGTAGGAT GGCATGAACA 2040
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 65 AACTCGCGTA CCCGTAGAT ACATTGTGCA ACGTCTTCT GTTATTCCCT TGAGGTGTA 2340
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 AAATCATGTA ACGCAGATA GGAAGGCTC ACCTGGGGAA ACTCTGGTT CCGATGGGAC 2580
 70 AGGAAAGTCA TACGGCAAC AGTATGCGGA AAGTACGTTT TTTAAGTAA AAAACAAAG 2640
 CAACCTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAG 2700
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Seq ID NO: B36 Protein sequence
 Protein Accession #: NP_055094.1

75 1 11 21 31 41 51
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 80 APQQTMCERD ARTKQLRQLL SKVQNMQSIS EVLDRRTQRD LQYVEKMEHQ MKGLESKFKQ 120
 VESSHQHLA RQPKAIKAKM DELRLPLIPVL REYKADAKLV LQFKEEVQNL TSVLNEHQE 180
 IGAYDYDELQ SRVSNLEERL RACMQKLACG KLTGISDFVT VRTSGSRFGS WMTDPLAPEG 240
 DNRVWYMDGY HNNRFVREYK SMVDFMNTDN FTSHRLPHPW SGTGQVYVNG SIYPNKPQSH 300
 IIRPDLKTE TILKTRSLDY AGYNNMYHYA WGHSDIDL M VDBSGLWAVY ATNQNAQNV 360

VSRLDPVSLQ TLQWTNTSY KRSAGEAFII COTLYVTNGY SGGTKVHYAY QTNASTYEYI 420
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5 Seq ID NO: B37 DNA sequence
Nucleic Acid Accession #: NM_006334.1
Coding sequence: 286..693

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   CCTGCCCAGC CCTGCCCGGA GGCAGACGCG CGGGAACCGG GACGCGATAA ATATGCAGAG 120
   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCGG CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCGCGGTCCA GCGAGCGCGC GGCCGGCCAG CACCCAGGGC CCTGCATGCC AGGTGTTTGG 300
15  AGGTGGCAGC GAGACATGCA CCGGCGCCCG AAGCTCCTCA GCCTCCTCTT CCTCATCTCT 360
   ATGGGCACTG AACTCACTCA AGTGTCTGCC ACCAACCTTG AGGAGAGCTG GCAGGTGTAC 420
   AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCCGCCC ACAGCAGACC 480
   ATGTGTTTCA GGGATGCGCG CACAAACAGC CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
   ATGTCTCAAT CCATAGAGGT CTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
20  AAGATGGAGA ACCAATAGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
   AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACCTAAAA GAGTTTTTTC AATGCTGCAG 720
   TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCATGAAAGA GAGCCAGAGA GCTTTTTGCA 780
   CCATGCATTT TTACTATTAT TTTCCAATAC TTAGCACCAT TTCACTAAGG AACCTTGAAT 840
   ACAACCGAGA TCCTCCTTTG CATGCGACTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900
25  TGTCAATGCA TTTTTTGAAG AAGAAAGAAA AAAAAAATT CGTGTATGTG ACTCAAAGCA 960
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30 Seq ID NO: B38 Protein sequence
Protein Accession #: NP_006325.1

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   APQQTMCSDR ARTKQLRQLL EKVQNMSSQSI EVLDRRTQRD LQYVEKMNQ MKGLESKFKQ 120
35  VESSHKQHLA RQPKG

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40 Seq ID NO: B39 DNA sequence
Nucleic Acid Accession #: NM_058199.1
Coding sequence: 286..795

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   CGGAGGCTTC GCGCAGCAGA GCCCGCGCGC CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
   GGGACACGAG CCAGGCGCGG CGCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
   TCGCGGTCCA GCGAGCGCGC GGCCGGCCAG CACCCAGGGC CCTGCATGCC AGGTGTTTGG 300
   AGGTGGCAGC GAGACATGCA CCGGCGCCCG AAGCTCCTCA GCCTCCTCTT CCTCATCTCT 360
   ATGGGCACTG AACTCACTCA AAATAAAGA GAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
50  GAGAGCGAGA GGAAGACCAC AGGAGAGAAG ACACTGAACG AGCTTCCCTT GTTTTGCCTG 480
   GAAGCCACAG CTGGCTCCCT GGCTCTGCCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
   GTGGGGTTAT GTCGTCCCGC TTACCTTCAG AGCCCTTCTC CTGGTGCTGC CCAGAGCATC 600
   AGCCAGTCCC TCCTGAGAGG GTTCTGCATG GCCTCTAGGA GAGAAGTTT CTGGGCCCCA 660
   GGAAGGCTGT GTGAGGGGTG GTGGTTGTGC ACTGTTGCTG GACAGATGCA TTCATTTCATG 720
55  TGCACACACA CACACACACA TGCACACACA GGGAGCAGA TACCTGCAGA GAAGAGCCAA 780
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   ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTTGAGC ATGGCCGCAC CCAAGGGCCC 900
   TCCAGGCTT AATGGACCCC TGAAGCTCC ATGCCAGGC CAAAGATGC TTTTCTCCC 960
60  TAAAAA AAAAAA

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65 Seq ID NO: B40 Protein sequence
Protein Accession #: NP_478106.1

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1      11      21      31      41      51
65  |      |      |      |      |      |
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   PLFCLERHAG SLALPRMCSP NPNPAVGLCR PAYPQSPSPG AAQTISQSLR ERPCMASRRB 120
   VFLAPGRPGG GHWLCTVAGQ MHSFMCETHH THAHTGEQIP AEKSQPGPD

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70 Seq ID NO: B41 DNA sequence
Nucleic Acid Accession #: AY038071.1
Coding sequence: 1..1686

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   CCAACTTTGC TCTCCTCTTA CTGCATGAC AGCATCCTGG GCGGAGGAG CCCGTGCATA 120
   ATGCGGTTGC TGGGAGCCGC GCAGAGCTTG CCTGCTCCCG TGACCAAGCCG CGCCGACCCG 180
   GAAAAGGCCG TGCAAGGCTC CCTAAGAGC AGCAGGCCCC CGTTGAGGCG CAGAGCTGCAC 240
80  CTGCCGCCCA AGCTGCGCGG CCTGTACGCG CCGGGCGGGG GCGGCTCCTT TCAGGGTGGG 300
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   CCAAGCGGGG AGGCCCCCTC GCGGCCACCG CCAACGCGCG GCGCGGGGGA ACGGCGGAGC 420
   GCGCGAGGGG CCGCGCGCGC AGCGCGCGCG GCGGCGCGCG GCGCTGGGA CAGCTCAAG 480
   ATCAGCCAGG CGCGCAGGT GAGCATCAGC GCGAGCAAGT CGTACCGGGA GAACGGGGCG 540

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CCCTTGTGTC CGCCGCGGCC CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCAACGAC 600
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ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA 720
GAGGAACCTG TGAGGAGACG CGAGGAGGAG CTGCTGGAGG ACGACGCCCG CGCGCTGCTC 780
AAGGAGCCCC GGCCTGTGTC TGTGGCCGCC ACTGGCGCCG TGGCGCGAGC AGCTGCGGCT 840
GCAGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAGG AGCTGCTGCT GCACCCGGAA 900
GACGCTGAGC GCAAGGACGG CGAGGACAGC GTGTGCCCTC CTGGCGGACG CGACTCGGAG 960
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GAGGAACCTG AGCGGGCCTT CCAGAAGACG CACTACCCGG ACGTCTTCAC CAGGGAGGAA 1080
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CGCGGGCGCG TCTCGGCCAC CCACCCGCTC AGCCCTTACC TGGACGCCAG CCGCTTCCCT 1260
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CTGAGACAGC CCAACACCCG CGTGGAGGGC GCAGTGGCAT CGGGCGCCCT GGCGGACCCG 1560
GCCACGCGCG CCGCAGACAG ACGCGCTCT AGCATAGCCG CGCTGAGGCT CAAGGCCAAG 1620
GAGCACGCGG CGCAGCTCAC GCAGCTCAAC ATCTGCGCGG GCACCAAGCAG GGGCAAGGAG 1680
GTGTGC
  
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Seq ID NO: B42 Protein sequence
Protein Accession #: AAK93901.1

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1 11 21 31 41 51
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PRGEAPPPPP PPARPGERPD GAGAAAAAAA AAAAAADTLK ISQAPQVSIS RSKSYRENGA 180
PFVPPPPALD ELGGPGGVTH PEERLGVAGG PGSAPAAGGG TGTEDEBEL LEDEDEDDEE 240
ELLEDDDEEE LLEDDARALL KEPRRCFVAA TGAVAAAAAA AVATEGGBELS PKEELLLHPE 300
DAEGKDGEDS VCLASGSDSE EGLLKRKQRR YRTTFTSYQL EELERAFQKT HYPDVTREE 360
LAMRLDLTEA RVQVWFQRR AKWRKREKAG AQTHPPGLFF PGPLSAATHPL SPYLDASFPF 420
PEHPALDSAW TAAAAAATAA FPLPFPPOS ASLPPSGAPL GLSTFLGAAV FRHPAFISPA 480
FGRLFSTMAP LTSASTAAAL LRQPTFAVEG AVASGALADP ATAAADRRAS SIAALELKAK 540
EHAQLTLQIN ILPGTSTGKE VC
  
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Seq ID NO: B43 DNA sequence
Nucleic Acid Accession #: CAT cluster

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CTGCTCTCTT CCGCTCTCAT GCGCCTTTCA GCTCCTACTC TGGTGTGCTC CCGCTCCCTC 180
GCTCGTTTCT CTGTGCTCTC TCCTTCCCGG TTGCTGTCTC GCTTCTTCTG GTTCCCTCTC 240
GTCTGTGTTT GTGGGTGCTC CTCTGCGTCC TGCTCTTTTC TCTTGCCTTT CCGCGCGGCT 300
CGTGTGTTGG TCCCTCTGGT TCTGCGCGGG TTCTGTGTGC GCGGGCGCGC CCGTCTTTTC 360
TTGTGTGCTT GCTCTGCTC TCTGTCTGCT GTTCTCGGCC GTCTGTGCTT TCTCTCTTTT 420
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AATGTGGAGA CTTGTGAGCC TGTGTCCGGC CCGTAACCTC CAAGCACAGG GCAGGCTTCC 660
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Seq ID NO: B44 DNA sequence
Nucleic Acid Accession #: NM_014421.1
Coding sequence: 718..1497

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AGTGCAGCTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCGTC CCGGGACGTC 180
TCCTGATCCC CTAATAAGC GCCTGCTAAC TTTGAAAAGG AGCACTGTGT CCGTCAAAGT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAAGGA 300
GCTGATGCGG GCCTCCTGAT CAATTAAGAG GAGAGTTAAA CCGCGAGAT CCGCGCGGGA 360
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CTTTGATTC CCAAGCCCTC GGGCTTTGCG TCTTCTGCG GACCCCTTCC CCGGAGATG 720
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 5 TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGSCCTGTC TTGCAAGTA 1440
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTGAGAA AATTGATCA 1500
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 35 TCAGTTCTAA ATACTTTGTC TGGAGCACAA AACATAAAA GGTATCTTA TAGTTGTGAC 3120
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Seq ID NO: B45 Protein sequence
 Protein Accession #: NP_055236.1

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 50 MAALMRKSDS SCCLLLLAAY LMVSSQIGS SRKLNLSIKS SLGGETPQQA ANRSAGMYQG 60
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 RCNNGICIPV TESILTPIHP ALDGTNRDR NRHGHYNHDL GWQNLGRPHR KMSHIKHEG 180
 DPCLRSSDCI EGFCCARHFV TKICKPVLHQ GEVCTKQRKK GSHGLEIFQR CDCAKGLSCK 240
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Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_019885.1
 Coding sequence: 1..1539

1 11 21 31 41 51
 60 ATGCTCTTTG AGGGCTTGA TCTGGTGTG GCGCTGGCCA CCTCGCCG GTGCCTGGTG 60
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 CGCGACAAGA GCTGCAAGCT GCCCATCCCC AAGGGATCCA TGGGCTTCCC GCTCATCGGA 180
 65 GAGACCGGCC ACTGCTGCT GCAGGGTTCT GGCTTCCAGT CGTCGCGGAG GGAGAAGTAT 240
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 70 AAGCGCAAGG TCTTCTCAA GATCTTCAGC CACGAGGCC TGGAGAGTTA CCTGCCCAAG 480
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 75 AAGGACTACT TGGACGCCCT GGACCTCCTC ATTGAGAGCA GCAAGGAGCA CGGGAAGGAG 840
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Seq ID NO: B47 Protein sequence
 Protein Accession #: NP_063938.1

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 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGCPCE GTLRDLTSLG LRYLDCVIRE 360
 VMRLFTPISG GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPVFKDYN VFPDRFSQA 420
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Seq ID NO: B48 DNA sequence
 Nucleic Acid Accession #: AB040527.1; AL136582.1
 Coding sequence: 94..2319

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 10 AGGCAAGAGG ACCAAGAAGT CCAAGCACCT GGATGATGAG TATGAGAGCA GCGAGGAGGA 1140
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 15 TGTATCAGA GAATATGATG AACATTTCCT TGAGTCATT GAACGAGCAA CGTACACCT 1440
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 20 GAAGATCCCC AACACCAACC CACCTGAGTA TGAATTCCT TGGGCGCTGC GAGCCCGCCA 1800
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 TATGCGCCAG GAACATGCCA GGGCCAGAT AGGGGCCAG ATGAATATCG GGGATGAAGC 1980
 25 GCTGATTGGA CCGTGGAGCT GGGATGACAT ACAAGTCGAG CTCTGACCT GGGATGAGGA 2040
 CGGAGATTTT GCGATGCTC GGGCCAGGAT CCGCTTGTCT TTCTGGGCA GATACCATCA 2100
 GTACATTCTG AATAGCAACC GTGCCAACAG GAGGCCACG TGGAGAGCTG GCGTCAGCAG 2160
 TGGACCAAT GAGGGGCCA GCACCAGCGT CCTAGATGGC CCCAGCACCA GCTCCACCAT 2220
 CCGGACCAAG AATGCTGCCA GAGCTGGGCG CAGCTTCTTC TCCTGGATCC AGCACCGTTG 2280
 30 ACGAAGTCCA GCGATCTTAC TGGCCAAAGC AGAGCGCCTC CTCTCAGATT CCTTCTGAC 2340
 ACAGCACCTC AGCGGCTTC TTCTGTCTAG TCGAGGTGG CATGCAAGAT GAAGCTCTCT 2400
 TTGCTCTCC TGCTTTCTAT TTGTGCTTTT CCTTGTGTTT TCATGTTTTT GGTATCAGTG 2460
 TTACATTAAA GTTGCAAAAT TAAA

Seq ID NO: B49 Protein sequence
 Protein Accession #: BAB33378.1; CAB66517.1

1 11 21 31 41 51
 40 MAEGSFVSQS ESYSVEDMDE GSDEVGEEM VEGNDYEEFG AFGGYGLTIS FDIHILRAF 60
 SLGFGRLRLS NEPWELNPFV LAQTLVEALQ LDPETLANET AARAANVARA AASNRAARAA 120
 AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQOPT PEPPLASQPT SQMLVTSKMA 180
 APRAPATSAQ SQTGSPAQEA ATEGPSSACA FSAQCAREV DANRPFSTAF LQNDVDFDTQ 240
 PAGVSGMAFP RPKRPAPAQE AATEGPSAAS GVPQTGPGR VAAATRPKTK SGKALAKTRW 300
 45 VEPQNVVAAA AAKAKMATSI PEPBGAAAAT AQHSAEPWAR MGGKRTKKSK HLDDEYESS 360
 EERETPAVFP TWASQPSLT VRAQLAPRPP MAPRSQIPSR HVLCLPRNV TLLQERANKL 420
 VKYLMIDYK KIPIKRADML KDVIREFDEH FPEIIRATY TLEKKFGIHL KEIDKEERLY 480
 ILVCTRDSSA RLIGKTKDTP RLSLLLVILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540
 PLGLRLRLIT DDFVKQKYLE YKIPNSNFP EYEFWLGLRA RHETSOMRVL RPIAQNQNRD 600
 PREWKAFLE AVDDAFKTM DMAEHHARA QMRAQMNIGD BALIGRWSWD DIQVELLTWD 660
 50 EDGDFDQAWA RIPPAPWARY HQYILNSNRA NRRATWRAGV SSGTNGGAST SVLDGPFSTSS 720
 TIRTRNAARA GASPPSWIQH R

Seq ID NO: B50 DNA sequence
 Nucleic Acid Accession #: XM_084965.1
 Coding sequence: 356..2014

1 11 21 31 41 51
 60 GACCTAGCGT GTGCTCAGCT CTGGACAAGA CATGGATGTA GGCAGACATG CTTCTGCTC 60
 GCTGGGCTTA GTGCACCAAT GCTAAGGACA GACATGAAGG GCTTGGGAAA GGCATGAAGA 120
 TGCAGGAGT CTAGGAGAGA GGATAAGAAA AACAAGCATT TTGTGGTGGG TTGAATTGCG 180
 TTGTGCTTT TAGAGGCATT TCGTATGATG TGGTTGCGCT CCGTGAAGA GCGAGTCTAG 240
 AGAAGGAATC CGAAGCGGCG GCGGCGAGCG CGGCTCAGGT TGATTAGAA TACGGGTGAC 300
 65 AGTGGCTTGG CGGAGGCCA CTGCTGACGA AAGCGGCTTA TCCGCGCGCG TTTCATGGA 360
 GACGAGCGCG AGCCGCGGCG GCGGCGGGCG TGTCAGCGAG CGCGGCGGAG CTGGCGGCTC 420
 CGTGGGGTCT TGACGAGGGA AGGCGGAGGC CGGCGCGGCG ACCCGGACCC TCGCGGCAGA 480
 CATGGACTTG CATTGTGACT GTGCCGCGGA AAGCGCGGCC GCGGAGCCGC CGTGGGGGAA 540
 GATTAATAAA GCTGCTTCA AATTATTCAA GAAGAGGAAA TCGGTGCGA CCATGCCCAG 600
 70 CATTTTTGGG GTCAAAAACA AAGGGGACGG GAAAAGCTCG GGTGCGACGG GGCTGGTGAG 660
 GAGCAGGACC CACGACGAC TTGCGCAGGT GCTGGTGTG GAGAGCGCA GGAAGGAGGA 720
 GCGGCGCGCG GGGGCGGACA GCGGCGGGGG CGGCGGGGGG CGGCCGAAAC CGGGGCCCCC 780
 CAGAGCGCGA GGGCCCGCGG GGGGCTCCCT CGCCAGCAGC TGGGTGGCCA AGTCGCACAG 840
 CTTCTTCTCG CTGCTGAAGA AGAAAGGGCG CTGCGAAAAC GGCAGGGAGG AGCCTGTGGA 900
 CGGAGCAAAG CGCGCGCGCA AACAAGAGCG GGGGCTGCGG GGGCTTTCA GCGGCATGCG 960
 75 CTGGCACAGG AAGACAAGC GGGCCAAGCG GAGGCGCGCG GAGGGGCGCG CGCCCGGGGG 1020
 CGGCTTGATC CTACCCGCTC CGCTCACCGC CAGCTTGGAG TGGCTCAAGG AGGAGACGCC 1080
 CAGAGCGCGC CGGAGCGCG AGGAGCCGAG CCAGGACGCC CCGGAGAGC CAGCAGGCTG 1140
 TGGAGATATT ATTGCAAGC AAGAGGAAGA GGCAGGTCCT AGCTGTGACA AGCATGTCC 1200
 80 CGGCGCAGCG AAGCGGCTC TGTCTAAAAA GAACCCCGCG GTGGTGGCCT ACCAAGGAGG 1260
 CGGGGAAGAG ATGCCAGACC CGGACGAGGT GAGCGACAC TATCTACAGG AGTTCTGGGA 1320
 CATGCTCTCC CAGACCGAGG AGCAGGGACC CGAGCCCGAG GAGGGCGCG CTAAGGTGTC 1380
 AGCTGCGCTG GAAACCAAGG TGGTGGCGGA GACCCCAAAA GACACAGGT GTGTGGAAAG 1440
 GGCCAGGAC GGTCTCTCG TCAAGCGCAG GAGGCTCAAC CGGATTCCCA TCGAGCCCCA 1500
 TCCTAAGGAG GAGCCCAAGC ACCCGAGAGG GAGCAGCAG GAAGGCGTCC CCAACAGCGA 1560

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OGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620
GAAGGCGGGC ATCCCCCGGG ATAGCTACAG CGGGGAGCGG CTCTATGATC TCTATGCTGA 1680
CCCGGACGGA AGTCCAGCAA CCCTTCTCGG AGGGAAGGAC AACGAGGAGA CGTCTCCCT 1740
GTCCCGGTTA AAGCCCGTAT CTCCAGGCAC CATCACTGTG CCCTGCGGAA CACGAGGACG 1800
CTTGCTGAAG GACTCTAAGA TCCTATTAG CATCAAGCAC CTGACCAACC TTCCATCTAG 1860
CCATCCCGTG GTGCACACAG AACCTCCAG GAGTGAGATG CCCAGAACAA AAATCCCGGT 1920
TTCCAAAGTG CTGGTCCGCA GAGTCAGCAA CCGGGGCTTG GCTGGGACCA CCATCAGAGC 1980
AACGCGCTGC CACGACAGTG CCAAAAAGTT GTGAGGTCTT CCAGGCCAAG GTGGATGGGC 2040
CCCATGCGAA GGAATACAA TTTTCCCTGG AAACCACTAA AGTAAGTTT GCTTTTCTTA 2100
AAGAAGTCT TTTAGACAC CACCCGTCC CCGCCCTGCT CCAGAGCGTG GACCGAGGAG 2160
GTCTTTGTGC CCTGAGCAGG GACCGATAA CACCAGAAAG AGGGATGCTA CACGGGGGTT 2220
TCTCTCTCA AGATAAGTCC CTGAGAATTA TTTTCAAGCA CTTTTCCTT TTTTACCTTT 2280
AAGTTTTTCT TCCTTTTGT TTAATATACT GAACACTTGG AAGTCACCTT TACTTGCCTT 2340
TGCAGAAAC AGAAGTTAG CAAACCTAAG TAAGAGTCAT GCCTGGATAT TGGGATAAGC 2400
CAGTGTCTAG AGGCTGAAG GAACCGCTGA AGAACAGAG GAGATCTCCT CTTCCAGAC 2460
ACGTTTCCTT CCTTCCCTTC TTTCTCTT TCTTCCAGT T
  
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Seq ID NO: B51 Protein sequence
 Protein Accession #: XP_084965.1

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1 11 21 31 41 51
| | | | |
METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDC AETPAABPPS 60
GKINKAAPFL FKRRKSGGTM PSIFGVKNKG DGKSSSGPTGL VRSRTHDGLA EVLVLESGRK 120
EEPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKGN GRSENGKGEP 180
VDASKAGGKQ KRGLRGLPSG MRWHRKDKRA KAEAAEGRAP GGGILILPGSL TASLECVKKE 240
TPRAAREPEE PSQDAPRDPF GCGDIIADQE EAGPSCDKH VPGPGKPLS KKNPGVVAYQ 300
GGGEHASPFG EVDVTYLQEF WMLSQTEEQ GPEPQEGAAG VAALETKVVP PETPKDTRCV 360
EAAADASSVK RRLNRIPIE PHPKEBPKHP EKEQQEGVPN SDEGYWDSIT PGPEEDSSSS 420
GKKAAGPRDS YSGDALYDLY ADPDGSPATL PGKDNNEETS SLRLKPVSP GTITCPLRTP 480
GSLKDKSKIP ISIKHLTNLP SSHPVVHQPP SRSEMPRTKI PVSKVLVRRV SNRGLAGTTI 540
RATACDSAK KL
  
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Seq ID NO: B52 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2016

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1 11 21 31 41 51
| | | | |
ATGGAGACGA GCGGAGCCG CGGCGGCGGC GGGGCTGTCA GCGAGCGCGG CGGAGCTGGC 60
GCGTCCGTGG GGGTCTGCAG GAGGAAGGCG GAGGCGCGGG CCGGGACCGG GACCTCGCG 120
GCAGACATGG ACTTGCATTG TGACTGTGCC GCGGAAACGC CGGCGCGCGA GCGCGCGTCG 180
GGGAAGATTA ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAATTCGGT TGGCACCATG 240
CCAGCATTTT TTGGGGTCAA AAACAAAGGG GACGGGAAAG GCTCGGGTCC GACGGGGCTG 300
GTGAGGACGA GGACCCACGA CGGACTTGCC GAGGTGCTGG TGCTGGAGAG CGGCAGGAAG 360
GAGGAGCCGC GCGCGCGGGG CGACAGCGGC GGGGCGCGCG GGGGCGCGCC GAACCGGGG 420
CCCCCAGAG CCGCAGGGCC CGGCGGGGCG TCCTCGCCA GCAGCTCGGT GGCCAAGTCG 480
CACAGCTTCT TCTCGCTGCT GAAGAAGAAC GGGCGCTCGG AAAACGGCAA GGGAGAGCCT 540
GTGGACGCGA GCAAGGCCGG CGGCAACAA AAGCGGGGCG TGCGGGGCT GTTCAGCGGC 600
ATGCGCTGGC ACAGGAAAGA CAAGCGGGCC AAGCGGAGG CCGGGAGGG GCGCGCGCCC 660
GGGGCGGGCT TGATCCTACC CGGCTCGCTC ACGCCAGGCC TGAGTGTGCT CAAGGAGGAG 720
ACGCCACAG GCGCGCGGGA GCGGAGGAG CCCAGCCAGG ACGCCCGCGG AGACCCAGCA 780
GGTGAAGCCG CAGGGGGAGA GGAGGTGCCC GCGCCCGCGG ACGCGCGCCC AGCGCGGAGC 840
TGCGGAGGAG CAGAGGGGCT CGGCAACCCG GCGGACACCG GCGCGCGGGG AGAGGACGCG 900
GCGGGGCATC GCGCGCGCGA GCGCGGGCCC GGGGAGGTCC GCACGGCAGA GGACGCTTCC 960
AGGACGGGGG CGGTTCCCGT AAAGAGCGTC CCCTTGTGCG ACTCCGAAGG CGGCAGCGGC 1020
CGGGCGCCCG CGGCGCCGCA CCCTGCTCT GTGATCCAC CACTCAGACC GTGCGCAGAT 1080
CGTATTGTGT TGATGTTTTC TGAAGTACT TCACTGAAAG GCTTTGACTC TCTTACAGGC 1140
TGTGAGATA TTATTGCAGA CCAAGAGGAA GAGGCAGTTC CCAGCTGTGA CAAGCATGTG 1200
CCCCGGCCAG GCAAGCCGCG TCTGTCTAAA AAGAACCCTG GGTGTGTGGC CTACCAAGGA 1260
GGCGGGGAAG AGATGGCCAG CCGGACGAG GTGGAAGACA CCTATCTACA GGAGTCTCTG 1320
GACATGCTCT CCCAGACCGA GGAGCAGGGA CCGGAGCCCC AGGAGGGCGC GGCTAAGGTG 1380
GCAGCTGCGC TGGAAACCAA GGTGGTGGCC GAGACCCCCA AAGACACCAG GTGTGTGGA 1440
GCGGCCAAGG ACGCTGCTCT GGTCAAGGCG AGGAGGCTCA ACGGATTCC CATGAGCCCC 1500
CATCCTAAGG AGGAGCCCAA GCACCCGAG AAGGAGCAGC AGGAAGGCGT CCCCACAGC 1560
GACGAGGGCT ACTGGGACTC CACACGCCCA GGGCCAGAGG AAGACAGCTC GAGCAGCGGG 1620
AAGAAGGGCG GCATCCCCCG GGATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT 1680
GACCCGAGCG GAAGTCCAGC AACCTTCTCT GGAGGGAAGG ACAACGAGGA GACGCTCTCC 1740
CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACT GTCCACTGCG AACACGAGC 1800
AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACCTGACCAA CCTTCCATCT 1860
AGCCATCCCG TGGTGCACCA GCAACCTTCC AGGAGTGAGA TGCCAGAAAC AAAAATCCCG 1920
GTTTCCAAAG TGCTGGTCCG CAGAGTCAGC AACCGGGGCT TGGCTGGGAC CACCATCAGA 1980
GCAAGCGGCT GCCACGACAG TGCCAAAAAG TTGTGA
  
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Seq ID NO: B53 Protein sequence
 Protein Accession #: FGENESH predicted

80

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1 11 21 31 41 51
| | | | |
METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDC AETPAABPPS 60
GKINKAAPFL FKRRKSGGTM PSIFGVKNKG DGKSSSGPTGL VRSRTHDGLA EVLVLESGRK 120
EEPRGGGDSG GGGGGRPNPG PPRAAGPGGG SLASSSVAKS HSFFSLKKGN GRSENGKGEP 180
VDASKAGGKQ KRGLRGLPSG MRWHRKDKRA KAEAAEGRAP GGGILILPGSL TASLECVKKE 240
TPRAAREPEE PSQDAPRDPF GEPAGGEEVP APADRAPARS CREAGLAHP GDTGARGEDA 300
  
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5 AGHRRABPGP GEVTRAEAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPPSDPSAD 360
 RICLMPDSVT SLKSPDSLTV CGDIIADQEE EAGPSCDKHV PGPGRPALSK KNPGVVAYQG 420
 GGSEMASPDE VDDTYLQEFW DMLSQTEQQ PEPQEGAAKV AAALSTKVVP ETPKDTRCVE 480
 AAKDASSVRK RRLNRIPIEP HPKEEPKHPE KEQGBGVNPS DEQYWDSTTP GPEEDSSSSG 540
 KKAGIPRDSY SGDALYDLVA DFDGSPATLP GGDNEETSS LSRLKPVSPG TITCPLRTPG 600
 SLKDSKIPI SLKHLTNLPS SHPVVBOQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660
 ATACHDSAKK L

10 Seq ID NO: B54 DNA sequence
 Nucleic Acid Accession #: NM_014138.1
 Coding sequence: 60..854

15 1 11 21 31 41 51
 CTGCAGAGAC TTCCACAGGAA GGTCCAGGCG CCTCTCAGCC TTGTACTCA GAACAGCCGA 60
 TGATGGGCTT CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCAG 120
 AGGGGCTGCT CGCCAGCCGG TACAGAGAGG AGAAGACCTT GGAAGAGCGG CGGTGGGAGA 180
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240
 ATCAGATGGC CCGCTATGCT GTTGGGAGGG AAGCCAGAAAT CTCCCATTA GTTGACAGAA 300
 20 GTCAGAAATG ATTCCGATGT GAATGTGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360
 GGATCCCTGG GGAGAGTAAC AGGGCCCCAC ATCCCTCTCT CTGGGAGACG CTGGTGCAGG 420
 GGCTCAGTGG CTTGACTCTC AGCCTAGGCA CCAACCAGCC CGGGCTCTG CCTGAAGCGG 480
 CACTCCAGCC ACAGAGAGCA GAGGAGAGAG GCCAGCGAGA GAGGACGAG GAGAGCAAAA 540
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCCATG 600
 25 GGATGGAGAC CCGAAGGGAC TCAGACGGAG CCGCGGTGT GGCAGCGCT GGGTGTGGGC 660
 CCATTTTGGG GACCAACAG CAAGCTGTGG TCGATGAGT GCCAGGACCT GTGTACCGGG 720
 ACACGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCG AGGAAGTTC TCATGTTTGG 780
 TGCTGTGAT TCTGGATGG CTGTGAGGCA TTCTTTGGCA AGGACGCTG CGTACCAGCG 840
 GTCTCAGCG CATCTACAT GGTCTCTGT ATGCATGTT TCGCTTTCC ACCCGGATC 900
 30 TCCATCTCTC TTCCCTCTCT GCTGTGATG AGAGATCACA TGTCTGTGA GTGTGAATGC 960
 TTTGTGCTG TCCTGTGCTT TTGCAACAT GAGTTGACT CCTCTGAGAA GCAGCACTAG 1020
 GCCTGTTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTT AAGAATGGCG AGGTAAACGC 1080
 ATGTGTGGAA AGGAATGTGG AATGAGAACT TGTGTGTTCA CCGCTGTACT ATTTGTGTAA 1140
 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTT CAATACCCCT AACAGTCGAG 1200
 35 TAGTAGTCTC CCTTACAGGA ATTTTGTACG GGGTTCCTCA TCATCAATAC CAAATAAATA 1260
 TAGTAGGAAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

40 Seq ID NO: B55 Protein sequence
 Protein Accession #: NP_054857.1

45 1 11 21 31 41 51
 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA PLRHVRRHRH 60
 DHMAPYAVGR EARISPLGDR SQNRFRCEBR YQSHRPNLS GIPGESNRAP HPSSWSTLVQ 120
 GLSGLTSLSG TNQPGPLPEA ALQPQETEEK RQRERQESK IMPQRLKQW LEEEN

50 Seq ID NO: B56 DNA sequence
 Nucleic Acid Accession #: NM_000025.1
 Coding sequence: 198..1424

55 1 11 21 31 41 51
 GCTACTCTCT CCCCAGAGAC GGTGGCACC GGGAGTTGG GTTGGGGGGA GGCTGAGCGC 60
 TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTCCGCTCT ATGCCCTTGT 120
 GTCCCTCTCC CTGAGCCAGG TGATTGGGA GACCCCTCTT TTCTTTCTTT CCTACCCGC 180
 CCAGCGCGGA CCGCGGGATG GCTCCGTGGC CTCACAGAG CAAGCTCTCTT GCCCATGGC 240
 CGGAGCTCCC CACCTCTGGG CCAATACCG CCAACACAG TGGGCTGCCA GGGGTTCGT 300
 60 GGGAGGGGGC CTAAGCCGGG GCCCTGCTGG CGCTGGGGGT GCTGGCCACC GTGGGAGGCA 360
 ACCTGTGCTT CATGTGGGCC ATCGCTGGA CTCCGAGACT CCAAGACCAT ACCAAGTGT 420
 TGTGACTTTC GTGGGCGCA GCGACCTGG TGATGGGACT CTGGTGGTGG CCGCGGGCGG 480
 CCAGCTTGGC GCTGACTGGC CACTGGCGGT TGGGCGCCAC TGGCTGGAG CTGTGGACCT 540
 CGGTGGAGCT GTGTGTGTG ACCGCCAGCA TCGAAACCT GTGCGCCCTG GCGTGGAGCC 600
 65 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GTTCACCAAG CGCTGGGCC 660
 GGACAGCTGT GGTCTGTGT TGGGTGTGT CCGCGCGGT GTGTTTGGG CCCATCATGA 720
 GCCAGTGTGT GCGGTAGGG GCGGAGCGG AGGCGCAGG CTGCCACTCC AACCGCGCT 780
 GCTGTGCTGT CGCTCCAAAC ATGCCCTACG TGTGCTGTG CTCTCTCGTC TCCTTCTACC 840
 TTCTCTCTCT CGTGTGCTT TTGCTCTACG CGCGGTTTT GTGTGTGGCT ACGGCGCAGC 900
 70 TGGCTTGTCT GCGCGGGGAG CTGGGCGGCT TTCCGCGCGA GAGTCTCCG CCGCGCGCT 960
 CGCGCTCTCT GCGCGCGGCC CCGGTGGGGA GTGCGCTCC GCCCGAAGGG GTGCGCGCT 1020
 GCGCGCGGCG GCGCGCGGCG CTCTGCGCT TCGGGGAACA CCGGCGCTG TGCACTTGG 1080
 GTCTCATCAT GGGCACTTTC ACTCTCTGT GGTTCGCTT CTCTCTGGCC AACTGTCTGC 1140
 GCGCGCTGGG GCGCGCTTCT CTAGTCCGG GCGCGGCTTT CTGTGCTGT AACTGGCTAG 1200
 75 GTTATGCCAA TTCTGCTTC AACCGCTCA TCTACTGCG CAGCGCGAC TTTGCGAGG 1260
 CCTTCGCGCG TCTTCTGTG CCGTGGCGCC GTGCGCTCC TCGGAGGCC TCGCGCGCG 1320
 CCGCGCGGCG CCGCTTCCCG TCGGGGCTTC CTGGGCGCTG GAGCAGCCCA GCGCAGCCCA 1380
 GGCTTGGCA ACGGCTGAC GGGGCTTCTT GGGGAGTTTC TTAGGCTTGA AGGACAAGAA 1440
 80 GCAACACTC TGTGTATCAG AACCTGTGA AAACCTCTG CCTCTGTTC GAATGAGTC 1500
 CATGGGATTC CCGGCTGTG AACTCTACC CTCCAGAAC TGACGACTGG GCCATGTAC 1560
 CCAAGAGGGG ATCCTTACCA AGTGGGTTT CACCATCTC TTGCTCTCTG TCTGAGAGAT 1620
 GTTTTCTAAA CCGGCGCTT GAACCTCCT CCGCTCTAG TGGTAGTGC CAGGTGCGT 1680
 GGAGCAGCAG GCTGCTTTG GTAGGGGAC CCAACAACCG GCTTGCCTGT GCAGTCACTG 1740
 AGTGCTTAGG GCAAGAGAG CTCCTCTGT TCCATTCTT CTGCCACCA AACCTGATG 1800

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTTGGG GTTTTATCTC TGGTTCCCTT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGGTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTGCCCAGGG 1980
TTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATTAG AACAGATCCC TTCTTTTCCT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTTAT CCTCGGCCCA CTTCCTCTCC 2100
GTTTGTTCCT TTTTCATAAT CCACCTACTC CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCGAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAAACAAAA 2220
AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCTTTCCTG AAACCTTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGCCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400
GCATTGTGCC CCTCCATGCT ATAATCCAGT GGTGCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGCGTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTG CTTGGGTTGG 2520
TCAATGTCT TGTGTCAATA ATATATTCTG ATGTTTCCCA GCCTTCCAC AACCTCTACC 2580
TTCCACTCA CCTTCCCCAG CTACAAAAAT CTGTATTATC CTCCTAAAGT AAAACTGGAG 2640
TTAC

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Seq ID NO: B57 Protein sequence
Protein Accession #: NP_000016.1

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1      11      21      31      41      51
|      |      |      |      |      |
MAPWPHENSS LAPWPDLPFL APNTANTSGL PGVPWEAALA GALLALAVLA TVGGNLLVIV 60
ALAMTRELQT MTNVFVTSIA AADLVMGLLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
VTASIELTCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VMVVSAAVSF APIMSQWHRV 180
GADAEARQCH SNPRCCAFAS NMPYVLLSSS VSFYLPPLVM LFVYARFEVV ATRQLRLLRG 240
ELGRFPPEES PPAPRSRAP APVGTCAPE GVPACGRRA RLLPLREHRA LCTLGLIMGT 300
FTLCWLPFFL ANVLRALGGF SLVPGPAFLA LNWLYANSA FNPPLYCRSP DFRSAFRRL 360
CROGRLPPE PCAAARPALE PSQVPAARSS PAQPRLCQRL DGASWGS

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Seq ID NO: B58 DNA sequence
Nucleic Acid Accession #: NM_032553.1
Coding sequence: 37..1038

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1      11      21      31      41      51
|      |      |      |      |      |
CACCATTAGG CAAAGATAGT TTCTCTAGAG AGAATCATGC CTGCTAATTA CACGTGTACC 60
AGGCCAGATG GAGACAATAC AGATTTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC 120
ATTCTGTGTC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGTATTTCTA TGGTTATATG 180
AAGAAGACAA AACGAGCTGT GATATTTATG ATAACTTAG CCATTGCTGA CTACTACAA 240
GTTCTTTCCT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGSCC ATTTGGGCCT 300
GGTCTCTGCA TGTCTGTTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGGTCTGCA TCAGTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTCG CTTCCATGAC 420
TGCAACAGCA AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCTTGCC 480
TGTGTACTCT TTCACTCTCT CAGAACCAGT GATGATAOCT CTGGCAATAG GACCAATGTC 540
TTTGTGGATC TTCTACCCAG GAATGTCAAC CTGGCCCACT COGTTGTTAT GATGACCATT 600
GGCGAGTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAAGACG 660
GTTTATCAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TTGAAGATGA TTCTAACCTG TGCAGGGGTA TTCTTAATTT GCTTTGCACC TTATCATTTT 780
AGTTTTCTCT TAGATTCTCT GGTGAAGTCC AATGAAATTA AAGCTGCTCT AGCCAGAAGG 840
GTGATTTCTA TATTTTCAATC TGTGGCATTG TGTCTTGCTA GTCTGAATTC ATGTCTTGAC 900
CCAGTCATAT ACTACTTTTC CACTAATGAG TTCCGAGAGC GGCTTTCAAG ACAAGATTTC 960
CATGACAGCA TCCAACCTCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
ACACCTGAAT TATGTAAACA CAAAAAACA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080
CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAAC ACAGCTTTTC 1140
AGTTCTGCTC TATCTACTG CTATGGGGAA TTCACTTCTT CAAAGCAGGA CCTATTTTGA 1200
GCATTACCAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTT CTTCAGAT

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Seq ID NO: B59 Protein sequence
Protein Accession #: NP_115942.1

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1      11      21      31      41      51
|      |      |      |      |      |
MPANYTCRTP DGDNDIFRYP IYAVTYTVIL VPGLIGNILA LWVFYGYMKE TKRAVIFMIN 60
LAIDLQLVL SLPLRIPYYL NHDWPPGPGL CMFCFYLYKV NMYASIFLV CISVRFWFL 120
MYPPRFHDCQ QKYDLYISIA GWLIICLACV LFPLLRSTSD TSGNRTKCFV DLPTRNVLNA 180
QSVVMTTIGE LIGFVTPLLI VLYCTWKTVL SLQDKYFMAQ DLGEKQKALK MILTCAGVFL 240
ICFAPYHFSF PLDFLVKSNE IKSCLARRVI LIPHSVALCL ASLNSCLDPV IYYPSTNEFR 300
RRLSRQDLWD SIQLHAKSFV SNHTASTMTF ELC

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Seq ID NO: B60 DNA sequence
Nucleic Acid Accession #: CAT cluster

75
80

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1      11      21      31      41      51
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Seq ID NO: B62 Protein sequence
Protein Accession #: NP_055337.1

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Coding sequence: 140..931

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 TATTGTTGAG ACCAAGATCT GTCAAGAGTA AGAGGCAACA GATAGAGTGT CCTTGGTAAT 960
 AAGAACTCAG AGATTTACAA TATGACTTTA ACATTAAGGT TTATGGGATA CTCAGATAT 1020
 TTACTCATGC ATTACTCTA TTGCTTATGC CGTAAAAAAA AAAAAAAAAA AAAAAAAAAA 1080
 AA

Seq ID NO: B66 Protein sequence
 Protein Accession #: NP_004858.1

1 11 21 31 41 51
 MVKIAFTPT AVQKEARQD VEALLSRTVR TQILTGKELR VATQSEKGGSS GRCLMTLLGL 60
 SPILAGLIVG GACIYKYFMD KSTIYRGEMC PFDSEDPANS LRGGEPNPLP VTEADIRE 120
 DNIAIIDVPEV PPSFSDSDPAA IIEDFEKGMT AYLDLLLGNC YLPLANTSIV MPPKNLVLEP 180
 GKLASGRYLP QTVVVRDLV AVEEIRDVSN LGIPIYQLCN NRKSFRLRRR DILLGPNKRA 240
 IDKCKIRHF FNEFIVETKI CQE

Seq ID NO: B67 DNA sequence
 Nucleic Acid Accession #: XM_083862.1
 Coding sequence: 121..813

1 11 21 31 41 51
 ACGCGGAGG TCTGAGCTGT GGGCTGAGGC AGCGCAGCG CTGCGCCAGG GTGCGCGATG 60
 CCTTGAACCT GGGAACTAT GTGAAGCAAC ACTCTGGATT TTGAAAGACA TCTTTTCATC 120
 ATGGGACAGC AAATTTCCGA TCAGACACAG TTGGTTATTA ACAAGTTACC AGAAAAAGTA 180
 GCAAAACATG TTACGTTGGT TCGAGAGAGT GGCTCCTTAA CTTATGAAGA ATTTCTCGGG 240
 AGAGTAGCTG AGCTTAATGA TGTAAACGGCT AAAGTGGCTT CTGGCCAGGA AAAACATCTT 300
 CTCTTTGAGG TACAACCTGG GTCTGATTCC TCTGCTTTT GGAAGTGGT TGTACGGGTG 360
 GTCTGTACCA AGATTAAACA AAGCAGTGGC ATTGTGGAG CATCACGGAT CATGAATTTA 420
 TACCAGTTTA TTCAACTTTA TAAAGATATC ACAAGTCAAG CAGCAGGAGT ATCGGCACAG 480
 AGCTCCACCT CTGAAGAAC TGAATGAAAC TCATCCTCTG TAACATCTTG TCAGGCTAGT 540
 CTTTGGATGG GAAGGGTGAA GCAGCTGACC GATGAGGAG AGTGTGTAT CTGTATGGAT 600
 GGGCGGGCTG ACCTCATCTC GCCTTGTGCT CACAGCTTTT GTCAGAAAGT TATTGATAAA 660
 TGGAGTGATC GACACAGGAA TTGCCCTATT TGTGCGCTAC AGATGACTGG AGCAATGAA 720
 TCTTGGGTGG TATCAGATGC ACCCACTGAA GATGATATGG CTAACATAT TCTTAACATG 780
 GCTGATGAGG CAGGCCAGCC CCACAGGCCA TGACCTTGAA GTGAAAGTCT TCTGTGCTA 840
 TGTGGGGCTC AAATATTGGT TCATGGGGGA AGAATGTAGG GTTGTGGCAC TGGCAGAGAC 900
 ACAGGAAAT CCATTTTCCC CACTCTTTTA TTTTGTCTAT TCTGATCAT TGTCCCTCT 960
 TAAAAATAA ACTTCCCATG TCTTCCAAA AAAAAAAAAA AAAAA

Seq ID NO: B68 Protein sequence
 Protein Accession #: XP_083862.1

1 11 21 31 41 51
 MGOQISDQTO LVINKLPEKV AKHVTLVRES GSLTYEEPLG RVABLNDVTA KVASGQEKHL 60
 LFEVQPGSDS SAFWKVVVRV VCTKINKSSG IVEASRIMNL YQFIQLYKDI TSQAAGVLAQ 120
 SSTSEEPDEN SSSVTSCQAS LWMGRVKQLT DEBECCICMD GRADLILPCA HSPQCCKIDK 180
 WSDRHRNCPI CRLQMTGANE SWVVSAPTE DDMANYILAM ADEAGQPHRP

Seq ID NO: B69 DNA sequence
 Nucleic Acid Accession #: NM_002975.1
 Coding sequence: 180..1151

1 11 21 31 41 51
 CGACCAACGG ACGGACAGGA GACGAGGAGA GGAACAGGAA GAGAGAAGCT GGGAGAAATCG 60
 GGAACCTGGG GGTAGTGAC CTGCACACAG GGCAGGGGCA CTCGGCAGTT CCCAGAGGCC 120
 ACCCTCCCA CCCCAGACAT CCAGACATCT GGAACCTTTG GTGCCAAGAG TCCAGCTTAA 180
 TGCAGGCAGC CTGGCTTTTG GGGCTTTTG TGGTCCCCCA GCTCTTGGGC TTTGGCCATG 240
 GGGCTCGGG AGCAGAGAGG GAGTGGGAGG GAGGCTGGGG AGGTGCCAG GAGGAGGAGC 300
 GGGAGAGGGA GGGCTGATG CTGAAGCATC TGCAGGAAGC CCTAGGACTG CCTGCTGGGA 360
 GGGGGGATGA GAATCCTGCC GGAACCTTTG AGGGAAGA GAACCTGGAG ATGGAGGAGG 420
 ACCAGGGGGA GGAAGAGGAG GAGGAAGCAA CGCCAAACCC ATCCTCCGGC CCCAGCCCTC 480
 CTCCACACCC TGAGACATC GTCACTTACA TCCTGGGCGG CCTGGCCGGC CTGAGCCAG 540
 GCCTGCACCA GCTGCAGTTC CTTCTGCACG CTTTGGACAC CGCGTGGTTC GAGCTGACCC 600
 AGGGGCTGGG GCAGCTGGGG AACGGGCGAG GCGACACCGG CGATGCCGTG CAGCCCTTGC 660
 AGGAGGGGCA GAGTCCGGCC GAGCGCGAGC ACGGCCGCTT GAGGGGCTGC CTGAGGGGCG 720
 TGGCGCTGGG CCAAGAGTGC TTCTGTCTCT CGCGGCACTT GGAAGCTCAG GGGCGGGGCG 780
 AGGCGGGTGG CAGCGCGGGG GCGGGGAGCC TGGCGGAGCC GGCAGACCGC CAGCAGATGG 840
 AGGCGCTCAC TCGGTACTGT CCGCGCGGCG TCGCTCCCTA CAACCTGGCC GTTGGCTGG 900
 GCGTGCACGA TGGCGCGGCC GAGGGCTCTT ACCTCTTGA AAACGGCCAG CGCGTGTCTT 960
 TCTTGGCCTG GCATCGCTCA CCCCCTCCCG AGCTCGGCGC CCAGCCAGCG GCCTCGCGCG 1020
 ATCCGCTCAG CCGGACAGG CCAACCGGTG GCAACGCTCA GAACTGCGTG GCGCAGGCTC 1080
 CTGACGAGCG CTCCTGGTGG GACCAAGACT GCGAGCGGGG TCTCTACTAC GTCTGGAGT 1140
 TCCCTTCTTA CGCGGGCGCG TACCCCGCTT CCTTGGCCAT CCCACACCC GGCCTTTCCC 1200
 TGGCGCGTGC CCACCTCTCT CCGGAATCGC CCTTCCCTTC CTGGCCACGA ATGGCAGCGT 1260
 CCTCCCGAGC CCCCAGTCTG GCGGCTTCTG GAGGGGCTCT TGGGTGCGCG GCATCTCTCC 1320
 TGTGTAAGTGT CTTTCTTGA AGGGGCGGGC ACCAGGCTAG GTCCGGTGCC AATAAATCTT 1380
 TGTGGAATCT GAAAAAAA AAAAAA

Seq ID NO: B70 Protein sequence
Protein Accession #: NP_002966.1

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5      1      11      21      31      41      51
|      |      |      |      |      |
MQAANLLGAL VVPQLLOFGH GARGAEREWE GNGGAQEER REREALMLKH LQBALGLPAG 60
RGDENPAGTV EGKEDWEMEE DQEEEEEEEA TPTSSGSPSP SPTPEDIVTY ILGRLAGLDA 120
GLHQLHVRLL ALDRVRVELT QQLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGLCKLG 180
10    LRLGHKCFLL SRDPEAQAAA QARCTARGGS LAQPADRQOM BALTRYLRAA LAPYNWVWNL 240
GVHDDRABGL YLPENGQRVS FPAWHRSPRP ELGAQPSASP HPLSPDQPNG GTLENCVAQA 300
SDDGSWHDHD CQRLYYVCE FPF

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Seq ID NO: B71 DNA sequence
Nucleic Acid Accession #: BC000839.1

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15      1      11      21      31      41      51
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CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG 60
TGGGGCTTTG TGAAGGACAA ATAGGCGATG GCGGGCCGTG TAGGTCCCCC TTCTATGAT 120
GAGGACCTTT TCACAGACTT GTACTGAGCT CCGTGAGGAT AAGTAACTCT GAGGAGATGG 180
GCCCTGCAAG CCTCTCTCTT AGCCGCTCTG TCAGAAAATA GCGTTTTCGA AATGCCCTGA 240
GTTGACCTAA TGTCTTATTC GGCTCTCTGC TGCAGGATTT ACGGSCACGT TGGAAACCGAA 300
GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA 360
25    GACCCATCTT TATGCAAGC CAGCGTTACA GTAAATGTTCC AGCATCTCAT AATCTATCCT 420
GGGJAATTCG GCTGCCCTCC AGGTGAATA CAGTATTCC TGATGACAGT CTGCCTCTAT 480
CTTACAGAGC AGCTTGTGTC TATATACCAT TGAAGAGCCT TCAGAGCTGA GAGGTACTAC 540
TAACCAATAA CCTGCTTGGC TCAAGGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
TTGAGGAATA CTAGGTGTCT GTGTTCACTC CAGGCTGAAG TTACAGTCTC GAGCAATAAA 660
30    GGTGTATAAA AAATGGAATC TGTCTTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT 720
GGACAACCTA CTTGTTGAAA AGCTTCTGCG GTTTGGGGGG TATTTCAGAT GTACCTTAAA 780
GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT 840
GTGTATCACA TTCTGTATTT TTATCACCCC CTTCCTGCAA CATTATTATC CTGGAATCTA 900
CCTGCCCTTT TGTTTTITAG ATACAAGGGC TTGGTTTGTG TACCCAGGCT GGTTTCAAGG 960
35    CCATAGCTTT AAGAGATCTC CTCACCAAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
TTCATGSCAC CCGAGCTTTC CTGCCCTTCT TACATGATCC AGGCCAGAA CCCAACTCA 1080
GGCACTGTAT AGATGACCAC TTTGTAAAC TACTGACCTA GCTTGTGACC AATGTTGAT 1140
TGAAGTCTCC ATAACTCCAC TTCTGTCTGT TACAGCCACC TTCTGTCTCC 1200
40    GTCACTGAGC TTAGGTCTC CATTTGCATA TGCATAATC TATGTTCCAT GTAGGTAGCT 1260
CATTCAGGCG CTGCTCTTC ACTTCAAAA AGGTTCCTTT GAGGACTGGC TGTCAATTTG 1320
TGTGCTGTGG TTGTTTGTGG ATGAAAAATA TAAATGATT GATTACATAA AAAAAAAA 1380
AAAAAA

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Seq ID NO: B72 DNA sequence
Nucleic Acid Accession #: CAT cluster

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45      1      11      21      31      41      51
|      |      |      |      |      |
TGCTAGTAGG GCCTGGGTTA ATCGGCCGAG GGTGGCTTGG TGGTCTTTAT AGCTGTTACT 60
CTTTGTACTT GTCTTTTTCT TTTATTTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA 120
CGCACTATGG CACGAGGCTC GTGCTGCCCTG GCGAGGGCGA CTGGGGATA AGGTCTTTGG 180
CGTGGCCTCG AGGCTTAAAA GTAGCAGTGG GGCTTTGTGA AGGACAAAAT GCGGATGGCG 240
GGCCGCTGAG GTCCCCCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCCG 300
TGAGGATAAA TAACCTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTTCA 360
55    GAAAATAGCG TTTTGGAAAT GCGCTGAGTT GACCTAATGT CTTATTGGGC TCCTGTCTGC 420
AGGATTTACG CGCAGCTTGG AACGGAAGAG AGCTCTGTTG TTGCAATGTT CAGCCACAA 480
GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCAAGGCCAG CGTTACAGTA 540
ATGTTCCAGC ATCTCATAAT CTATCCTGGG GAATTCAGCT GCGTCCACGG GTGAATACAG 600
GTATCTCTGA TGACAGTCTG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCAATTGA 660
60    AAAGCCTTCA GAGCTGAGAG GTACTACTAA CCAATAAACC GCTTGGCTCA AAGGGCCAGC 720
ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGTCTGTG TTCACTCCAG 780
GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAACTCTG CTTGGAGGAC 840
ATCAGAAGGT GAATTTTCCA AGTTCTTGGA CAACCTAGCT GTTGAAGAAC TTCTTGGGTT 900
TGSGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAAAG CACTGGGAGC 960
65    CAATGAACA GCAGTTGAGG GTTTGCTGTG TATCACATTT CTGATTTTAA TCACCCCTTT 1020
CCTGCAACAT TATTTATCTG GAATCTACCT GCGCTTTTGT TTTTATGATA CAAGGGCTTG 1080
GTTTGTGTAC CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
TCCAAAGTGC TGGGATTGCA GGTGTGATTC ATGGCACCCA GACTTTGCTG CCTTTCTTAC 1200
ATGATCCAGG CCCAGAACCC AAACCTCAGG ACTGTATAGA TGACCACTTT CGTAAACTAC 1260
70    TGACCTAGCT TGTGCTCAAT TGTTGATTGA ACTTCCATA ACTCCACTTC GTGTCTGTTT 1320
CTCTGTATAC AGCCACCTTC TGTTCCTGTC ATGAGCCTTT AGGTCTCCAT TTGCATATTG 1380
CAAAATACTAT GTTCCATGTA GTTAGCTCAT TCAGGGCCCT GCTCTTCACT TCAAAAAAGG 1440
TTCCCTTGAG GACTGCTGCT CAATTTGTGT TGCTGTGTTG GTTGTGTATG AAAAAATAAA 1500
75    AATGATTGAT TACATAAAAA AAAAAAAA AAAAAAAA CACAAAAAAC 1560
GCGCGGCTTT TTTCCCGGGC GCACAAAGTT ATAAAGGCC GTCCATC

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Seq ID NO: B73 sequence
Nucleic Acid Accession #: NM_000222.1
Coding sequence: 22..2952

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80      1      11      21      31      41      51
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GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGCGGCG CCTGGGATTT TCTCTGCGTT 60
CTGCTCTTAC TGCTTGGCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120

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	CCGTCCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGACTGTA	TCCGGGCTTT	GTCAATATGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACAGT	GCACCAACAA	ACACGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCGAAGC	TTTTCTCTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCACAGA	CCCAGAAGTG	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGCGAT	CATGATCAAA	540
	AGTGTGAAAC	GGGCTTACCA	TGGGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTCTGT	CGGAAAAATT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAGGC	TGTGCCCTGT	660
	GTGTCTGTGT	CCAAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTCAAC	AGTGACGTGC	720
	ACAAATAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAAAGTGGA	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTCAAGCA	840
	ACGTGTGACTA	TCAGTTCTAGC	GAGAGTTAAT	GATTCTGGAG	TGTTTCATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCAACACA	ACCTTGGAA	TAGTAGATAA	AGGATTCAAT	960
	AATATCTTCC	CCATGATAAA	CACATACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTGT	1020
	ATTGTTGAAT	ATGAAGCAAT	CCCCAAACCT	GAACACGAG	AGTGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAGTAA	TATCAGATAC	1140
	GTAAAGTAAC	TTCACTCTAAC	GAGATTAAAA	GGCACCAGAG	GAGGCACTTA	CACATTCTTA	1200
20	GTGTCCAATT	CTGGGCTCAA	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAAATCTCGA	CTTAGCAGAC	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTTC	1320
	CCAGAGCCCA	CAATAGATTG	GTATTTTGTG	CCAGGAACCTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGATGTGCA	GACACTAAAC	TCATCTGGGC	CACCGTTTGG	AAAGCTAGTG	1440
	GTTCAGAGTT	CTATAGATTTC	TAGTGCATTTC	AAGCACAATG	GCACGGTTGA	ATGTAAGGCT	1500
25	TACACAGATG	TGGGCAAGAC	TTCTGCTAT	TTTAACTTTG	CATTAAAGG	TAACAACAAA	1560
	GAGCAAAATCC	ATCCCCACAC	CCGTGCTACT	CCTTTGCTGA	TTGTTTCTGT	AATCGTAGCT	1620
	GGCATGATGT	GCATTATTGT	GATGATTCTG	ACCTACAAAT	ATTTACAGAA	ACCCATGTAT	1680
	GAAGTACAGT	GGAGAGTTGT	TGAGAGAGATA	AATGGAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAATTC	CTTATGATCA	CAAAATGGAG	TTTCCAGAA	ACAGGCTGAG	TTTTGGGAAA	1800
30	ACCCCTGGTG	CTGGAGCTTT	CGGGAAGGTT	GTGAGGCA	CTGCTTATGG	CTTAATTAA	1860
	TCAGATGCGG	CCATGACTGT	CGCTGTAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGGAAGCCC	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TTGTAATCA	CATGAATATT	1980
	TGGAATCTAC	TTGGAGCCCTG	CACCATTTGA	GGGCCACCCC	TGGTCATTAC	AGAATATTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTTGAGA	AGAAAAAGTG	ATTCAATTAT	TTGTTCAAAG	2100
35	CAGGAAGATC	ATGCAGAAAG	TGCACCTTAT	AAGAATCTTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAAGGATA	GTACTTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCCG	ACAAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCGCCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAGGTGG	CAAGGGGACT	GGCTTTCTCT	GCCTCCAGAA	ATTGTATTCA	CAGAGACTTG	2400
40	GCAGCCAGAA	ATATCTCTCT	TACTCATGGT	CGGATCAAAA	AGATTGTGTA	TTTTGGTCTA	2460
	GCCAGAGACA	TCAAGAAATGA	TTCTAATTAT	GTGGTTAAAG	GAACGCTCG	ACTACCTGTG	2520
	AAGTGGATGG	CACCTGAAAG	CATTTTCAAC	TGTGTATACA	CGTTTGAAAG	TGACGCTGG	2580
	TCCTATGGGA	TTTTTCTTTG	GGAGCTGTTT	TCTTTAGGAA	GCAGCCCTTA	TCCTGGAATG	2640
	CCGCTCGATT	CTAAGTTCTA	CAAGATGATC	AAGGAAGGCT	TCCGGATGCT	CAGCCCTGAA	2700
45	CAOGCAGATA	ACAGTTGGCC	TGACATAATG	AAGACTTGCT	GGGATGCAAA	TCCCTTAAAA	2760
	AGACCAACAT	TCAAGCAAAAT	TGTTTCACTA	ATTGAGAAAG	AGATTTCAGA	GAGCACCAAT	2820
	CATATTACT	CCAACCTAGC	AAACTGCAGC	CCCAACCGAC	AGAAGCCGCT	GGTAGACCAT	2880
	TCTGTGCGGA	TCAATTCTGT	CGGCAGCACC	GCTTCTCTCT	CCGACCTCT	GCTTGTGCAC	2940
	GACGATGCT	GAGCAGAAATC	AGTGTTTGGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCTTCCATGA	TGTTTATTGT	CTTTTCTTTC	AACTTGCAATC	CAACTCCAGG	ATAGTGGGCA	3060
	CCCCACTGCA	ATCCTGTCTT	TCTGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTATCAGC	3120
	CACCATCTTA	TTGCAAGGTT	TCCAACCTGA	TATATTCCCA	ATAGCAAGCT	AGCTTCTACC	3180
	ATGAACAGAA	AACATTCTGA	TTTGGAAGAA	GAGAGGGAGG	TATGACTGG	GGCCAGAGT	3240
	CCTTCCCAAG	GCTTCTCCAA	TTCTGCCCAA	AAATATGTTT	GATAGTTTAC	CTGAATAAAT	3300
55	GGTAGTAATC	ACAGTTGGCC	TTCAAGAACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
	AGCTGAAAC	CTAAGTCTCT	TATGTGGAAA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAGA	AATCTAGTAT	TTTATGCTGG	GAATGAGACA	TAGGCCATGA	3480
	AAAAAATGAT	CCCCAAGTGT	GAACAAAAGA	TGCTCTCTCT	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGGTTTT	TAAATAGAGT	TTGCTATTAG	AGCATTTAAT	TGGAGAGAA	3600
60	GCTCCCTAG	CCAGCACTTG	TATATAAGCA	TCTATAAATT	GTCCGTGTTT	ATACATTGA	3660
	GGGGAACA	CCATAAGGTT	TGTTTCTGT	ATACAACTCT	GGCATTTATG	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACAG	TTAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAGACA	CAGTTTGAAC	AAAATCTCCT	CTTTTAGCTG	ATGAACCTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAAATG	GCATTTGACT	CAATGGATT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCACT	GCATGGCTCC	CACAGGAGTG	GGAAAACACT	3960
	GCCAATCTAG	TTTGGATTCT	TATGTAGCAG	GAATAAAGT	ATAGTTTAG	CCTCCTTGGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTAGCTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGGCCC	TGAGTCCAA	AGGGTCCCTT	AGTACCTGAA	4140
	AAGTAACCTG	GCTTTTCATTA	TTAGTACTGC	TCTTGTCTCT	TTTCACATAG	CTGTCTAGAG	4200
70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCACTTC	ACCTGCACCT	AAGGCACCTC	GTTATTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTTAGACT	4380
	GTAGCCTGGA	TATTATTCTT	GTAGTTTACC	TCTTTAAAAA	CAAAAACAAA	CAAAAACAAA	4440
	AACTCCCTCT	CCTCACTGCC	CAATATAAAA	GGCAAAATGTG	TACATGGCAG	AGTTTGTGTG	4500
75	TTGTCTTGAA	AGATTCAAGT	ATGTTGCCCT	TATGTTTCC	CCCTTCTACA	TTTCTTAGAC	4560
	TACATTAGA	GAAGTGTGGC	CGTTATCTGG	AAGTAACCAT	TTGCACTGGA	GTTCTATGCT	4620
	CTGCACTCTT	TCCAAAGTTA	ACAGATTTTG	GGGTTGTGTT	GTCAACCAAG	AGATTGTGTT	4680
	TTGCCATACT	TTGTCTGAAA	AATTCTTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTGTG	TAGTTATAGA	TGTCTAGGTA	CTTCAGGGGC	ACTTCAATTGA	GAGTTTGTCT	4800
80	TTGCCATACT	TTGTCTGAAA	AATTCTTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTGTG	TAGTTATAGA	TGTCTAGGTA	CTTCAGGGGC	ACTTCAATTGA	GAGTTTGTCT	4920
	AATGCTCTTT	GAATATTTCC	AAGCCCATGA	GTCTCTGAAA	ATATTTTCTA	TATATACAGT	4980
	AACCTTTATGT	GTAAATACAT	AAGCGGCTTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
	TTATCTCTGT	ATGTTGTCCA	ATTGTTGACA	GTTCTGAAGA	ATTC		

Seq ID NO: B74 protein sequence
Protein Accession #: NP_000213.1

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5      1      11      21      31      41      51
|      |      |      |      |      |
MRGARGANDF LCVLLLLLRV QTGSSQSPSVS PGEPSPPSIH PGKSDLIVRV GDEIRLLCTD 60
PGFVKMTFBI LDETNNKQN EWITEKAEAT NTGKYTCTNK HGLSNSIYVF VRDPAKLFLV 120
DRSLYGKEDN DTLVRCPLTD PEVTNYSLSKQ CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAFKA VPVVSVSAS YLLREGEEPT VTCTIKDVSS 240
10     SVYSTNWKREN SQTKLQEKVN SWHHGDFNYE RQATLTISSA RVNDSGVFMC YANNTFGSAN 300
VTTLEVVVDK GFNIFPFIN TTVFVNDGEN VDLIVEYEF PKPEHQMIY MNRTFTDKWE 360
DYPKSENESE IRYVSELHLT RLKQTEGGTY TPLVNSDVN AAIAPNVYVN TKPEILTYDR 420
LVNGLQCVAA AGPPEPTIDW YFCPTGEQRC SASVLPVDVQ TLNSSGPFPG KLVVQSSIDS 480
SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPT LFTPLLIGFV IVAGMMCIIV 540
15     MILTYKYLQK PMYEVQWQV EEBINGNVYV IDPTQLPYDH KWEFFRNRLS PGKTLGAGAF 600
GKVVETATYG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLVSYLGNH MNIVNLLQAC 660
TIGGPTLVIT EYCCYGLLIN FLRRKRDSPI CSKQEDHAEA ALYKLLHSK ESSCSDSTNE 720
YMDMKPGVSY VVPTKADKRR SVRIGSYIER DVTFAIMEDD ELALDLEDLL SFSYQVAKGM 780
APLASNCHH RDLAARNILL THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAFES 840
20     IFNCVYTFES DVMSYGFILW ELPSLGSSPY PGMFVDSKPY KMIKEGFRML SPEHAPAEY 900
DIMKTCDWAD PLKRPFPKQI VQLIEKQISE STNHIYSNLA NCSFNQKQPV VDHSVRINSV 960
GSTASSSQPL LVHDDV

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Seq ID NO: B75 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58..2298

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30     1      11      21      31      41      51
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GAATTCGCGG CGACGCGCGG GAACAACGCG AGTCGCGCGG CGGGACGAAG AATAATCATG 60
GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAGTTTGTT GCGCGAAGCG TGTAATAATCA 120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCA ATCGTCAGAA AATTTTGAAA AGAACGGAAA TCTTAAACCA AGAATGGAAA 240
CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGACTAGG 300
35     GAGTGTTCGG TGACCACTGA CTTGGATTTT CCAACACAAG TCATCCCAT TAAAGACTCTG 360
AATGCAGTTG CTTGAGTACC CATAATGTAT TCTTGGTCTC CCTACAGCA GAATTTTATG 420
GTGGAAGATG AAACCTGTTT ACATAACATT CCTTATATGG GAGATGAAGT TTAGATCAG 480
GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAAATTTTT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
40     AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
GATCTGGAGG ATCACCAGAG TGATAAAGAA AGCCGCCAC CTGCGAAATT TCCTTCTGAT 720
AAAATTTTGG AGGCCATTTC CTCATGTGTT CCAGATAAGG GCACAGCAGA AGAACTAAAG 780
GAAAATATAT AAGAACTCAC CGAACAGCAG CTCCAGGCG CACTTCTCC TGAATGTACC 840
CCCAACATGA TTGACACAAA TGCTAAATCT GTTCAGAGAG AGCAAGCTT ACACCTCTTT 900
45     CATACGCTTT TCTGTAGGCG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCCAACA CTTTATAGCG GAAGAACACA GAAACAGCTC TAGACAACAA ACCTTGTGGA 1020
CCACAGTGTT ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCCACCAA ACCTCCAGGA GCGCGCAGAA GAGGACGGCT TCCCAATAAC 1140
50     AGTAGCAGGC CCAGCACCCC CACCATTAA TGTCTGGAAT CAAAGGATAC AGACAGTGAT 1200
AGGGAAGCAG GCACTGAAAC GGGGGGAGAG AACAATGATA AAGAAGAAGA AGAGAAGAAA 1260
GATGAAACTT CAGCTCTCTC TGAAGCAAAT TCTCGGTGTC AAACACCAAT AAAGATGAAG 1320
CCAAATTTTG AACCTCTCTG GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAA 1380
GTCTCTATTG GCACCTACTA TGACAAATTC TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
55     ACATGTAGAC AGGTGTATGA GTTAGAGTCA AAGAATCTA GCATCATAGC TCCAGCTCCC 1500
GCTGAGGATG TGGATACTCC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA 1560
CACTGCAAGAA AGATACAGCT GAAAAAGGAG GGCTCTCTTA ACCATGTTTA CAACTATCAA 1620
CCCTGTGATC ATCCACGCGA GCCTTGTGAC AGTTCTGTCC CTGTGTGAT AGCACAAAAT 1680
TTTTGTGAAA AGTTTGTGCA ATGTAGTTCA GAGTGTCAA ACCGCTTCC GGGATGCCGC 1740
60     TGCAAAAGCAG AGTGCAACAC CAAGCAGTGC CGTGTCTACC TGGCTGTCCG AGAGTGTGAC 1800
CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATTGGG ACAGTAAAAA TGTGTCTGTC 1860
AAGAAGTCCA GTATTACAGG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGAGCTG 1920
GCAGGCTGGG GGATTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAAATC 1980
TGTGGAGAGA TTATTCTCAA AGATGAAGCT GACAGAAAGG GGAAAGTGTG TGATAAATAC 2040
65     ATGTGCAGCT TTCTGTTCAA CTTGAACAA TATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
AACAAAAATC GTTTTGCAAA TCATTGGGTA AATCCAAACT GCTATGCAAA AGTTATGATG 2160
GTTAAGCGTG ATCAGAGGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCCG CATCGAAAGA 2280
GAAATGGAAG TCCTTGACA TCTGCTACCT CCTCCCCTCT CTCTGAAACA GCTGCTCTAG 2340
70     CTTCAGGAAC CTGAGTACT GTGGSCAAT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
AATTTGCAAA GTACTGTAG AATAATTTAT AGTAATGAGT TAAAAATCA ACTTTTAT 2460
GCCTCTCAC CAGCTGCAAA GTGTTTTGTA CCAATGAAAT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAACCTGAA AAAAAA AAAAAA

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Seq ID NO: B76 Protein sequence
Protein Accession #: NP_004447

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80     1      11      21      31      41      51
|      |      |      |      |      |
MQQTGKKSEK GPVCRKRKVK SEYMRLRQLK RFRRADEVKS MPSSNRQKIL ERTEILNQEH 60
KQRIQFVHI LTVSVSLRGT RECSVTSDDL PPTQVIPLKT LMAVASVPIM YSWSPLOQNP 120
MVDEDTVLIN IPYMGDEVLD QDGTFTIEELI RNYDGKVGHD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDPEERESEK KDLEDHRDDK ESRPFRKFPK DKILEAISSM PPDGTAEREL 240
REKYKELTEQ QLPKALPPEC TPNIDGPNAX SVQREQSLHS PHTLFCRRCP KYDCFLPHFP 300
ATPNTYKRNK TETALDNKPC GPQCYQHLEG AKFPAAALTA ERIKTPPKRP GRRRRGLRPN 360

```

NSSRPSTPTI NVLESKDTDS DREAGTBTGG ENNDKESEK KDETSSSSEA NSRCQTPIKM 420
 KPNTPEPEVW EWSGAEASMF RVLIGTYVDN FCAIARLIGT KTCRQVVEFR VKESSIIAPA 480
 PAEDVDTPPR KKKRKHRLMA AHCRIQLKK DGSSNHVYNY QPCDHPQPC DSSCPCVIAQ 540
 NPCEKFCQCS SEQNRRPFGC RCKAQCNKQ CPCYLAVREC DFDLCLTCGA ADHWDNRNVS 600
 CKNCISIQRGS KKHLLLPASD VAGWGIPIKD PVQKNEPISE YGSEIISQDE ADDRKGKVDK 660
 YMCSPLENLN NDFVVDATRK GNKIRFANHS VNFNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 ELFVDYRYSQ ADALKYVGIE REMEIP

Seq ID NO: B77 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1..1005

1 11 21 31 41 51
 15 ATGACAGAGA ACTCGACAA AGTTCCCAT GCGCTGGTG GACCTGATGA CGTGGAAATTC 60
 TGCAGCCCC CGCGTAGCG TACGCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120
 AAGGTGGGAG CCGTGGTCTT CATTTCGGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
 GCGTCTTACT TCTGGAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300
 20 TTTAAATGG GAAGTGAAG TGAAGAAGCA ATTGCAGTTA ATGATTTCGA GAATGGCATC 360
 ACAGGAATTC GTTTTGTCTG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
 ATTCTGAGG TGGGCGCGGT GACCAACACG AGCATCTCCT CCAAACTGGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAAGA AATTTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 GACAAACAGT TCTTGAATTC TAAGGTGTTA GAACCTCTCG GTGACCTTCC TATTTTCTGG 600
 25 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAATA CCACAAAAG ACCACACAGT GACCCACGGA GCAACCCAGG CGCTGGAAGA 720
 CTGAATAATG AAACAGAGCC CAGTGTTCAG GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780
 CCTTATCATC AGCAGGAAGG GGAAGACATG ACATTGAGCC CTAGACTGGA TCAGGAAGGA 840
 30 ATCTGTTGTA TAGAATGTAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
 GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCTG CAGAGTCATC 960
 ATGCCATGTA GCTGGTGGGT GCGCGTATC TTGGGCTATG TGTGAATCA CTTCATATAT 1020
 CAGTGTCTGT AAAATAAGAA CTAGCTGAAG AGACAACCA AAGAGCATTA AGGCAGGTTG 1080
 ATGCTGATGG GACCATAAAA TATTTTACA CGCAGCTGA GCGGTTATTC TTGACACTCT 1140
 35 TAACAGAAAT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAATGCA CTGAAAGGGT 1200
 AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTTGTTAT TTTTATTTC ATTGATTTC 1260
 CATAGTCTT CCCTTGCTG CATCTCCAA AGCTATTTG AAATAAACAC GAAATTTAC 1320
 AGTTTGCC

Seq ID NO: B78 Protein sequence
 Protein Accession #: NP_008946

1 11 21 31 41 51
 45 MTENSDKVPV ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFGAIG 60
 APYFWKGSDE HIYVNVHTMS INKQLDQSM EIDAGNLET FPMGSGAEEA IAVNDFQNGI 120
 TGIRFAGGEK CYIKAQVKAR IPEVGAUTKQ SISKLEGGI MPVKYEENSL IWVAVDQPVK 180
 DNSFLSKVL ELCDLPIFW LKPTYPKETQ RERREVRKI VPTTKRPHS GPRSNPAGR 240
 LNNETRFVSQ EDGQAFNPDN PYHQEGESM TFDPRLDHEG ICCIECRRSY THCQKICEPL 300
 50 GGYYPWFYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: B79 DNA sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

1 11 21 31 41 51
 55 CCGAGACTCA CGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 AATTAAATGA AAGCAGAAAA GACATCAACA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120
 60 GGAGAAATTT AGAAGAAGAC GATTATTGCT ATAAGGACAC GGGAGAGACC AGCATGCTAA 180
 AAAGACCTGT GCTTTTGCAT TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAATTCCA GCACACACAG GAACTCTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTCTTTACA CTCTCTGAG GGAAGTAATT CACCTTTTAG 360
 CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCTATCAAC AAAGTCTTGC 420
 65 CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
 TCCAACITCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTTTGC TGTACTGCAT GCAATTATA 600
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660
 AGGTCCAACA AAATAAGAGG GATGCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720
 70 ATGTGTCTCT GGAATTTGTG GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTG 780
 CATCTGTGAG TGACTCTTTC ACATGGAGAG AATTTCATA TATTAGAGC AAGCTAGGAA 840
 TTGTTTCCCT TCTACTGGGC ACAATACAGC CATTGATTTT TGCTTGAAT AAGTGGATAG 900
 ATATAAAGCA ATTTGTATGG TATACACCTC CAACITTTAT GATAGCTTTT TTCTTCCAA 960
 75 TTGTTGTCTT GATATTTAAA AGCATACTAT TCTGCGCATG CTTGAGGAAG AAGATACTGA 1020
 AGATTAGACA TGGTTGGGAA GACGTACCAA AAATTAACAA AACTGAGATA TGTTCCTCAGT 1080
 TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATGA TATATTTTAT CACCAACATT 1140
 TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence
 Protein Accession #: NP_036581.1

1 11 21 31 41 51
 80 MESRKDITNQ EELWVKMPRR NLEEDDYLHK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60
 LQHTQELFPQ WHLPKIAAI IASLTFLYTL LREVIHPLAT SHQYFYKIP ILVINKVLPM 120

VSITLLALVY LPGVIAAIVQ LHNGTKYKFP PHWLDKMLT RKQFGLLSFF FAVLHAIYSL 180
 SYPMRRSYRY KLLNWAYQQV QNKEDAWIB HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 VSDSLTWREF HYIQSKLIV SLLLOTIHAL IPAMNKWIDI KQFVWYTPPT FMIAVFLPIV 300
 VLIFKSLFLP CLRRKKILKI RHGMEDVTKI NKTBCSQL

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Seq ID NO: B81 DNA sequence
 Nucleic Acid Accession #: NM_000684
 Coding sequence: 87..1520

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1	11	21	31	41	51	
TGCTACCCGC	GCCCCGGCTT	CTGGGGTGTT	CCCCAACCC	GGCCACAGCC	TGCCACACCC	60
CCCCCCCCCG	GCTCTCGCAG	CTGGGCATGG	GCGCGGGGGT	GCTCGTCTTG	GGCGCCTCCG	120
AGCCCGGTAA	CCTGTGTGCG	GCCGCAACGC	TCCCGACGG	GCGGCGCAC	GCGGCGCGCG	180
TGCTGTGTC	CGCTGCGCG	CCCGCTCGT	TGCTGCTCC	CGCCACGGAA	AGCCCGAGAG	240
CGCTGTCTCA	GCAGTGAACA	GCGGCATGG	GTCTGTGAT	GGGCTCATC	GTGCTGCTCA	300
TGCTGGCGGG	CAATGTGCTG	GTGATCGTG	CCATCGCCAA	GACGCGCGG	CTGCAGACGC	360
TCACCAACCT	CTTCATCATG	TCCCTGGCCA	GCGCGGACCT	GGTCATGGGG	CTGCTGGTGG	420
TGCGTTTCG	GGCCACCATC	GTGGTGTGG	GCGGCTGGGA	GTACGGCTCC	TTCTTCTGG	480
AGCTGTGGAG	CTCAGTGGAC	GTGCTGTGCG	TGACGGCCAG	CATCGAGACC	CTGTGTGTCA	540
TTGCCCTGGA	CCGCTACCTC	GCCATCACCT	CGCCCTCCG	CTACCAGAGC	CTGCTGAAGC	600
GCGCGCGGG	GCGGGGCTC	GTGTGCACCG	TGTGGGCCAT	CTCGGCTCTG	GTGTCTCTCC	660
TGCCCATCCT	CATGCACTGG	TGGCGGGCGG	AGAGCGACGA	GGCGCGCGCG	TGCTACAAGG	720
AGCCCAAGTG	GGCCACTTTC	GTCAACCAAC	GGGCTTACGC	CATCGCTCTG	TTCGTAGTCT	780
CCTTCTAGT	GCCCCGTGCG	ATCATGGCT	TGCTGTACCT	GCGGGTGTTC	GCGAGGCGCC	840
AGAAGCAGT	GAAGAAGATC	GACAGCTGCG	AGCGCGTTC	CCTGGGCGCG	CCAGCGCGCG	900
CGCCCTCGCC	CTCGCCCTCG	CCCGTCCCG	CGCCCGCGCC	GCCCGCCGGA	CCCGCGCGCC	960
CGCGCGCGCG	CGCGCCAC	GCCCCGCTGG	CCAACGGGCG	TGCGGGTAAG	CGCGCGCCCT	1020
CGCGCTGTCT	GGCCCTACGC	GAGCAGAAGG	CGCTCAAGAC	GCTGGGCATC	ATCATGGGCG	1080
TCTTCAAGCT	CTGCTGGCTG	CCCTCTTCC	TGGCCAACGT	GGTGAAGGCC	TTCCACCGCG	1140
AGCTGTGTCC	CGACCGCTCT	TTGCTTCTT	TCAACTGGCT	GGGCTACGCC	AACTCGGCTC	1200
TCAACCCCAT	CATCTACTGC	CGCAGCCCG	ACTTCCGCA	GGCCTTCCAG	GGACTGTCTC	1260
GCTGCGCGCG	CAGGGCTGCC	CGCCGCGCGC	ACGCGACCCA	CGGAGACCGG	CGCGCGCGCT	1320
CGGGCTGTCT	GGCCCGGCGC	GGACCCCGCG	CATCGCCCGG	GCGCGCTCG	GACGACGAGC	1380
ACGACATGT	CGTGGGGGCC	ACGCGCGCGC	CGCGCTGCT	GGAGCCCTGG	GCGCGCTGCA	1440
ACGCGCGGGC	GGCGCGGAC	AGCGACTCGA	GCTGGACGA	GCGGTGCGCG	CCCGGCTTGG	1500
CCTGGGAATC	CAAGGTGTAG	GGCGCGGCGC	GGGGCGGGGA	CTCGCGGCAC	GGCTTCCAG	1560
GGGAACGAGG	AGATCTGTGT	TTACTTAAGA	CGGATAGCAG	GTGAACCTGA	AGCCCAACAT	1620
CCTGCTGGA	ATCATCCGAG	GCAAGAGAA	AAGCCACGGA	CGGTGTCACA	AAAAGGAAAG	1680
TTTGGGAAGG	GATGGAGAG	TGGCTTGCTG	ATGTTCTCTG	TTG		

Seq ID NO: B82 Protein sequence
 Protein Accession #: NP_000675.1

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1	11	21	31	41	51	
MGAGVLVLGA	SEPNLSSAA	PLPDGAATAA	RLLPASPPA	SLLPPASESP	EPLSQWNTAG	60
MGLLMALIVL	LIVAGNVLVI	VALAKTPRLQ	TLTNLFIMSL	ASADLVMLGL	VVPFGATIVV	120
WGRWEYGSFF	CELWTSVDVL	CVTASIELTC	VIALDRYLAI	TSPFRYQSL	TRARARGLVC	180
TVWIAISALVS	PLPILMEHWR	AESDEARRCY	NDPKCCDFVT	NRAYAIASSV	VSPFYVPLCIM	240
AFVYLRFVRE	AQKQVKKIDS	CERRFLGGPA	RPPSPSPSPV	PAPAPFPGPF	RPAAAAATAP	300
LANGRAGKRR	PSRLVALREQ	KALKTLGIIM	GVFTLCWLPF	FLANVVKAFH	RELVPDRLFV	360
FFNWLGYANS	AFNPPIYCRS	PDFRKAPOGL	LCCARRAARR	RHATHGRDPR	ASGCLARPGP	420
PPSPGAASDD	DDDDVVGATP	PARLLEPWAG	CNGGAAADSD	SSLDEPCRP	FASESEKV	

Seq ID NO: B83 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence: 2..421

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1	11	21	31	41	51	
GGCTCAGCTG	CGGGGCTGCT	CCGTTTGGA	ACGCCAAGCC	AGCTGCGGTC	CTAATCCAAA	60
AGCCATGAAC	AGCGGCGTGT	GCCTGTGCGT	GCTGATGGCG	GTACTGGCGG	CTGGCGCCCT	120
GACGCGAGCG	GTGCTCCCG	CAGATCCCGC	GGGCTCGGG	CTGCAGCGGG	CAGAGGAGGC	180
GCCCCGTAGG	CAGCTAGGG	TATCGCAGAG	AACGGATGGC	GAGTCCCGAG	CGCACTGGG	240
CGCCCTGCTG	GCAAGATACA	TCCAGCAGGC	CCGGAAGCT	CCTTCTGGAC	GAATGTCCAT	300
CGTTAAGAAC	CTGCAGAAC	TGGACCCAG	CCACAGGATA	AGTGACCGGG	ACTACATGGG	360
CTGGATGGAT	TTTGGCGGTC	GCAGTGCCGA	GGAGTATGAG	TACCCCTCTC	AGAGGACCCA	420
GCGGCCATCA	GCCCAACGGA	AGCAACCTCC	CAACCCAGAG	GAGGCAGAA	AAGACAACAA	480
TCACACTCAT	AACTCATTTG	CTGTGGAGTT	TGACATTGAA	TGTATCTATT	TATTAAGTTC	540
TCAATGTGAA	AATTGTGTCT	GTAAGATTGT	CCAGTGCAAC	CACACAGCT	CACCAGAAGT	600
TGTGCAAACT	GAAGACAAAA	CTGTTTCTT	CATCTGTGAC	TCCGTGTCG	AAAATGTTGT	660
TATGCTATTA	AAGTGATTTC	ATTCTGCC				

Seq ID NO: B84 Protein sequence
 Protein Accession #: NP_000720.1

80

1	11	21	31	41	51	
MNSGVCLCVL	MAVLAAGALT	QVFPADPAG	SGLQRAEAP	RRQLRVQSRT	DGESRAHLGA	60
LLARYIQQAR	KAPSGRMSIV	KNLQNLDPSE	RISDRDYMGW	MDFGRRSABE	YEYPS	

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis	
5	A1 DNA SEQUENCE
	Gene name: endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number: Hs.154210
	Probeset Accession #: M31210
10	Nucleic Acid Accession #: M31210
	Coding sequence: 251-1396
15	TCTAAAGGTC GGGGGCAGCA GCAAGATGCG AAGCGAGCG TACAGATCCC GGGCTCTCCG 60
	AAAGCTACAC CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAAGGA 120
	AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT 180
	CTGGCTCGC CCTCTAGGCT TGGTCTGGAG TAGCGCCACC CCGGCTTCTC GGGGACACAG 240
	GTTTGGCACC ATGGGGCCCA CCAGCGTCCC GCTGGTCAAG GCCCACCGCA GCTCGGTCTC 300
	TGACTACGTC AACTATGATA TCATGCTCCG GCATTACAAC TACAAGGAA AGCTGAATAT 360
	CAGCGCGGAC AAGGAGAACA GCATTAACT GACCTCGGTG GTGTTCAATC TCATCTGCTG 420
20	CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCAT TGGAAAACCA AGAAATTCCA 480
	CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTGG CAGGAGTAGC 540
	CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CGGCCAGTG 600
	GTTTCTGCGG GAAGGGAGTA TGTTTGTGGC CCTGTCAAGC TCGGTGTCA GTCTCTCGC 660
	CATCGCCATT GAGCGCTATA TCACAATGCT GAAATGAAA CTCACAAAGC GGAGCAATAA 720
	CTTCGCGCTT TTCTGCTTAA TCAGCGCTG CTGGGTCTAT TCCCTCATCC TGGGTGGCCT 780
25	GCCTATCATG GGCTGGAATC GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCCGCT 840
	CTACCAACAG CTAACATCTC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT 900
	CGTCATTCTG TACTGCAGAA TCTACTCCTT GGTCAAGACT CCGAGCGGCC GCCTGACGTT 960
	CCGCAAGAAC ATTTCCAAAG CCAGCGCGAG CTCTGAGAAT GTGGCGCTGC TCAAGACCGT 1020
	AAATATCGTC CTGAGCGTCT TCATCGCCTG CTGGGACCCG CTCTTCATCC TGCTCTGCTG 1080
30	GGATGTGGGC TGCAAGGTGA AGACCTGTGA CATCCTCTTC AGAGCGGAGT ACTTCTGCTG 1140
	GTTAGCTGTG TCAACTCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACAAGGAGAT 1200
	GCGTGGGGCC TTCATCGGGA TCATGCTCTG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG 1260
	CAAAATTCAG CGAGCCATCA TCGCGCGCAT GGAATTCAGC CGCAGCAAT CGGACAATTC 1320
35	CTCCACCCCG CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTAATGCTT CTGGAAACGT 1380
	CAACTCTTCT TCCTAGAACT GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTGG 1440
	CTGGCCACCC CAGGTGTTGG AAAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT 1500
	GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGTGGTGTG CCGGTGTTGG 1560
	TGGGTAGAGT TAGTTCCTGT GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCCCT 1620
40	GGAAATATA TTCTACCCCG CTGGAGCTTT GATTTTGAC TGAAGCAAG GTCTAGCAT 1680
	GTCAAGCTCC TAAAGGGTTC ATTTGGCCCC TCCTCAAAGA CTAATGTCCC CATGTGAAAG 1740
	CGTCTCTTGG TCTGAGCTTT TGAGGAGATG TTTTCTTCA CTTTAGTTTC AAACCCAACT 1800
	GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCCCTGTACA TCCCACACCC CACCTCCCT 1860
	TCCTTCTATA CCCCTCTCA ACGTCTTTT ACTTTATACT TTAACCTACT GAGAGTTATC 1920
45	AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAT AGGCTATGTT GAGTAGCTAG 1980
	GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAACAAT GTCTTCTGCT GAGGCCAAAG 2040
	TTTCCATGTA AGCGGAATCC GTTTTGTGA ATTTGGTTGA AGTCACTTTG ATTTCTTTAA 2100
	AAAACATCTT TTCAATGAAA TGTGTTACCA TTTCAATACC ATTGAAGCCG AAATCTGCAT 2160
	AAGGAAGCCC ACTTATCTTA AATGATATTA GCCAGGATCC TTGGTGTCTT AGGAGAAACA 2220
50	GACAAAGCAA ACAAGTGA AAACGAATGG ATTAACCTTT GCAAAACCAAG GGAGATTTCT 2280
	TAGCAATAGA GTCTAACAAA TATGACATCC GTCTTCCCA CTTTGTGTA TGTTTATTTT 2340
	AGAATCTTGT GTGATTCATT TCAAGCAACA ACATGTTGTA TTTTGTGTG TTAAGATGTA 2400
	TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTATGGA TTTTCTTAAC 2460
	CCGTGTTAAC TTTTCTAGAA TCCACCCTCT TGTGCCCTTA AGCATTACTT TAACCTGGTAG 2520
55	GGAAAGCCAG AACTTTTAAG TCCAGCTATT CATTAGATAG TAATTGAAGA TATGTATAAA 2580
	TATTACAAAG AATAAAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAATC 2640
	CGAGAGATGT CTTGTTTTTT TAAAAAGAA AGTATTTAAT AGGTTTCTGA CTTTGTGTGA 2700
	TCATTTTGCA CATAGCTTTA TCAACTTTTA AACATTAATA AACTGATTTT TTTAAAG
60	A2 Protein sequence:
	Gene name: endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number: Hs.154210
	Probeset Accession #: M31210
65	Protein Accession #: AAAS2336
	Signal sequence: none found
	Transmembrane domains: 50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Cellular Localization: plasma membrane
70	1 11 21 31 41 51
	MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKINISAD KENSIKLTSTV VFILICCFII 60
	LENIFVLLTI WKTKFHRPM YYFIGNLALS DLLAGVAYTA NLLLSGATTY KLTPAQWFLR 120
	EGSMFVALSA SVFSLAIAI ERYITMLKMK LHNGSNFRL PLLISACWVI SLILGGLPIM 180
75	GMNCISALSS CSTVPLPYHK HYILFCTTVP TLLLSIVIL YCRIYSLVRT RSRRLTFRKN 240
	ISKASRSSEN VALKTVIV LSVFIACWAP LFILLLLDVG CKVKTCDILF RAEPFLVLAV 300
	LNSGTNPILY TLTKMKMRA FIRIMSCCKC PSGDSAGKPK RPIIAGMEPS RSKSDNSSHP 360
80	A3 DNA SEQUENCE
	Gene name: G protein-coupled receptor 51
	Unigene number: Hs.198612
	Probeset Accession #: AA452928
	Nucleic Acid Accession #: NM_004624.1

Coding sequence: 1-2826 (underlined sequences correspond to start and stop codons)

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5 1 11 21 31 41 51
| | | | | |
ATGGCTTCCC CGCGGAGGTC CGGGCAGCCA GGGCGGCCGC CGCCGCCGCC ACCGCCGCC 60
GGCGGCTTGC TACTGCTACT GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCTTGG 120
GGCTGGCGCG CGGGGCGCCC CGGGCGCGCG CCCAGCAGCC CGCGGCTCTC CATCATGGGC 180
CTCATGGCGC TCACCAAGGA GGTGGCCAAG GGCAGCATCG GGCGCGGTGT GCTCCCGGCC 240
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ATAAAATACG GGCGGAACCA CTTGATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC 420
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CTGTCTCTAG CCGATAAGAA AAAATACCCT TATTTCTTC GGACCGTCCC ATCAGACAA 540
GGGTGAATC CAGCCATTCT GAAGTGTCTC AAGCACTACC AGTGAAGCG CGTGGGCAAG 600
CTGACGCAAG ACCTTCAGAG GTTCTCTGAG GTGCGGAATG ACCTGACTGG AGTTCGTAT 660
GGCGAGGACA TTGAGATTTC AGACACCGAG AGCTTCTCCA ACGATCCCTG TACCAGTGT 720
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GCAAAAGTGT TCTGTGTGTC ATACGAGGAG AACATGTATG GTAGTAAATA TCAGTGGATC 840
ATTCCGGGCT GGTACGAGCC TTCTTGGTGG GAGCAGGTGC ACACGGAAGC CAATCATCC 900
CGCTGCCTCC GGAAGATCT GCTTGTCTGC ATGAGGGCT ACATTGGCT GGAATTGAG 960
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CGGCACCAGC GGAATCCAGGA CTTCACCTAC ACGGACCACA CGCTGGGCGG GATCATCTCT 1200
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GAGTACAACG CTGTGGCGCA CACACTGGAG ATCATCAATG ACACCATCAG GTTCAAGGA 1380
TCCGAACCA CAAAGACAAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCCTACCT 1440
CTCTACAGCA TCCTCTCTGC CCTCACCATC CTGGGATGA TCATGGCCAG TGCTTTCTC 1500
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CCACCGCCA GCCCGGCCA CAGACATGTG CCACCTCTCT TCCAGTCTAT GGTCTCGGCG 2820
CTGTAA

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55 A4 Protein sequence:

Gene name: G protein-coupled receptor 51
 Unigene number: Hs.198612
 Probeset Accession #: AA452928
 Protein Accession #: NP_005449.1
 Signal sequence: 1-42
 Pfam domains: 7tm_3 [481-754], ANF_receptor [130-204]
 Transmembrane domains: 22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744
 Cellular Localization: plasma membrane

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65 1 11 21 31 41 51
| | | | | |
MASPRRSQGP GRPPPPPPPP ARLLLLLLLL LLLPLAPGAW GWARGAPRPP PSSPPLSIMG 60
LMPLTKEVAK GSIGRGVLPV VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAFYDA 120
IKYGPNNLMV PGVVCPSVTS IIAESLQGNV LVQLSFAATT FVLADKKKYP YFRTVPSDN 180
AVNPAILKLL KHYQWKRVTG LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SPSNDPCTSV 240
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RCLKGLLLAA MEGYIGVDPE PLSSKQIKTI SGKTQQQYER EYNKRSRGV PSKPHGYAYD 360
GIWVIKTLQ RAMSTLWASS RHQRIQDFNY TDHTLGRILL NAMNETNFFG VTGQVVRNG 420
75 ERMOTIKFTQ PQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPDKTKII LEQLKKISLP 480
LYSILSALT I LGMIMASAFI PFIKNNRNRK LKIMSSPYM NLIIILGMLS YASIFLFGLD 540
GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTRVHEA IFKNVKKKKK IIKDKLLVI 600
VGGMLLDLC ILICWQAVDP LRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGITV 660
YAYKGLMLF GCPLAWETRN VSIPALNDSK YIGMSVYVNG IMCIIGAAVS FLTRDQPNVQ 720
80 FCTIVALVIF CSTITLCLVF VPKLITLRTN PDAATONRRF QFTQNKKED SKTSTSVTSV 780
NQASTSRLES LQSENHRLRM KITELDKDLE EVTMQLQDTP ERTTYIKQNH YQELNDILNL 840
GNFTBSTDGG KAILKHLDDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH 900
HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L

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A5 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 ProbeSet Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCCG GGGAACTACT TCACCAATGA 120
GTGCAACATA CCAGGCAACT TCATGTGACG CAATGGACGG TGCAATCCCG GCGCCTGGCA 180
GTGTGACGGG CTGCGTGACT GCTTGGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
15 GTCGAAATGT GGCACAACTT TCTTCCCTCG TGCCAGCGCG ATCCATTGCA TCATTGGTGG 300
CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
AAACCCCTCG CTTTGCTCCA CGGCCCGCTA CCACTGCAAG AACGGCTCT GTATTGACAA 420
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CCTGCTGGCA CTGGTCTTGC ACCACCAAGC GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
GCACCGGCTG CAGCAGCGTG TGCTGCTGTC CCGCTTGGTG GTCTGGGACC ACCCCACCA 720
CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGGGAGGCA 780
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25 TGGTGGTATG GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
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GAAACCTCTG CCAAGAAAAA GGTGGCAGGA ATCTCCACA CCAAGAAAAA ACGCGCCGGG 4020
GGAAACCGCA GAGTGTGTCG TAAACCAAC CCGAAGAGAG AACTCAGAG CACACAAGCG 4080
80 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

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A6 Protein sequence:

Gene name: ESTs

Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 5 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51
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 KNGLCIDKSF ICDGNNOQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 15 VIFVLVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHRCN VTYNVNNGIQ 240
 YVASQAQNA SEVGSPPSYS EALLDQRPWA YDLPPPPYSS DTESLNQADL PFYRSRSGSA 300
 NSASEQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

20 A7 DNA SEQUENCE
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Nucleic Acid Accession #: NM_002205
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

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 CTCAGGCTC CAGCCACCTC TGATGCTGGA

A8 Protein sequence:

5 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Protein Accession #: NP_002196
 Signal sequence: 1-42
 Transmembrane domains: 998-1020
 10 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036
 Cellular Localization: plasma membrane

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 LESSLSSEEG EEPFVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DFGVTCYLSL 180
 20 DNPTRILEYA PCREDPSWAA QGGYCCGGPS AEPTKTRGVV LGGPGSYFNQ QQILSATQEQ 240
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 QQGVVVPFPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGG YPDLVGSGF 480
 25 VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNPV ACTINLSFCLN ASGKHVADSI 540
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 SASSGPQILK CPEAEFCRLR CELGPLHQQE SQSLQLHFRV WAKTFLOREH QPFLQCEAV 960
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 35 YKLGFFKRSI PYGTAMEKAQ LKPPATSDA

A9 DNA SEQUENCE

40 Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

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 50 TCTGCACGAT GTGATGATT AGAAGCCTTA AAAAAGAAGG GTTGCCTCC AGATGACATA 240
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 AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGG AAAACAGCGC 720
 ATATCTGGAA ATTTGGATTG TCCAGAGGT GGTTCGATG CCATCATGCA AGTTGCAATT 780
 60 TGTGGATCAC TGATTGGCTG GAGGAATGTT ACAAGGCTGC TGGTGTTC CACAGATGCC 840
 GGGTTTCACT TTGCTGGAGA TGGGAACTT GGTGGCATTG TTTTACCAA TGATGGACAA 900
 TGTCACTGCC AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
 CACCTTGCTC AGAAACTGAG TGAATAATAT ATTCAGACAA TTTTGCAGT TACTGAAGAA 1020
 TTTCAAGCTG TTTTCAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
 65 TCTGCAAAAT CTAGCAATGT AATTCAGTTG ATCATTGATG CATAAATTC CCTTTCCTCA 1140
 GAAGTCATT TGGAAACCG CAAATGTGCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
 TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCCATT 1260
 GGAGATGAGG TTCAATTGTA AATTAGCATA ACTTCAAAAT AGTGTCCAA AAAGGATTCT 1320
 GACAGCTTGA AATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
 70 ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
 AATGGGACAT TTGAGTGTGG CGCGTCGAGG TGCAATGAAG GCGGTGTGG TAGACATTGT 1500
 GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
 AGTTCAGAAA TCTGAGTAA CAATGGAGAG TGCCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
 AGGGATAATA CAAATGAAAT TTATCTGTCG AAATCTGTCG AGTGTGATAA TTTCACTGT 1680
 75 GATAGATCCA AGAGCTTAAT TTGTGGAGGA AATGTTGTTT GCAAGTGTG TGTGTGTGAG 1740
 TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTCT TGGATAC TAGTCTGTGA 1800
 GCCAGCAAGA GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGTGTG CTGTAAAGTGT 1860
 ACAGATCCGA AGTTTCAAGG GCAAAAGTGT GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
 GCTGAGCATA AAGATGTGTG TCAGTGCAGA GCCITCAATA AAGGAGAAAA GAAAGACACA 1980
 80 TGCACACAGG AATGTTCCCTA TTTTAACTT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
 CAGCGGTGCC AACCTGATCC TGTGTCCCAT TGTAAGGAGA AGGATGTTGA CGACTGTTGG 2100
 TTCTATTTTA CGTATTCACT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAA 2160
 CCAGAGTGTG CCACTGTGTC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220

GTCTTATTG GCCTTGCACT ACTGCTGATA TGGAGCTTT TAATGATAAT TCATGACAGA 2280
 AGGGAGTTTG CTAATTTTGA AAAGAGAGAA ATGAATGCCA AATGGGACAC GGGTGAAAT 2340
 CCTATTATA AGAGTGCCCT ACAACTGTG GTCATCCGA AGTATAGGG AAAATGA

5

A10 Protein sequence:

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDP2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Protein Accession #: NP_002202.1
 Signal sequence: 1-21
 Transmembrane domains: 732-754
 INB domain: 34-464
 PSI domain: 26-76
 Cellular Localization: plasma membrane

10

15

1 11 21 31 41 51
 20 MNLQIPFIWG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
 SARODDLLEAL KKKGCPDDI ENPRGSKDIK KNKNVTNRSK GTAELKLPED ITQIQPQQLV 120
 LRLRSGEPQT FTLKPKRAED YPIDLYLYMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
 RIGFGSFVEK TUMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKG VFNELVKGQR 240
 25 ISGNLDSPG GFDALMQVAV OGLSLGWNRV TRLLVPSTDA GFHFAGDGKL GGIVLFPNDGQ 300
 CHLENNMYTM SHYYDYP9IA HLQVQLSENN IQTIPAVTEE PQPVYKELKN LIPKSAVGTI 360
 SANSSNVIQL IIDAYNSLSS EVILENGKLS EGVTSYKSY CKNGVNGTGE NGRKCSNISI 420
 GDEVQFEISI TSNKCPKQDS DSFKIRPLGF TEEVEVILQY ICECEQSEGE IPBSPKCHGE 480
 NGTFECGACR CNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCQGVQCRK 540
 30 RENTNEYISG KFCEDNFWNC DRSNGLICGG NGVCKCRVCE CNFNTYSAC DCSLDSTTCE 600
 ASNGQICNGR GICECGVCKC TDPKFCQQT C EMCQTCLGVC AEHKECVQCR AFNKGKKKDT 660
 CTQECSEYFNI TKVESRDKLP QVQPDVPSH CKEKDVEDCW FYFTYSVNGN NEVMVHVVEN 720
 PECPTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIHDR REPAKFEKEK MNAKWDGTEN 780
 PIYKSAVTV VNPKEGK

35

A11 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

40

1 11 21 31 41 51
 45 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60
 GCCTGGTCTT ACACACCTCT CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAAGT ACACACACTT GATTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
 TCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATTGT 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAAGAAG CCAAGAACTG GGCTCCAGGT 300
 50 GAACCCAAAC ATAGGCAGAA AGATGAGGAC TGCCTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGGCTGTA CCAATACATC CTGCAGTGGC CACGCTGAAT GTGTAGAGAC CATCAATAAT 480
 TACACTTGA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAATGT 540
 ACAGCCCTGG AATCCCTGGA GCATGGAAAG CTGGTTTGCA GTCACCCACT GGGAAACTTC 600
 55 AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCACT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCTGTG AATGTTTCCA AAACCCCTGA 780
 AGCTTCCCAT GGAACACAAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840
 GCCCAGAGCC TTCACTGTAC CTATCTGGG AATTGGGACA ACAGAAAGCC AACGTGTAAA 900
 60 GCTGTGACAT GCAGGGCCCT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CTGTCTGGAG AGTTACCTTT CAAATCATCC TGCAACTTCA CTGTGAGGA AGGCTTCATG 1020
 TTGCAGGGAC CAGCCCAGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAATCCCA 1080
 GTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCCTAGTG CTTCCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
 65 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAAC 1260
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTATTCCTCC TATTGGAGAA TTCACCTACA AGTCTCTCTG TGCCCTTCAGC 1380
 TGTGAGGAGG GATTGAATTT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCCGGGA 1500
 70 AAGATCAACA TGAGCTGCGAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCCCTGT 1560
 CCTGAAGGAT GGAGCTCTCA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 CTTCCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740
 TGCTTACGGA AAGCAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAGCCT TGAATCAGAC 1800
 75 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

75

A12 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 Transmembrane domains: 555-573
 C-lectin domain: 23-139

80

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKKEIEYLN 60
 SILSYSPSY WIGIRKVMNV WVVVGTOXPL TEBAKWAPG EPNNROKDED CVEIYIKREK 120
 DVGWNDERC SKKLLALCYT AACTNTSCSG HGECVETINN YTCKDPGFS GLKCEQIVNC 180
 10 TALESPHGS LVCSHPLGNP SYNSSCSISC DRGYLPSSME TMQOMSSGEW SAPIPAQNVV 240
 ECDVATNPAN GFVECPQNP SPFWNTTCTF DCEGPELMG AQLQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEGFM LQGPQVBECT TQGGWTQQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEPSCBQ GFVLKSGSKRL QCGPTGEWDN 420
 EKPTCEAVRC DAVHQPQKGL VRCAHSPIGE PTYKSSCAPS CEEGFELYGS TOLECTSQGQ 480
 15 WTEEVSPSQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 GSYQKPSYIL TSNIFLVLG LSAAGLSLLT LAPFLMLRK CLRRAKFPVP ASSQSLESD 600

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 ATGGCTTCAC CCAGCCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGT CTGATCATC 120
 TTCTGATGG GCCTTCTGGG GAACAGCGCC ACCATTGGG TCACCCAGGT GCTGCAGAAG 180
 30 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240
 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 ACCTCCAGCT ACACCTGTG CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC 420
 35 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGCTCG 480
 GTCACTCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGACTGA GTACCCCTG 540
 GTGAACGTGC CCGCCACCG GGTCTCACT TGCAACCGCT CCAGCACCG CCACCAAGAG 600
 CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGGTTC 660
 CAGTCCAGCA TCTTCGGCGC CTTCGTGGTG TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGCTCGCT GGCCGGGGC 780
 ACGCGGCTCT CCGAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCG CAGGAGGCAG 840
 ACCATCATCT TCTTGAGGCT GATTGTTGTG ACATTGGCGG TATGCTGGAT GCCCAACCA 900
 ATTCCGAGGA TCATGGCTGC GGCCAAACCC AAGCACGACT GGAACGAGTC CTACTTCCG 960
 GCGTACATGA TCTTCTCTCC CTTCCTCGAG ACGTTTTTCT ACCTCAGCTC GGTATCAAC 1020
 45 CGCTCTCTGT ACACGGTGTG CTCGCGAGCAG TTTCGGCGGG TGTTGCTGCA GGTGCTGTGC 1080
 TGCGCGCTGT CGCTGCAGCA CGCCAAACCA GAGAAGCGCC TGCGGTGACA TGCGCACTCC 1140
 ACCACCGACA GCGCCGCTT TGTGACGCG CCGTTGCTCT TGCGTCCCG GCGCCAGTCC 1200
 TCTGCAAGSA GAAGTGAAG GATTTCCTTA AGCACTTTTC AGACGAGGC CGAGCCCCAG 1260
 TCTAAGTCCC AGTCAATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACACGCC 1320
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 60 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 Cellular Localization: plasma membrane

65 1 11 21 31 41 51
 MASPSLPQSD CSQIIDHSHV PEFEVATWIK ITLLVLYLII FVMGILLGNSA TIRVTQVLQK 60
 KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHVLTL FERYIAICHP FRYKAVSGPC QVKLLIGFVN VTSALVALPL LFAMGTEYPL 180
 VNVPSHRLGT CNRSSTRHHE QPETSNMISC TNLSSRWTFV QSSIFGAFVV YLVVLLSVAF 240
 70 MCKNMQVLM KSQKSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLLIV TLAVCWMPNQ 300
 IRRIMAAKPF KHDWTRSYFR AYMILLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360
 CRLSLQAHNE EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STPQSEAEQP 420
 SKSQSLSLBS LEPNSGAKPA NSAAENGFOE HEV

A1 ProstateA15 DNA sequence

80 Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5	GGGTCGCGG	CACACCTCCC	CGGCGCGCG	CGGCCACCGC	CGGCACTCCG	CCGCGCTGTC	60
	CGGCAACCGC	TGAGCCATCC	ATGGGGGTG	CGGGCCGCAA	CGGTCCCGGG	GCGGCTGGG	120
	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCGCG	CACCTGCTGCT	GCTGGCGGGG	GCGTCCCGC	180
	CGGTCGCGG	CGGTGCGCG	GGGCGCGAG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCCAAGGCG	CTGTGTGAGA	ACACACCCAC	CTCCTACAAG	TGCTCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTTTGA	ATATTCCAGG	CAATTATCGT	TGCACTTGT	420
10	TGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCCTGG	480
	AGAACAAATG	CGGTGCGCAG	CATACCTGTG	TCAACGTCTAT	GGGAGCTAT	GAGTGTGCT	540
	GCAAGGAGGG	GTTTTTCTCT	AGTGACAATC	AGCACACCTG	CATTCAACGC	TCCGAAGAGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCACAT	CTGCAAGGAG	GCCCCAAGGG	660
	GCAGCGTCG	CTGTGAGTGC	AGGCCTGGTT	TTGAGCTGGC	CAAGAACCAG	AGAGACTGCA	720
15	TCCTGACCTG	TAAACATGGG	AACGCTGGGT	GCCAGCACCT	CTGTGACGAT	ACAGCGATG	780
	GCCAGAGTG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCTTG	840
	AGGAGAGGGA	CACCTGTCTG	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAAACGGGT	GAAACGGCGG	CTGCTCATGG	AAACGTTGTC	TGTCAACRAAT	GGAGGCTGTG	960
	ACCGCAGCTG	TAGAGATACT	TGACACAGGT	TCCACTGCGG	TTGTCTCTGT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAAGACA	TGTAAAGATA	TTGATGAGTG	CCAGACCCCG	AATGGAGGTT	1080
	GTGATCAATT	CAGTAAAAAA	ATCGTGGGCA	GTTTGACTG	CGCTGCAAG	AAAGGATTTA	1140
	AATTATTAA	AGATGAGAAG	TCTTGCCAA	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCAAG	CTGCATCAAC	CACCTTGCCA	CATTGCTTTG	TGCTTGCAAC	CGAGGGTACA	1260
	CCCTGTATG	CTTGACCCAC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
25	GTGACGAGGT	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGCCAC	CCTGGGTACA	1380
	AGCTCAATT	GAAATAAAAA	GACTGTGTGG	AAGTGAAGGG	GCTCCTGCCC	ACAAGTGTGT	1440
	CACCCCGTGT	GTCCCTGSCAC	TGCGTAAGA	GTGGTGGAGG	AGACGGGTGC	TTCTCTCAGAT	1500
	GTCACTCTGG	CATTCACTCT	TCTTCAGATG	TCACCAACAT	CAGGACAAGT	GTAACTTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAATA	ATGCTGAGCT	GTTCCTCGAG	GGTCTGCGAC	1620
30	CAGCACTACC	AGAGAGGAC	AGCTCAGTAA	AAGAGAGCTT	CCGCTACGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAGCAAGTGC	CCAGGAGCCC	CTGGCCGACC	AAGCACCCCT	AAGGAATGT	1740
	TTATCATCTG	TGAGTTTGAG	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGATC	CGTAAAGGGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCGGTCCA	CAGGAGGAG	TTTCACTTCC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAAGCCTCC	CAGAAATCT	GAAAGCCAGG	CAGAGTCTTG	TGGAGTGGGC	CAGGGTCTAG	1980
	CAGAAACCA	ATGTGTCAAT	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CGAGAACGCT	2040
	GCATTTTATG	TCCAAATGGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATCT	GGGCGCTTGA	AGACCCGAGA	AGCTTGGAAAT	ATGTCTGAAT	2160
	GTGGAGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCAACCT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CAGCTTCCAG	CCTGAAGCTG	GTGCAACTTC	CTGCTTCCCT	TGTGGAGGAG	2280
	GCCTTGCCAC	CAAACTCAG	GGAGCTACTT	CCCTTCAGGA	CTGTGAAACC	AGAGTTCAAT	2340
	GTTCACCTGG	ACATTTCTAC	AACACCACCA	CTCACCGATG	TATTCTGTGC	CCAGTGGGAA	2400
	CATACAGCCG	TGAATTTGGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTAOGACTG	2460
	ACTTTGATGG	CTCCACAAAC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
45	GAGATTTTAC	TGGGTACATT	GAATCCCCAA	ACTACCCAGG	CAATTACCCA	GCCAAACCGG	2580
	AGTGTACCTG	GACCTCAAC	CCACCCGCCA	AGCGCCGCAT	CCTGATCGTG	GTCCCTGAGA	2640
	TCTTCTGCCC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
	CCAAATCTGT	GACAACATAT	GAAACCTGCC	AGACCTACGA	ACGCCCCATC	GCCTTCACTT	2760
	CCAGCTCAAA	GAACTGTGG	ATTCAAGTTCA	AGTCCAAATGA	AGGGAACAGC	GCTAGAGGGT	2820
50	TCCAGTCCCC	ATACGTGACA	TATGATGAGG	ACTACCAAGG	ACTCATTTGAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAACC	ATCAGGAAAT	ACTTAAGGAT	AAGAAACTTA	2940
	TCAAGGCTCT	GTGTGATGTC	CTGGCCCATC	CCCAGAACTA	TTTCAAGTAC	ACAGCCGAGG	3000
	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TCCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTGAAGACC	TTACAAATGA	CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
55	GTTTGGTGGG	ACAGAGCTGT	CTTCTCTCTG	CATGTACGCA	CAGTCCGGTA	TTGCTGCCTC	3180
	CGTATCAGT	GACTCATTAG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GAACTTGGTT	TTTCTTTCCC	AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGGCTGGCT	GAGCTGGACT	3360
	TTGGTCAGCC	TGCTGAGAGC	TCACTGTGCC	TTCTGGGGTC	TTACTCTCTC	TCAAGGAGTC	3420
60	TGTAGTGGAA	AGGAGGCCAC	AGAAATAGCT	GCTTATTCTG	AAACTTCAGC	TTCTCTAGC	3480
	CGGCGCTCT	CTAAGGGAGC	CCTCTGCAC	CGTGTGCAGG	CTCTGACCAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCTGCGAGG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGTATCC	CAGGAACCTG	3660
65	AGTTCTAAGC	AGTGTCTGTG	AAAAAATAAA	GCAGAAAGAA	TTAGAAATAA	ATAAATACTA	3720
	AGCACTTCTG	GAGACAT					

A16 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like domains [49-84,132-167,177-213,286-321,407-442]
 CUB domain [809-918]
 Cellular Localization: may be secreted

80	1	11	21	31	41	51	
	MGVAGNRNRP	AAWAVLLLLL	LLPPLLLLAG	AVPPGRGRAA	GPQEDVDECA	QGLDDCHADA	60
	LCQNTPTSYK	CCKPKGYQGE	GRQCEDIDEC	GNEINGGCVH	DCLNIPGNRY	CTCFDGFMLA	120
	HDGHNCLDVG	ECLNENGGCQ	HTCVNVMGSY	ECCCKSGFPL	SDNQHTCIHR	SEELGSCMNK	180
	DHGCSTHCKE	APRGSVACBC	RPGPELAKNQ	RDCILTCNHS	NGGCGHSCDD	TADGPECSCH	240
	PQYKMTDQR	SCLEREDTVL	EVTESNTTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300

5 STGVHCSCPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFKLITDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGPTH CGDTNECBIN NGGCOQVCVN 420
 TVGSYEQCH PGYKLHWNK DCVEVKGLLP TSVSPRVSLH CGKSGGDCG FLRCHSGIHL 480
 SSDVTITRTS VTFKLNEGKC SLKNAELFPE GLRPALEPKH SSVKESFRYV NLTCSSGKQV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYYDGA RERCILCPNG 660
 TFQNEEGQMT CBPCPRPGNS GALKTPPEAWN MSECGLQCP GREYADGAP CQLCALGTFQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHPY NTTHRCIRC PVGTYPQEFQ 780
 KNNCVSCPGN TTDFDGTSTN ITQCKNRRCG GELGDFGTGI ESNFYPGNYP ANTECTWTIN 840
 10 PPFKRRLIV VPEIFLPIED DCGDYLVMRK TSSNSVTY ETQTYERPI APTSRSKLW 900
 IQPKSNEGNS ARGQVPPVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
 LAHPQNYFYK TAQBSREMPF RSPIRLLRSK VSRFLRPYK

15 A17 DNA sequence
 Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Nucleic Acid Accession #: none found
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

20 1 11 21 31 41 51
 CAAAAGAAA TAGATAAAAT AAATGGAAAA TTAGAAGAGT CTCCTGATAA TGATGGTTTT 60
 25 CTGAAGGCTC CCTGCAGAAAT GAAAGTTTCT ATTCCAACCTA AAGCCTTAGA ATTGATGGAC 120
 ATGCAAACTT TCAGAGCAGA GCTCCCGAG AAGCCATCTG CCTTCGAGCC TGCCATTGAA 180
 ATGCAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240
 GATCAGATGT TCCCTTCAGA ATCAAAACAA AAGAAAGTTG AAGAAAATTC TTGGGATTCT 300
 GAGAGTCTCC GTGAGACTGT TTCACAGAAAG GATGTGTGTG TACCCAAGGC TACACATCAA 360
 30 AAAGAAATGG ATAAATAAG TGGAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420
 GATACAGTTT ATTCTTGTGA AAGAACAAGG GAACITCAAA AAGACCCCTG TGACCCACGT 480
 TCAGAAAA

35 A18 Protein sequence
 Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Protein Accession #: none found
 Signal sequence: none
 Transmembrane domains: none
 40 Cellular Localization: nuclear

45 1 11 21 31 41 51
 QREIDKINGK LEESPDNDGF LKAPCRMVKS IPTKALELMD MQTFKAEPPE KPSAFEPAIE 60
 MQKSVFNKAL ELKNEQTLRA DQMFPSESQK KXVEENSWDS ESLRETVSQK DVCVPKATHQ 120
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDFCDPR SGK

50 Breast

55 A19 DNA SEQUENCE
 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 ACCGGGCACC GGACGGCTCG GGTACTTTTCG TTCTTAATTA GGTCAATGCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACAGTGTGGC CTACTATCTC TTCCGTGGTG 120
 65 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180
 AGAGGTCTCG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGGG CCTTGATGAT TTGAAAATAA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTGACTGC 420
 70 TCAGGGAAGT ACAGATGTGG CTCACTCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGGT GGTGTGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGC 600
 AAGGGTCACT ACGCAATGT TGCCTGTGCC CAAGTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 75 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGAGGGGA 780
 TGTGCTCTGC CCAAGTGTG TACCTTGCAG TGCACAGCCT GTGGTTCATG AAGGGGCTAC 840
 AGCTCACGCA TGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCGCAC 900
 CTTGAGTTCC AGGGTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCCCT GTGGATCATC 960
 ACTGCTGAC ACTGTGTTTA TGACTGTGAC CTCCCAAGT CATGACCAT CCAGTGGGT 1020
 80 CTAGTTTCCC TGTGGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATGCCCC TTATGAAGCT GGCCTGGGCA 1140
 CTCAGTTTCA ATGAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTCCCC 1200
 GATGGAAGAG TGTGCTGAGC GTCAGGATGG GGGGCCACAG AGGATGAGAC AGGTGAGGCC 1260
 TCCCTGTCC TGAACCAAGC GGCGGTCCCT TTGATTCCA ACAAGATCTG CAACCAAGG 1320
 GACGTGTACG GTGGCATCAT CTCCCCCTCC ATGCTCTGCG CGGCTACCT GACGGGTGGC 1380

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 20

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GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGGAGCCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAGAGG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620
TCCTCCCTG GACTCCCGTG TAGGAACTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCCTCCA TCTGATTCCA GCACAACCTT 1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
TTGCCCTCAG TGTCCCACTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACTAATTT 1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
CCTCAAATGA TGTGCTGCTC TCAGCCTCCC ACAGTGCTGG GATTACAGGC ATGGGCCACC 2040
ACGCCTAGCC TCAGCTCCTT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCACTT TTCATCTCTA GGGACCAGAA 2280
CCAAACCCAC CCTTCTACTT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTGTTT TAAGGCCTAT TTTCTATGAT TCTTTGTAGC ATTTGTGTCT TGACGTATTA 2400
TTGTCTCTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
AAAAA
  
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 30

A20 Protein sequence:

Gene name: TMPRSS3a

Unigene number: Hs.298241

Probeset Accession #: AI538613

Protein Accession #: BAB20077

Signal sequence: none found

Transmembrane domains: 43-65, 239-261

Tryp_Spc domain: 216-444

Cellular Localization: not determined

35
 40

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1 11 21 31 41 51
MGENDPFAVE APFSFRSLFG LDDLKISPIVA PDADAVAAGI LSLPLKFFP IIVIGIILI 60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVP 120
TAASWKTMCS DDWKGHYANV ACAQLGPPSY VSSDNLRVSS LEQGFREFEV SIDHLLPDDK 180
VTALEHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQPGYH 240
LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGKVCWT SGWGATEDGA GDA9FVLNHA 360
AVPLISNICK NHRDVGIGII SPSMLCAGYL TGGVDSQCGD SGGFLVCQER RLWKLVGATS 420
FGIGCAEVNK PGVYTRVTSF LDNIHEQMER DLKT
  
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45
 50

A21 DNA SEQUENCE

Gene name: ESTs; opposite strand to TRPS1

Unigene number: none

Probeset Accession #: AA428090

Nucleic Acid Accession #: AA428090

Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

55
 60
 65
 70
 75
 80

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1 11 21 31 41 51
ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG 60
CAAGTTGTGG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120
TTTTGAGACA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAACCGT 180
GATTTCTGTG GGCTTCCTGG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240
GGAAAAACAA CTAACTCAG CCAATTGCCC AATTTCCACC TTGCTAGTTA TCAGAGTTCA 300
CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGAATTT TATTCTGAGC 360
AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAC ATTGCCTCCA GCTGCAAAAGC 420
AAGGGCATTG CCATTATGAA AGCCCTCAA AGACTCTCTG CTATTTTCAA AACATGGAAA 480
GAAAAGGGA AAAAAAGAAA AAAAATAATA ATTAGAAGGA TTGTTCCTT AATTGGGGCT 540
CCCAAAATG AGAAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACCTCTC 600
CAAGCAATTC TTCTGAAGCA ATCAATTATT TATATACITT ATGTTCTGTC TTTTGTATT 660
TTTCTCTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCCTTCCT ATCTGGATCT 720
GTTCTGCTCT ATTTCTCTTT CAAAGTCATC TTTGAGGAA CTGCCCCTGA TTAATTTGAT 780
TTTAACCAAA CAAATAAGAT ATTTGATATA TTAATTTAAA CTTTTTGAGA TGATGTGATTA 840
GGAAATGCAT CATGTTTACA TGAGTATACC GAATTCAAAG TTAACCTTCA TAAGCAGGAG 900
TTTTTACACA TCGTAACATA ATCAATTACC AATACTCGAG ACTCAATATT TGATACTCAA 960
CTGAATGTTT TTGAAATAAA CACATTTTTA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020
CTTTTTACAC AAAATATATC AGTGAGAGAG TGTTTGTTTA AGAAAAAAA TCAAAGCACA 1080
ACAAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTITAGA ATGGTGATTT 1140
GATTTCACCA TTTCATTCGA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200
TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCCTATTGC TAGAAGGATG 1260
AAAGTGAATC CATATAAAC CATTACACG CGTTATGTGT AACTGTGTGT AAAACTTTAT 1320
TATTCAAGTT TAGATGTAAC AGACATCTTT GCTGCCTGAA GATTGTTTGC ATAAGAAATA 1380
CACCAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAAAAACAA ATAAAAATAA 1440
ACGAAAAAAT TTCAATGTGT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA 1500
ATCAGGACTA CAAATGGAAT TCTTTTCTT AGCAACATGA AATCATTTCA TATGAAGAC 1560
ATTTTCTGCT GGTGAATATT GCTGTAAAGT AAATTTTACA TTGGCATTTT GAGATGTTCC 1620
CCCCATATGC CTCCCCCAAA GTTTTCCATG TGGTGTGCAA ATAGTCCGC
  
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A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 113-129
 Cellular Localization: not determined

10 1 11 21 31 41 51
 MKPSLKHWD IKMPSBIDQR QVVGSEIHLQ VVSVSYLVEN FSDTDDLMSI VEESDSCYNR 60
 DSVGLPGRAG DRLQPKTKPR GKTTLNLSHP NFHLASYQSS LLFLKQGSYY GNLLVEFILS 120
 KCFVQLAVLK QKHCHLQLQS KGIAIMKAPQ RLSAIFKTKW EKGKKEKKII IRRICSLIWA 180
 PKNEK

A23 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCCGGGCTCT 60
 CGGCGCCGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG 120
 CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGAGATG GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAACCAAGG GTGAGCCGGC GCGGGGCCCT AGGCGGGCCC TGCTCCCCA GGCACACTCA 300
 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCGCCCTCCG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420
 CCTGTATGCC AACCCAGTGG GTACAGGTTC TGGGGGACCT GGACAGATGC CGCTACCTCT 480
 AGCCGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAAG TGCTGCTCTC GGGAAAGCCCA 540
 GGGCCTGAGG TCATTGCAGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCCT 600
 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGTG TTCCTTGCCA CTGTGCCAAG 840
 GCACTTCCCC ATCTTGACAG CGGCCCCAC CCAGCCGAGG ATCTGGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA 960
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCACTGCCCA GGGCTCTCCC TTCCAGGGA 1020
 GACATGGAGA AGGGGCTTGA GGGAGGGGCC TTCCCTAGCC GCTGTGGCAA CTCAGTGG 1080
 CTGTCTGGG CAAAGTGTGG CCCAAGTGG CAGCCCCAGC CTGTGAGTGC TGGGGACGCT 1140
 GACAGGACAC GGGAGAGGGC CATGCTTTCC CTGGGACCT GCTGTTCATG GTGTCCCAAG 1200
 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTTG 1260
 GGGCTCTGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGAGGAGCC CAGCCCTGCG 1320
 AGGCTGAAGG AGGGCTCTCT ACGGACACAC AGGCCAGGAG GCAAGGCTGG GCCTCTTGG 1380
 GGGGTAGAG CCGACACTGT GCGCTCTCTC GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCATCTCTAA TTCAGCCAA TCCTAAGGCA AGGCCAGGCC CCAGCCCGG 1500
 TCTTCAACA AGCAAGATTG AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGCA GGCAGAAAG 1620
 GAGAAAGCAG AGGCTCTAA TGCAGGAGCT GCTGTATGG GGAACAGCCA GCACAGGGC 1680
 AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCTTGC CCTTCCCTCT GCGAAAGCCC 1740
 ACCACACTTA GGCAGTGCGA AGTGTCTATC CGGAGCTGT GGAATACCAA CCTCTGACAG 1800
 ACCCAAGAGC TGCGCACTCT CRAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
 CCGAGGAGAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920
 AAGAGCCTCT CCAAGAAATG CTTAGCCCA CCTGTGGGG AGCGTGCCAT CCTCCCGCA 1980
 CTGAAGCAGA CCCGAAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
 AAACGGGGCC TGCACTGCTC AGTGTCTTGA

A24 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

75 1 11 21 31 41 51
 MSGAGVAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAH S TLPLPQHRNT AINSSTRLGS 120
 GGTQDGEPLQ TVLAHLAALA FVCPSPGYRF WGTWDAATS SRGWIMLC SQ AQHVLLSGSP 180
 GPEVIAGRQV ATGCSFDLFP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH 240
 MLGAQGIWTH SIQGLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDGSPH PAQDPQLNSQ 300
 AHFPLSLQLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVGGP PPSRCGNSE 360
 LFWAKCGPSR QQPCCSAGDA DRTREEMLS LGTCCSMCPK PSCFPDGPSP NHLRSASAPL 420
 GARWVCINGV WVEPPGGSPA RLKEGSSRTH RPKGKRGLA GGSADTVRSP ADSLSMSSTQ 480
 SVKSIISNAN SQGKARPQPG SFNKQDSKAD VSQKADLEEB PLLHNSKLDK VPGVQQAARK 540

EKABASNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
 TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFPKVST KSLSKKCLSP PVAERAILPA 660
 LKQTPKQNTFA ERQKRLQAMQ KRRLHRSVL

5

A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Nucleic Acid Accession #: NM_000949
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

10

1 11 21 31 41 51
 15 GGAGGCTGAA ATCCCCAGAC GCGGGTTTTC TGGGCTGGGC TTTCGTCTTA CTCACCTCCT 60
 CTCCTCTCTT CTGGATTTTA COGACCGTTC GCGAAACAGC TTCCACACA ATGGAGCTTC 120
 ATGTCTCTGT GCAGGAAGTA CTCATCGACT GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180
 TAAAGAACTC TCCTATTTCAT GSAGGCGAAC ACTGAGGATG CTTCCACAT GAACCTTGAA 240
 GTGAACCTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300
 20 CATCTGCAAC CGTTTTCACT CTGCTACTTT TTCTCAACAC CTGCTCTCTG AATGGACAGT 360
 TACCTCTCTG AAAACCTGAG ATCTTTAAAT GTGCTTCTCC CAATAAGGAA ACATTACCT 420
 GCTGTGGGAG GCCTGGGACA GATGGAGGAC TTCTTACCAA TTATTCACTG ACTTACCACA 480
 GGGAGGAGAG GACACTCATG CATGAATGTC CAGACTACAT AACGGTGGC CCCACTCCT 540
 25 GGCATTCTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
 CTAAACAGAT GGGAGAGCAGT TTCTCGGATG AACTTTATGT GGACGTGACT TACATAGTTC 660
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAACAA GCCAGAGAGC AGAAAAACCT 720
 ACCTGTGGAT TAAATGTGCT CCACCTACCC TGATTGACTT AAAAAGTGGT TGGTTACGCG 780
 TCCTGTATGA AATTGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGACT CATTTTGCTG 840
 30 GGCAGCAAAAC AGAGTTTAAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900
 TTCTGTGCAA ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTCTGA 960
 TACCTAGTGA TCTCAACATG AATGATACAA CCGTGTGGAT CTCTGTGGCT GTCCCTTCTG 1020
 CTGTCACTGT TTTGATTATT GTCTGGGCGA TGGCTTTGAA GGGCTATAGC ATGTTGACCT 1080
 GCATCTTTCC GCGAGTTTCT GGGCCAAAAA TAAAGGATT TGATGCTCAT CTGTTGAGAG 1140
 35 AGGGCAAGTC TGAAGAACTA CTGAGTGCTT TGGGATGCCA AGACTTTCCT CCCACTTCTG 1200
 ACTATGAGGA CTGTCTGGTG GAGTATTTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
 TGTCACTCCA TTCAAAGGAA CACCCAGGTC AAGGTATGAA ACCCACAATC CTGGATCCTG 1320
 ACATGACTCT AGGCCGGGGG AGCTGTGACA GCGCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380
 AACCCAGGCG CAATCCCTCC ACATTCTATG ATCTGAGGT CATTGAGAGC CCAGAGAAATC 1440
 40 CTGAAACAAC CCACACCTGG GACCCCCAGT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500
 TTCTATGCTG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCAGC CAGCACAACC 1560
 CCAGATCCTC TTACCAACAAT ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG 1620
 CACCGGGCCAC TCTGTGAAT GAAGCAGGTA AAGATGCTTT AAAATCTCTC CAAACCATTA 1680
 AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGAGGT AGAAAGCTTC CATTCTGAGA 1740
 45 CTGACCAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCGCTTAAC 1800
 CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAGATGG TGCAATTATCA TTGCTACCAA 1860
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
 ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGGT GTTGTGCCCA GATCCACATG 1980
 50 CTAAAAAGCT GGCCTTGCTT GAAGAATCAG CCAAGAGGC CCCACATCA CTTGAACAGA 2040
 ATCAAGCTGA GAAAGCCCTG GCCAATCTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
 TGGGTGGTTT GGATTACCTG GATCCCGCAT GTTTTACACA CTCCCTTTCAC TGATAGCTTG 2160
 ACTAATGGAA TGATTGGTTA AAATGTGATT TTCTTTCAGG TAACACTACA GAGTAGCTGA 2220
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGCTCCA 2280
 TTTTAAACA CTTGCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCCT 2340
 55 AACTGTGATT TGTAGATTTA CTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAAT 2400
 AAAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAAG 2460
 GCTTTCATGA TGTGGCATGG GACAGACGGA AATGAAATTG TCAAAATTGT TTACCATAGA 2520
 AAGATGACAA AAGAAAAATT TCCACATAGG AAATGCCAT GAAAAATTGT TTTGAAAAAC 2580
 AACTGCATAA CCTTTACACT CTTGTTCCAT TTTATTAGGA TTACCCAAAT ATAACCAATT 2640
 60 AAAGAAAGAA TGCAATCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
 TTGCTGATAT GCAAGTAAGA AAT

65

A26 Protein sequence:

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Protein Accession #: NP_000940
 Signal sequence: 1-23
 Transmembrane domains: 237-253
 70 FN3 domains: 28-112, 127-215
 Cellular Localization: plasma membrane

75

1 11 21 31 41 51
 80 MKENVASATV FTLLFLNTLC LLNGQLPPGK PBIFKCRSFN KETFTCWWRP GTDGLPTNY 60
 SLTYHREGET LMHECPDYIT GGFNSCHFGK QYTSMTWTYI MMVNATNQMG SSPSDLYVD 120
 VTYIVQPDPP LBLAVEVKQP EDRKPYLMWK WSPPTLIDLK TGWFTILYBI RLKPEKAAEW 180
 EIHFAQQQTE FKILSLHPQG KYLVQVRCKP DHGYWSAWSP ATPFIQPSDF TMNDTTVWIS 240
 VAVLSAVICL IIVWAVALKG YSMVTCIPFP VPGPKIKGPD AHLLKKGKSE ELLSALGCOQD 300
 FPPTSDEYEDL LVEYLEVDSS EDQHLMSVHS KEHPSQGMKP TYLDPDTSQ RGSCEPSFLL 360
 SEKCEEPQAN PSTFYDPEVI EKPEPFETH TWDPQCISME GKIPYFHAGG SKCSTWPLPQ 420

PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQRBEV 480
 SPHSBTDQDT PWLLPQEKTP FGSAPKLDYV EHKVKNKGA LSLPKQREN SGKPKPGTTP 540
 ENNKKEYAKVS GVMDDNILLVL VPDPAKQVVA CPESAKEAP PSLEQNQAEK ALANFTATSS 600
 KCRLLQLGGLD YLDPACPTHSH FH

A27 DNA SEQUENCE

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)

Unigene number: Hs.169266

Probeset Accession #: L07615

Nucleic Acid Accession #: NM_000909.1

Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CATTCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATTG CAATATCGGG 120
 AATAAGAAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180
 ATAATCTATA ACAACCAAAAC CAATCAAAAT GAATTCAAAC TTATTTTCCC AGGTTGAAAA 240
 TCATTGAGTC CACTCTAATT TCTCAGAGAA GAATGCCAG CTTCCTGGCT TTGAAATGA 300
 TGATTGTCTAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTGCTTATG GAGCTGTGAT 360
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAC AAAAGGAGAT 420
 GAGAAATGTT AGCTAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480
 CATGTGTCTC CCCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGTTGAGGC 540
 GATGTGTAAG TTGAATCCTT TTGTGCAATG TGTTCATC ACCTGTGCTA TTTTCTCTCT 600
 GGTTCTCATT GCTGTGGAAC GACATCAGCT GATAATCAAC CCTCGAGGCT GGAGACCAAA 660
 TAATAGACAT GCTTATGTAG GTATTGTGCT GATTTGGGTC CTGCTGTGG CTCTCTCTTT 720
 GCCTTTCTCT ATCAACCAAG TAATGACTGA TGAGCCGCTC CAAATGTAA CACTTGATGC 780
 GTACAAAGAC AAATACGTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTTAA 840
 TACCCTTAGT TCTTGGTGGC TGCAATATT TGGTCCACT TGTTTTATAT TTATTTGCTA 900
 CTTCAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGACAAGA TGAGAGACAA 960
 TAAGTACAGG TCAGTGAAA CAAAAGAAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
 ATTTGCAGTC TGCTGGCTCC CTCTTACCAT CTTTAACACT GTGTTTGATT GGAATCATCA 1080
 GATCATTGCT ACCTGCAACC ACAATCTGTT ATTCCTGCTC TGCCACCTCA CAGCAATGAT 1140
 ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGAAAC AAAAATCTCC AGAGAGACTT 1200
 GCAGTTCCTT TTCAACTTTT GTGATTTCOG GTCTCGGAT GATGATTATG AAACAATAGC 1260
 CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTGGC 1320
 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
 TCTCCCAAGG AATGGGGTGG AAATCATTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500
 TTACTGCTTT TGTGTGATGT GTCATAATTA CATTTGGAAC AAAAGGTGTG GGCCTTGGGG 1560
 TCTCTGGAAG ATAGTTTGA CCAGACATCT TTGAAGTGCT TTTTGTGAAT TTATGCATAT 1620
 AATATAAAGA CTTTATATCT GTACTTATTG GAATGAAAT TCTTTAAGT ATTACGATGC 1680
 GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCAATAG ATTGGGTAT CTTGATTAGA 1740
 TTAGATTAGA TTGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
 TAGTGTGTTA CAATAGTAAC AGTATGCAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
 GAAGTCATTC AGAAGTGGTT TGAGGTCTCT GTTTTTTGGT GGTTTTGTGT TGTTTTTTTT 1920
 TTTTTTACC TTAAGGGAGC CTTTCATTTT CTCGCGACTG ATTGTCACTT AAATCAAAAT 1980
 TTAATAATGA ATAAAAAGAC ATACTTCTCA GCTGCAATA TTATGGAGAA TTGGGCCACC 2040
 ACAGGAATGA AGAGAGAAAG CAGCTCCCA ACTTCAAAAC CATTTTGGTA CCTGACAACA 2100
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
 TATATTATT TGAATTGATG GTCAAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAGTGT 2220
 TTGCAAGCT TCTGGTCTAA TATGACTCG AAAGACTTTC CGCTTAAAT TTGTAGAAAC 2280
 ACAATATCG TTTTCCATAC AGCAGTGCTT ATATAGTGAC TGATTTTAA TTTCAATGTC 2340
 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTAC TTTACCTAGC 2400
 AGGGAAAAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT 2460
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TACTGATAA GTTGTGTCAT 2520
 GTTAATGTGC CTAATTTCAT GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTGAGAG 2580
 AAATATATT TTAAGAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640
 TGTTTGATTT TAAAAGGGCG GACATTTTAT TAAATCAAT ATTGTTTGTG CTTTTTCTGA 2700
 GGAGTCTCTT TCAGTTTCAT TTTTCTCAT CCCATGACTT CCTCCGATG GT

A28 Protein sequence:

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds

Unigene number: Hs.169266

Probeset Accession #: L07615

Protein Accession #: NP_000900.1

Signal sequence: none found

Pfam domains: 7tm_1 [57-91]

Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286,

300-322

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MNSTLFSQVE NHSVSNFSE KNAQLLAFEN DCHLPLAMI FTLALAYGAV IILGVSGNLA 60
 LIIILKQKE MRNVNLIIV NLSFSDLLVA IMCLPPTFVY TLMDEWVFGE AMCKLNPFVQ 120
 CVSITVSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180
 DEFPQNVITLD AYKDKYVCFD QPPSDSHRLS YTTLLLVLYQ FGPLCPFIC YFKIYIRLKR 240
 RNNMDKMRD NKYSRSETKR INIMLSIVV AFVNCWLFLT IFNTVPDWNH QIIATCNHNL 300
 LFLLCILHAM ISTCVNPIFY GPLNKNPQRD LQFFNFPCDF RSRDDDYETI AMSTMHTDVS 360

KTSLKQASPV AFKKINNDD NEKI

A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

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5      1      11      21      31      41      51
|      |      |      |      |      |
10     |      |      |      |      |      |
15     |      |      |      |      |      |
20     |      |      |      |      |      |
25     |      |      |      |      |      |
30     |      |      |      |      |      |
35     |      |      |      |      |      |
40     |      |      |      |      |      |
45     |      |      |      |      |      |
50     |      |      |      |      |      |
55     |      |      |      |      |      |
60     |      |      |      |      |      |
65     |      |      |      |      |      |
70     |      |      |      |      |      |
75     |      |      |      |      |      |
80     |      |      |      |      |      |

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ATGCACACCG TGGCTACGTC CGGACCCAAAC GCGTCTCTGG GGGCACCCGG CAAAGCCTCC 60
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TCGCTGGTCA TCTAGTCACT CTGCGGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
ATCGCCAAAC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300
CTGCTGTACC CGTGGCCCGG CTGGGTGCTG GCGACTTCA TGTGCAAGTT CGTCAACTAC 360
ATCCAGCAGT ACTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCATGAG TGTGGACCGC 420
TGGTACGTGA CGGTGTTCCC GTTGGCGGCC CTGCACCGCC GCACGCCCGC CTTGGCGCTG 480
GCTGTACAGC TCAGCATCTG GGTAGGCTCT GCGCGGTGT CTGCGCCGT GCTCGCCCTG 540
CACCCTCTGT CACCCTGGCC GCGCGCTTAC TGCAGTGAGG CCTTCCCGAG CCGCGCCCTG 600
GAGCGCGCCT TGCACCTGTA CAACCTGTCT GCGCTGTACC TGCTGCGCT GCTCGCCACC 660
TGGCGCTGCT ACTCGGTGCA GGCCACGTGT GCGCGGCCAC CTGGGCGCGG TCGCGGTGCG CCGCGCGGCC 720
GCGCATAGCG CCTCGAGGG GCGAGGTGCT GCGAGCGCGC CAGGCGCGGT GCGGGCCAG 780
GTCTGCGCGC TGGTGGCGCC CGTGGTCTCT CTCTGCGCG CCGCTGCGG CCCATCCAG 840
CTGTCTCTGT TGTGCGAGG GCTGGGCCCC GCGGGCTCCT GGCACCCAG CAGCTACGCC 900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCCG 960
CTGCTCTAGT TCTCTCTGG CTGCACTTTC CGACAGGCGT TCGCGCGGT TCGCCCTGTC 1020
GCGCGCGGCC GCGCGCGCG CCGCGCGCG CCGGACCCCT CGGACCCCG AGCCCAACAC 1080
GCGGAGCTGC ACGCTCTGG GTCCACCCG GCGCGCGCA GGGCGCAGAA GCCAGGGAGC 1140
AGTGGGCTGG CCGCGCGCG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

Pfam domains: 7tm_1 [59-323]

Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

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45     1      11      21      31      41      51
|      |      |      |      |      |
50     |      |      |      |      |      |
55     |      |      |      |      |      |
60     |      |      |      |      |      |
65     |      |      |      |      |      |
70     |      |      |      |      |      |
75     |      |      |      |      |      |
80     |      |      |      |      |      |

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MHTVATSGPN ASHGAPANAS GCPGCGANAS DGPVPSPRAV DAWLVPLFFA ALMLLGLVGN 60
SLVIYVICRH KPMRTVTNFI IANLAATDVT FLLCCVPPTA LLYPLPGWVL GDFMCKFVNY 120
IQQVSVQATC ATLITMSVDR WYVTVPFLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAPFSRAL ERAPALYNLL ALYLLPLLAT CACVAAMLRH LGRVAVRPAP 240
ADSAIQGGVL AERAGAVRAK VSRLVAAVVL LFAACWGPQI LPLVLQALPG AGSWHPRSYA 300
AYALKTWAHC MSYNSALNP LLYAFLLGSHF RQAFRRVCPC APRRRPRPRR PGPSDPAAPH 360
AELHRLGSHP APARAQKPGS SGLAARGLCV LGEDNAFL

A31 DNA SEQUENCE

Gene name: CH22_PGENES.706; cadherin, BGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM_014246

Nucleic Acid Accession #: NM_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

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65     1      11      21      31      41      51
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70     |      |      |      |      |      |
75     |      |      |      |      |      |
80     |      |      |      |      |      |

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ATGGCGCGGC CGCGCGCGCC CGTGTCTGCC GTGTCTCTGC TCCTGGCGGC CGCGCGCGCC 60
CTGCCGCGCA TGGGGCTGCG AGCGGCGCGC TGGGAGCGCG GCGTACCCGG CGGGACCCGC 120
GCCTTCGCCC TCOCGCGCGG CTGTACTCTAC GCGGTGGGCG CCGCTTGACG GCGCGCGCGC 180
CGCGGGGAGC TGCTGAGCTG GGGCGCGGAT GGGCGGCTGG CAGGACGTGC GCGCGTCTCG 240
GGCGCGGGGC GCGCGTGCCT GCTGCAAGTC CGCTTGTGG CCGCAGTGC CCGGACGGCG 300
CTGAGCGGCC GCTGTGCGGC GCGCACGCGC CTTCCCGGCT GCGGAGCGCG TGCCCGGCTC 360
TGCGGAACCG GTGCCCGGCT CTGCGGGGCG CTCTGCTTCC CCGTCCCGCG CGGCTGCGCG 420
GCGCGCGAGC ATTGCGCGCT GCGAGCTCCG ACCACTTAC CCGCTTGCGG CTGCGCGCGC 480
CGCCCGAGCG CCGCTGTGTC GCGCGGTCCC ATCTGCTGCG CGCGGGCGCG CTCGGTCCGC 540
CTGCGTCTGC TGTGCGCCCT GCGCGCGCGG GCTGGCGCGG TCGGGGTGGG ACTGCGGCTG 600
GAGGCGCGCA CGCGCGGGAC GCCCTCCGCG TCGCCATCCC CATCGCGCGC CCTGCCCGCG 660
AACTTGCCTG AAGCCCGGCG GGGCGCGGCG GCGCGGGCGC GCGCGGCGAG GAGCGGCGAG 720
GGGAGCGCTA AGTTTCCGAT GCCCAACTAC CAGGTGGCGT TGTTTGAGAA CGAACCGGCG 780
GGCACCTTCA TCCTCCAGCT GCAAGCGCAC TACACCATCG AGGGCGAGGA GGAGCGCGTG 840
AGCTATTACA TGGAGGGGCT GTTGAAGGAG CGCTCCCGGG GCTACTTCCG AATCGACTCT 900
GCCACGGGCG CCGTGAGCAC GGACAGCGTA CTGGAACGCG AGACCAAGGA GACGACGCTC 960
CTCAGGGTGA AAGCCGTGGA CTACAGTACG CCGCGCGGCT CGGCCACCA CTACATCACT 1020
GTCTTGGTCA AAGACACCAA CGACCAAGC CCGGTCTTCC AGCAGTCCGA GTACCGGAG 1080
CGCGTCCGGG AQAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCCGCGC CAGCGACCGC 1140

5	GACTCGCCCA	TCAAAGCCAA	CTTGGCTTAC	CGGCTGTTGG	GGGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAACG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGCGG	TGCTGGACCG	GGAGGAGGCG	1260
	GCCGAGTACC	AGCTCCTGGT	GGAGGCCAAC	GACAGGGGCG	GCAATCCGGG	CCCGCTCAGT	1320
	GCCACGGCCA	CGGTGTACAT	CGAGGTGGAG	GACGAGAACG	ACAATCAACC	CCAGTTTCAG	1380
	GAGCAGAACT	ACGTGGTCCA	GGTGCCCGAG	GACGTGGGGC	TCAACAACGG	TGTGCTGCGA	1440
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	GGGAACTGTG	COGGCCAGTT	CTACCTGCAC	TGCTGAGCG	GGATCCTGGA	TGTGATCAAC	1560
	CCCTTGGATT	TOGAGGATGT	CCAGAAATAC	TGCTGAGCA	TTAAGGCCCA	GGATGGGGGC	1620
10	CGGCCCCCG	TCATCAATTC	TTCAAGGGTG	GTGTCTGTGC	AGTGCTGGA	TGTCAACGAC	1680
	AAOGAGCCTA	TCTTGTGAG	CAGCCCTTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTG	1740
	GGCTACCCCG	TGGTGACAT	TCAGGCGGTG	GACGCGGACT	CTGGAGAGAA	CGCCCGGCTG	1800
	CACATATCGC	TGGTGACAC	GGCCTCCACC	TTTCTGGGGG	GCGGAGCGC	TGGGCTTAAG	1860
	AATCCTGCCC	CCACCCCTGA	CTTCCCTTC	CAGATCCACA	ACAGCTCCGG	TTGGATCACA	1920
15	GTGTGTGCG	AGCTGGACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGGCGGTG	1980
	GACCAOCCGT	CGCCCCCAT	GAGCTCCTCC	ACCAGCGTGT	CCATCACGGT	GCTGGAOCTG	2040
	AATGACAACG	ACCCGGTGT	CAGCGAGCCC	ACCTAGGAGC	TTGCTGTGAA	TGAGGATCGG	2100
	GCCGTGGGGA	TGGTGACAC	GACCTGCAG	GCCCGGACC	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACCCAG	TCACAGGCGG	CAACACCCGG	AAOCCCTTTC	CACTCAGCAG	CCAGAGAGGG	2220
20	GGCGGCTCA	GCTACCTGCG	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	TACGTGCTGT	2280
	GCGGTGACAG	CATCCGAGCG	CACACGGTCC	CACACTGCGC	ATGTCTTAAT	CAACGTCACT	2340
	GATGCCAACA	CCACAGGGCC	TGTCTTTTCA	AGCTCCCAT	ACACAGTGAG	TGTCACTGAG	2400
	GACAGGCGCT	TGGGCACTCC	CATTGCTACC	CTCAGTGCCA	ACGATGAGGA	CACAGGAGAG	2460
	AATGCCCGCA	TCACCTACGT	GATTGAGGAC	CCCGTCCCGC	AGTTCCGAT	TGACCCGAGC	2520
25	AGTGGCACCA	GTGTACACCA	GATGAGCTGT	GACTATGAGA	ACCAGTCCGC	CTACAGCTGT	2580
	ACCATCATGG	CCACAGGACA	CGCATCCCG	CAGAAATCAG	ACACCAACAC	CCTAGAGATC	2640
	CTCATCTCTG	ATGCCAATGA	CAATGCACCC	CAGTTCCTGT	GGGATTTCTA	CCAGGGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTCGACCGC	ATCCTCCAGG	TCTCTGCCAC	GGACCGGGAC	2760
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30	TTCTACATCG	AGCCCACTGC	CGGTGTGATT	CGCACCCAGC	GCCGCTGGA	CCGGGAGAA	2880
	GTGGCCGTGT	ACAACCTTTG	GGCTCTGGCT	GTGGATCGGG	GCACTCCAC	TCCCTTTAGC	2940
	GCCTCGGTAG	AAATCCAGGT	GACCATCTTT	GACATTAATG	ACAATGCCCC	CATGTTTGAG	3000
	AAGGACGCTG	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGGTCCGT	GGTGGCAAGG	3060
	ATTGCTGCTA	ACGACCTTGA	TGAAGGCCCT	AATGCCGAGA	TCATGTATCA	GATTGTGGAA	3120
35	GGGGAACATG	GGCATTTCTT	CCAGCTGGAC	CTGCTCAACG	GGGACCTCGC	TGCCATGCTG	3180
	GAGCTGGAAT	TTGAGGTCCG	GCGGAGTAT	GTGCTGGTGG	TGCAGGCCAC	GTGGGCTCCG	3240
	CTGGTGAGCC	GAGCCACGGT	GCACATCTTT	CTGTTGGACC	AGAATGACAA	CCCGCTCTGT	3300
	CTGCCCGAT	TCCAGATCCT	CTTCAACAAC	TATGTCAACA	ACAAGTCCAA	CAGTTTCCCC	3360
	ACCGGCGTGA	TGGCTGTGAT	CCCGGCCCAT	GACCCGACCG	TGTGAGACAG	CCTCAACTAC	3420
40	ACCTTCTGTG	AGGGCAACGA	GCTGCGCTGT	TTGCTGTG	ACCCCGCCAC	GGGCGAATCT	3480
	CAGCTCAGCC	GCGACCTGGA	CAACAACCGG	CCGCTGGAGG	CGCTCATGGA	GCTGTCTGTG	3540
	TCTGATGGCA	TCCACAGCGT	CACGGCTTTC	TGCACCTTCG	GTGTCCCAT	CATCAAGGAC	3600
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	TCCCGCTGTC	TGGCCCTCTT	CGTGGAGGGG	GTGGCCCGCG	TGCTGTCCAC	CACCAAGGAC	3720
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	CAGGAGCAGA	TCTACTTGAA	TOGGAACGCT	CTGACCAACA	TCTCCACGCA	GCGCGTGTGT	3900
	CCCTTCCAGG	ACAACATCTG	CCCTGCGGAG	CCCTGCGAGA	ACTACATGAA	GTGCGTGTCC	3960
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50	ATCCACCCCA	TCACGCGCTG	GCGCTGCCGC	TGCCCGCCCG	GCTTCCACCG	CGACTACTGC	4080
	GAGACGGAGA	TGACCTCTGT	CTACTCOGAC	CCGTGCGGCG	CCAAACGCGC	CTGCCGACGC	4140
	CGCGAGGGCG	GCTACACCTG	CGAGTGCTTC	GAGGACTTCA	CTGAGAGGCA	CTGTGAGGTT	4200
	GATGCGCGCT	GCGCGCGCTG	TGCCAACGGG	GTGTGCAAGA	ACCGGGGCAC	CTGCGTGAAC	4260
	CTGCTCATCG	GCGGCTTCCA	CTGCGTGTGT	CCTCTGGGCG	AGTATGAGAG	GCGCTACTGT	4320
55	GAGGTGACCA	CCAGGAGCTT	CCCGCCCCAG	TCCCTTGTCA	CCTTCCGGGG	CCTGAGACAG	4380
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	TACAACGGCC	GCTTCAATGA	GAAGCAAGAC	TTCACTCGCC	TGGAGATCGT	GGACGAGCAG	4500
	GTGACGCTCA	CCTTCTCTGC	AGGCGAGACA	ACAACGACCG	TGGCACCGGA	GGTTTCCAGT	4560
	GGTGTGAGTG	ACGGGCGGTG	GCACTCTGTG	CAGGTGCAGT	ACTACAACAA	GCCCAATATT	4620
60	GGCCACCTGG	GCTTGCCTCA	TGGGCCGCTC	GGGGAAGAGA	TGGCGGTGTT	GACAGTGGAT	4680
	GATTGTGACA	CAACCATGGC	TGTGCGCTTT	GGAAAGGACA	TGGGGAACCA	CAGCTGCGCT	4740
	GCCAGGGGCA	CTCAGACCGG	CTCCAAGAAC	TCCCTGGATC	TGACCGGCCC	TCTACTCCTG	4800
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	GGGAAGAACT	GTGAGCAAGC	CATGCCCTAC	CCCCAGCTCT	TCAGCGGTGA	GAGCGTCTGT	5100
	TCCTGGAGTG	ACCTGAACAT	CATCATCTCT	GTGCCCTGGT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCGGAAGG	AGGACAGCGT	TCTGATGGAG	GCCACCAATG	GTGGGCCAC	CAGCTTTCCG	5220
70	CTCCAGATCC	TGAACAACCT	CCTCCAGTTT	GAGGTGTCCC	ACGGCCCTTC	CGATGTGGAG	5280
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	CCGCTGTGTG	GACCTTGCCA	CTGTGCGGTC	AGCAAGGCTT	TGATCCCGA	CTGTAAATAG	5940
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	CAGTGTGCTT	GCAAGCCCGG	CGTCACTGCG	CGCCAGTGCA	ACCGCTGCGA	CAACCGGTTT	6120
	GCGGAGGTCA	CCAAGCTCGG	CTGTGAAGTG	ATCTACAATG	GCTGTCCCAA	AGCATTTGAG	6180

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5	CGCAATGAGA	CGCAGGTGGA	CGCGGCCAGG	GCCCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
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	GCAGCCCTGC	TGGTGGCCTT	CGTCTCTCTG	AGCCTGGTCC	GCATGCTGCG	CTCCAACTCG	7500
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	GGGATCAACC	GACGCGAATA	CCCGTTTCTG	TGCAAGTGGG	TTGCCATCCT	CTCCCACTAC	7620
25	ATCTACATGA	GCACCTTTGC	CTGGACCTTC	GTGGAGAGCC	TGCATGTCTA	CCGCATGCTG	7680
	ACCGAGGTGC	GCAACATCGA	CACGGGGCCC	ATGCGGTTCT	ACTAGTCTGT	GGGCTGGGGC	7740
	ATCCCGGCCA	TTGTACACAG	ACTGGCGGTC	GGCCTGGACC	CCGAGGGCTA	CGGGAACCCC	7800
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	GCTGTTATAA	TATCAACAC	AGTCACTTCT	GTCTTATCTG	CAAAGGTTTC	CTGCCAAGAA	7920
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	CACCTGCGTC	TCAACGAGGA	GGTCCGGAGG	CACCTGAAGG	GCGTGTCTCG	CGGAGGAGAG	8160
	CTGCACTGAG	AGGACTTCGC	CACCAACAGG	GCCACCTGTC	TGACGCGCTC	CCTCAACTGC	8220
35	AACACCACTT	TCGGTGACGG	GCCTGACATG	CTGCGCACAG	ACTTGGGCGA	GTCCACCGCC	8280
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	GTGAGCGGCA	GCCAGCGAGA	GCCAGACCGG	TCCCTCATGC	CCAGGAGCTG	CAAGGATCCC	8400
	CCTGGCCACG	ATTCCGACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
	GCCTCTCTAC	ACTGTCAGAA	CAGCGAGGAC	GATGGGGTGG	GAGCTGAGGA	AAATGGGAC	8520
40	CCGGCCAGGG	GCGCGCTCCA	CAGCACCCCC	AAAGGGGACG	CTGTGGCCAA	CCAGCTTCGG	8580
	GCGCGCTGGC	CCGACAGAGG	CCTGGCTGAG	AGTGACAGTG	AGGACCCGAG	CGGCAAGCCC	8640
	CGCCTGAAGG	TGGAGACCAA	GGTCAGCGTG	GAGCTGCACC	GCGAGGAGCA	GGGCAGTCAC	8700
	CGTGGAGAGT	ACCCGCCGGA	CCAGGAGAGG	GGGGGCGCAG	CCAGGCTTGC	TAGCAGCCAG	8760
	CCCCCAGAGC	AGAGGAAAGG	CATCTTGAAA	AATAAAGTCA	CCTACCCCGC	GCCGCTGAGC	8820
45	CTGACGAGGC	AGACGCTGAA	GGGCGGGCTC	CGGAGAAAGC	TGGCCGACTG	TGAGCAGAGC	8880
	CCACATCTCT	CGCGCACGTC	TTCCTTGCGC	TCTGGCGGCC	CCGACTGCGC	CATCACAGTC	8940
	AAGAGCCCTG	GGAGGGAGCC	GGGGCGTGAC	CACCTCAACG	GGGTGGCCAT	GAATGTGGCG	9000
	ACTGGGAGCG	CCGACGCCGA	TGGCTCCGAC	TCTGAGAAAC	CGTGAGGCAA	GCCCGTCACC	9060
	CCACACAGGC	TGCGGCATCA	CCCTCAGACC	TTGGAGCCCA	AGGGGCCACT	GCCCTTGAAG	9120
50	TGGAGTGGGC	CCAGAGTGTG	GCGGTCCCCA	TGGTGGCAGC	CCCCCGACTG	ATCATCCAGA	9180
	CACAAAGTTC	TTGGTTCTCC	CAGGAGCTCA	GGGCGGTGCA	GACCTGGTGA	CAAGTGCCAA	9240
	AGGCCACAGG	CATGAGGGAG	GCGTGGACCA	CTGGGCCAGC	ACCGCTGAGT	CCTAAGACTG	9300
	CAGTCAAAGC	CAGAACTGAG	AGGGGACCCC	AGACTGGGCC	CAGAGGCTGG	CCAGAGTTCA	9360
	GGAAACGCGG	GCACAGACCA	AAGACCGCGG	TCCAGCCCCG	CCGAGGCGGG	CATCTCATGG	9420
55	CAGTGGCGAC	CCGTGGCTCG	CAGCCCGGCG	AGTCTTTTGC	AAAGGCACCC	CTTGTCTTAA	9480
	AATCACTTCG	CTATGTGGGA	AAGGTGGAGA	TACTTTTATA	TATTTGTATG	GGACTCTGAG	9540
	GAGGTGCAAC	CTGTATATAT	ATTGCAATCG	TGCTGACTTT	GTATCCCCGA	GAGATCCATG	9600
	CAATGATCTC	TTGCTGTCTT	CTCTGTCAAG	ATTGCACAGT	TGTACTTGAA	TCTGCACTGT	9660
	GTGAGCAAAA	CTGGTGCCCC	AGCAGATCAA	AGGTGGGAAA	TACGTGAGCA	GTGGGGCTAA	9720
60	AACCAAGCGG	CTAGAAGCCC	TACAGCTGCC	TTCCGCCAGG	AAAGTGAGAT	GGTGTGGGCC	9780
	CTCCCGCCCG	GCCCCCTGGG	TCCCCAGTGT	TGCGTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCGG	GCTGTGTGAA	TTCAAGACAG	GGCAGTGCAG	CACCTAGGAG	GTGTGAGGAG	9900
	CCCTGCTGAG	GTCATGTGGG	GGCAOGGTTG	CCACAGCGCT	GTCATTTTTC	ACCTGGTCAAT	9960
	TCTGTGACCA	CCACCCCTTC	CCCTCAGCTC	CTCCAGGTTG	GCCCGGGAGC	TGCAAGTGGG	10020
65	GATGGCTTTG	TCTTTTGTCT	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAGGT	10080
	TCTGTATTTG	GACAGAGGTG	TGGGGCCTTC	CAGGGCTTTC	CATACCTCCT	GCCAAATTCT	10140
	TAACTCTCTG	AGACTGCGAG	GATCTCCAGG	CAGGGTTCTC	CCCTCTGGAG	TCTGACCAAT	10200
	TACTTCAATT	TGCTTCAAA	GGCCAAATTG	GCAAGGGGAC	AAAGCCACAG	CCACACTCTT	10260
	CAACGCTTAC	CAAACTGTTT	TTGGAAATTC	ACACCAAGGT	CGGGCCCACT	GCAGGCAGCT	10320
70	GGCACAGGCT	GGCCCGAGGG	GCTGTGGAAC	GGGTCCCGGA	ACTGTGAGAC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTCTCT	CAAACTCAGG	GCCCAATAAA	GTGATCAGCA	CAGCTGCTTC	10440
	CAAAATAGAG	AAACCAATAA	ATAGGATGAA	AATCAAGTAA	AATGCAAGAA	TGTCCACACT	10500
	GTTTTAAACT	TGACCCGTAT	GAAATATGTA	GCATGTTTAA	CAGATGCCCT	TGGGAGAGGA	10560
	AAAGCGTATC	TGAAATATGT	CCAGGACAGG	AGGATGAAAT	GAGATCCGAG	AGTCTCTACA	10620
75	CCTGAATGAA	TTATACATGT	GCCTTACCAG	GTGAGTGGTC	TTTGGAGAGT	AAAAAACTCT	10680
	AGTCCCTTTA	AACGTTTGCC	CCTGGCGTTT	CCTAAGTAGG	AAAAGGTTTT	TAAGTCTTCT	10740
	AACAGTCTCC	TTTCATGACT	TTAACAGGAT	TCTGCCCCCT	GAGGTGTAAAT	TTTTTTGTTC	10800
	TATTTTTTTC	CAGCTACTCC	ACAGCCAACA	TCAAGAGGTC	TAATTTTTTA	TTTGATCAGA	10860
80	ACTGTTACCA	AAAAACAAC	GTCAAGTTTA	TTGAGATGGG	AAAAATGTAA	ACCTATTTTT	10920
	ATTACTTAAG	ACTTATATGG	AGAGATTAGA	CAGTGGAGGT	TTTTTAACAGA	AGTGTATTTT	10980
	ATTAAATGTT	AAAAACTCTG	AATTAACAAT	GAGAAGAGTC	TACAAATAAT	TAAGATTTTT	11040
	GAATTTGTAC	TTCTGCGGTG	CTGGTCTTTC	TCACAAACA	CCCCCGCCCC	TCCCCATGCC	11100
	CAGGGTGGCC	GTGGAAGGGA	CGGTTTACGG	ACGTGCAGCT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGAAACGT	GCCGGAACCT	TTTGTCCATT	CCCTAGTAGG	CCTGCCACAG	11220

CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTTGAGGAC TTTTTTTTTT TGCCATTATT 11280
 TCTTCAGTTT TCTTTTCTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340
 AGACGTTAGA CCTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTC

5 **A32 Protein Sequence**
 Gene name: CH22_PGENRS.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo
 (Drosophila) homolog (CELSR1),
 Hs.252387
 Unigene number:
 Protein Accession #: NP_055061
 Signal sequence: 1-20
 Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,
 1110-1199
 Pfam domains: Laminin EGF [2003-2048], 7tm_2 [2465-2708]
 Latrophilin/GPS domains: 2407-2460
 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51
 MAPPPFVPLP VLLLLAAAAA LPAMGLRAAA WEPRVPGGTR APALRPGCTY AVGAACTPRA 60
 PRELLDVGRD GRLAGRRRVS GAGRPLPLQV RLVARSAPTA LSRRLRARTH LPGCGARARL 120
 CGTGARLCGA LCPFPVPGCA AAQHSALAAP TTLPACRCPP RPRPRCPGRP ICLPPGGSVR 180
 25 LRLCALRRA AGAVRVGLAL EAATAGTPSA SPSPSPPLPP NLPEARAGPA RRARRGTSGR 240
 GSLKFPMPNY QVALFENEPA GTLILQLHAH YTEGEEERV SYMEGLPDE RSRGYFRIDS 300
 ATGAVSTDGV LDRETKEHV LRVKAVDYST PPRSATTYIT VLVKDTNDHS PVFEQSEYRE 360
 RVRENLEVGY EVLTIRASDR DSPINANLRY RVLGGAMVVP QLNESGGSVS TRAVLDREEA 420
 AEYQLLVEAN DQGNRPGLS ATATVYIEVE DENDNYPQFS EQNYVVQVPE DVGLNTAVLR 480
 VQATDRDQGG NAATHYSILS GNVAGQFYIH SLSGILDVIN PLDFEDVQKY SLSIKAQDGG 540
 30 RPPLINSRGV VSVQVLVDND NEPIFVSSFP QATVLENVPL GYPVVHIQAV DADSGENARL 600
 HYRLVDVST FLGGGSAGPK NPAPTDPFPP QIHNSSGMIT VCAELDREEV EHYSFGVEAV 660
 DHGSPPMSSS TSVSITVLDV NDNDPVFTQP TYELRLNEDA AVGSSVLTIQ ARDRDANSVI 720
 TYQLTGGRNR NRPALSSQRG GGLITLALPL DYKQEQYVL AVTASDGTSS HTAHLVINVT 780
 DANTRFPVQ SSHYTVSVSE DRPVGTSIAT LSANEDTGE NARITYVIQD FVPQFRIDPD 840
 35 SGTMYTMEL DYENQVAYTL TIMAQDNGIP QKSDTTTLEI LILDANDNAP QFLWDFYQGS 900
 IFEDAPPSTS ILQVSATDRD SGPNRLLYT PQGGDDGDGD FYIEPTSGVI RTQRRLDREN 960
 VAVYNLWALA VDRGSPPTLS ASVEIQVTIL DINDNAPMFE KDELELFVEE NNFVGSVVAK 1020
 IRANDPDEGP NAQIMYQIVE GDMRHFFQLD LLNGDLRAMV ELDFEVREY VLVVQATSAP 1080
 40 LVSRATVHIL LVQDMNPFV LPDFQILFNN YVTNKSNSFP TGVIGCIAPH DDPVSDSLNY 1140
 TFVQGNELRL LLLDPATGEL QLSRDLNMR PLEALMEVSV SDGHSVTAFL CYLRVTIITD 1200
 DMLTNSITVR LENMSQEKPL SPLLALFVGG VAAVLSTTKD DVPFVNVQND TDVSSNINLV 1260
 TFSALLPGGV RQGFPPSEDL QEQIYLNRTL LTTISTQRLV PPDNLCLE RECPNMYKCVS 1320
 VLRDSSSAPP LSSTTVLFRP IHPINGLCRC CPPGFTGDYC ETEIDLCSYD PCGANGRCRS 1380
 45 REGGYTCBCP EDPFTGCEVF DARSGRANG VCKNGGTCVN LLIGGFHCVC PGEYERPYC 1440
 EVTTRSFPPQ SFVTFRGLRQ RFHFTISLTP ATQERNGLLL YNGRPFNEKH FIALEIVDEQ 1500
 VQLTFSAGET TTTVAPKVPV GVSDDGRWHSV QVQYINKPNI GHLGLPHGFS GEKMAVTVTD 1560
 DCDTMAVRP QGDIGNYSCA AQGTQTGSKK SLDLTGPLLL GGVEPLPEDF FVHNRFVVGK 1620
 MRLNSVDGKH VDMAGFIANN GTREGCAARR NFCDGRRCON GGTGVNRNMM YLCBCPLRFG 1680
 50 GKNCEQAMPH PQLFSGESV SWSDLNIIIS VPMYGLMFR TRKEDSVLME ATBGGPTSFR 1740
 LQILNNYLQF EVSHQPSDVE SVMLSGLRVT DGEWHHLLIE LKNVKEDSEM KHLVTMTLDY 1800
 GMDQNKADIG GMLPGLTVRS VVVGASEDK VSVRRGFRGC MQGVRMGTP TNAVTLNMMN 1860
 ALKVRVKDGV QQFDLAATQD DVPDPCTSSP CPNNSRCHDA WEDYSCVCDK GYLGINCVDA CHLNPCERNM 1920
 ACVRSPGSPQ GYVCECGPSH YGPFYCNKLD LPCPRGWMGN FVCGPCHCAV SKGFPDPCNK 1980
 55 TNGQCCCKEN YKLLAQDTC LPDCCFPHGS HSRTCMMATG QCACKPGVIG RQCNRCDNPF 2040
 AEVTTLCGEV IYNGCPKAFB AGIWWPQTKF GQPAAVPCPK GSVGNAVRHC SGEKGLPPE 2100
 LFNCCTTISFV DLRAMNEKLS RNETQVDGAR ALQLVRALRS ATQHTGTLPF NDVRTAYQLL 2160
 GHVLQHEGSH QQFDLAATQD ADFHEDVIHS GSALLAPATR AAWBQIQRSE GGTAQLLRL 2220
 EGYFSNVARN VRRTYLRFV IVTANMILAV DIFDKFNFTG ARVPRFDITH EEPFRELSS 2280
 VSPFADFFRP PEEKGPLLR PAGRRTTTQT TRPGPOTERE APISRRRRHP DDAGQPAVAL 2340
 60 VIIYRTLQQL LPERYDPDRR SLRLPHRP11 NTPMVSTLVY SEGAPLPRPL ERPLVVEPAL 2400
 LEVEERTKPV CVFNNHSLAV GGTGWSARG CELLSRNRTH VACQCSHTAS FAVLMDISRR 2460
 ENGEVLPK1 VTYAAVLSL AALLVAFVLL SLVRMLRSNL HSIHKLAVA LFLSQLVPVI 2520
 GINQTNPFPL CTVAAILLHY IYMSTFAWTL VESLHVYRML TEVRNIDTGP MRFYVVGWG 2580
 65 IPAIVTGLAV GLDPQGYGNP DFCNLSLQDT LIWSPAGPIG AVIIINTVTS VLSAKVSCQR 2640
 KHHYGGKGI VSLRLTAPLL LLLISATWLL GLAVNRDAL SPHYLFAIPS GLQGPVLLP 2700
 HCVLNQEVRR HLKGLVGGRK LHLEDSATTR ATLLTRSLNC NTTFGQDPM LRTDLGSESTA 2760
 SLDSIVRDEG IQKLGVSGL VRGSHGEPDA SLMPRSCKDP PGHDSDSSE LSLDEQSSSY 2820
 ASSHSSDSED DQVGABEKWD PARGAVHSTP KGDVANHV P AGMPDQSLAE SDEDPSSGK 2880
 70 RLKVTETKVS ELHREEGSH RGEYPPDQES GGAARLASSQ PPEQRKILK NKVTYPPPLT 2940
 LTEQTLKGR LREKLADCEQS PTTSSRTSSLG SGGFDCAITV KSPGREPGRD HLGVMANVR 3000
 TGSQAQDSD SEKP

75 **A33 DNA SEQUENCE**
 Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 Probeset Accession #: X95876
 Nucleic Acid Accession #: X95876
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 CCAACCAAA GCACCAAGC AGAGGGGCG AGAGCACACC ACCAGCAGC CAGAGCACCA 60
 GCCACGCCAT GTCTCTTGAG GTGAGTGACC ACCAAGTGCT AAATGACGCC GAGGTGCGG 120

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CCTCTCTGGA GAACTTCAGC TCTTCTATG ACTATGGAGA AAACGAGAGT GACTCGTGCT 180
GTACCTCCCC GCCCTGCCCA CAGGACTTCA GCCTGAACTT CGACCGGGCC TTCTGCCAG 240
CCTCTACAGC CTCTCTCTTT CTGCTGGGGC TGCTGGGCAA CGGCGCGGTG GCAGCCGTGC 300
TGCTGAGCCG GCGGACAGCC CTGAGCAGCA CCGACACCTT CCTGCTCCAC CTAGCTGTAG 360
CAGACAGCGT GCTGGTGTG AACTGCGCGC TCTGGGCAGT GGACGCTGCC GTCCAGTGGG 420
TCTTTGGCTC TGGCCTCTGC AAAGTGGCAG GTGCCCTCTT CAACATCAAC TTCTAGCCAG 480
GAGCCCTCCT GCTGGCCTGC ATCAGCTTTG ACGCTACCT GAACATAGTT CATGCCACCC 540
AGCTCTACCG CCGGGGGGCC CCGGGCCGCG TGACCTCTAC CTGCTTGCTT GTCTGGGGGC 600
TCTGCTGCTT TTTCGCCCTC CCAGACTTCA TCTTCTGTG GGGCCACCAC GAGGAGCGCC 660
TCAACGCGAC CCACTGCCAA TACAACCTCC CACAGGTGGG CCGCAGCGCT CTGCGGGTGC 720
TGCAGCTGGT GGCTGGCTTT CTGCTGCCCC TGCTGGTCAT GGCTACTGCT TATGCCACCA 780
TCTTGCCCGT GCTGCTGGTT TCCAGGGGCC AGCGGGCCCT GCGGGCCATG CGGCTGGTGG 840
TGGTGGTGGT GGTGGCCTTT GGCCTCTGCT GGACCCCTCA TCACCTGGTG GTGCTGGTGG 900
ACATCCTCAT GTCTTCCCGC GCTTTGGGCC GCAACTGTGG CCGAGAAAGC AGGGTAGAGC 960
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ATGCTCTTGT AGGGGTCAAG TTCCGGGAGC GGATGTGGAT GCTGCTCTTG CGCCTGGGCT 1080
GCCCCAACCA GAGAGGGCTC CAGAGGCAGC CATCGTCTTC CCGCGGGATG TCATCCTGGT 1140
CTGAGACCTC AGAGGCTTCC TACTCGGGCT TGTGAGGCGG GAATCCGGGC TCCCTTTTGG 1200
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CAGCCGAGCC CTCCAGCTCA GCAGTGACTG TGGCCATGCT CCGCAAGACC TCTATATTG 1560
CTCTTTTATT TTATGTCTA AATCTCTGCT TAAACTTTT CAATAACAA GATCGTCAGG 1620
ACCAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA BHCLITERAT 1680
UREBHCBLAS TPEHCORTHO LOGUESMOUS ECKRMYLEV SERQVLDASD PAFLENST 1740
PYDGENESD FSDSPPCPD FSLNFDRTFL PALYSLFLFL GLLGNVAVAA VLLSQRTALS 1800
STDFTLLHLA VADVLLVLT PLWAVDAAVQ WVFGPLCKV AGALFNINFY AGAPLLACIS 1860
FDRYLSTVHA TQYLRDPRV RVALTCIVVW GLCLLPALED FYLSANYDQ RLNATHCQYN 1920
FPQVGRALR VLQLVAGPLL PLLVMAYCYA HILAVLLVSR GQRRFRFAMRL VVVVAAFAV 1980
CWTFPHLVVL VDILMDVGLV ARNCGRESHV DVAKSVTSGM GYMHCCLNPL LYAPVGVKFR 2040
EQMWMLPTRL GRSDQRPQR QPSSSRRESS WSETTEASYL GL

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A34 Protein sequence

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 Protein Accession #: P49682
 Signal sequence: none found
 Pfam domains: 7tm_1 [70-318]
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323
 DRY box: 148-149
 Cellular Localization: plasma membrane

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55

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1 11 21 31 41 51
| | | | |
MVLEVS DHQV LNDAEVAALL ENFSSSYDYG ENESDSCCTS PPCQDPFSLN PDRAFLPALY 60
SLFLPLGLLG NGAAVAALLS RRTALSTDT FLHLAVADT LLVLTLPWA VDAAVQWVFG 120
SGLCKVAGAL FNINFYAGAL LLACISFDYR LNVHATQLY RRGFPARVTL TCLAVWGLCL 180
LFALPDFIFL SAHDERLINA THQYNYFPQV GRTALRVLQL VAGFLPLPLV MAYCYAHILA 240
VLLVSRGQRR LRAMLVVVV VVAFALCWTP YHLVVLVDIL MDLGLARNC GRBSRVDAK 300
SVTSLGLVMH CCLNPLLYAF VGVKFRERMW MLLRLGCFN QRGLQRPSS SRDSSWSET 360
SEASYSGL

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A35 DNA SEQUENCE

Gene name: Differentially expressed CO16 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541 (start and stop codons are underlined)

65
70
75
80

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1 11 21 31 41 51
| | | | |
GGGGGCGCGC CGCGCTGACC CTCCCTGGGC ACCGCTGGGG ACAGTGGGCG TGCTGCCTT 60
GCTGCTGTGC GTGGCCCTAC CGCGGGTGTG GACAGACGCC AACCTGACTG CGAGACAAAG 120
AGATCCAGAG GACTCCAGC GAACGGACGA GGGTGACAAT AGAGTGTGGT GTCATGTTTG 180
TGAGAGAGAA AACACTTTGC AGTGCCAGAA CCGAAGGAGG TGCAAAATGGA CAGAGCCATA 240
CTGCGTTATA GCGGCGGTGA AAATATTTC ACCTTTTTC ATGGTTGCGA AGCAGTGCTC 300
CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGGTTTC TCCTGGAAGA 360
GCCCATGCCC TTCTTTTACC TCAAGTGTG TAAATTCGCT TACTGCAATT TAGAGGGGCC 420
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GCTGTGGCTG GCCATCTCC TGCTGCTGGC CTCCATTGCA GCCGGCTCA GCCTGTCTTG 540
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GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGCACTGG GGCACACGTT 1020
AGGGCTGCC CCATTCCAGT GGTGGAGGCG CTGTGGATGG CTGCTTTTCC TCAACCTTTC 1080

```

5 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTGTG AAGAAACTTA GACTTCACCC 1140
 ACCAGCTGGC ACAGGTGCAC AGATTTCATAA ATTCOCACAC GTGTGTGTTC AACATCTGAA 1200
 ACTTAGAGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAACAAT ACAAGGGGAC 1320
 TTCAAAGTT CACGAAAAA AAAAAAATA AAAAAAATA AAAAAAATA AAA

10 A36 Protein sequence:
 Gene name: Differentially expressed CO16 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Protein Accession #: AAH01291
 Signal sequence: 1-17 (first underlined sequence)
 Transmembrane domain: 146 - 162
 Cellular localization: plasma membrane

20 1 11 21 31 41 51
 MALLALLLVV ALPRVWTDAN LTARQRPED SQRTDEGDNR VWCHVCEREN TPECQNPRRC 60
 KWTEPYCVIA AVKIFPPFFM VAKQCSAGCA AMERPKPEEK RFLLEEFMPF FYLKCKKIRY 120
 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASTAA GLSLLS

25 A37 DNA SEQUENCE
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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 35 AGCAACGACG CGGGGACGG GGAGCGGCGG CCGCGCCATG TGGCTGCTGG GGCGCTGTG 60
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 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCAATCCCG GCGCCTGGCA 180
 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTCGAAATGT GGCCCAACCT TCTTCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTCG 300
 CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 40 AAACCCCTCG CTTTGCTCCA CGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
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 AAGTTCTCAA GAACCCGCA GTGGGACAGT GTTTGTGACT TCAGAGAACC AACTGTGTGA 540
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 45 CCTGCTGGCA CTGGTCTTGC ACCACCAAGC GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
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 50 CGACCTGCCC CCTTACGCTC CCGGTCGCG GAGTGCCAAC AGTGCCAGCT CCGAGGCAGC 960
 CAGCAGCTCT CTGAGCGTGG AAGACACCA CACAGCCCG GGGCAGCCCTG GCGCCACGGA 1020
 GGGCACTGCT GAGCCACGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCAATTC TAACAATTG 1140
 TGCTGAGTGG AAGCTCTTTA AGCACTGTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 55 AACTATCTCT GCATTCCCTC CTTCCCCAGC ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
 TGACATGATC TGTGTGTGCT CTTTCTGTC AGTCACTCT TCCCTTGGGA CCGAGATCA 1320
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 60 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCC CAAAAAATT CCATTGAGC 1560
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 65 GAGCCCCCTC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860
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 ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAGATC TGACCTGGCT 1980
 GTATGTCCCT GTGGCCACCA CCCAGCCTGT CTGTCTCATT CATGCAGCCT CAACACTGGC 2040
 70 CTCAAAAGTT CCGTTAACAC TTGCAAGTTC CTTTTACCT GTGCATTGGG ACTTGAGGAC 2100
 ACTGTTTCT ATCAGAGTGG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCTTGCTCC 2160
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 GGTCAGGGTC AGGCTCTTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 AGACAATTGT GAGTCAAGAT TTTCATTGTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 TGAACAAGTG TGTGTGTTT TTCCCTTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400
 75 AGCTGTCTCT TTTTGTGTT TTCCCTTAA AAGGTCCAAA GAAAGATGCA AAGGAGATC 2460
 ACACCTTGC CCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 ACATTGTGTC ATTGTGAC TTTGAGGTTA TTATTATCA AGTTCGTGAA GGAAGCAGAA 2580
 AGAGGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
 80 TTCTCTGTG CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACTGT 2700
 AGGTGTTGTT TGGCAGAAA CCACTGAC TGATGAGGGG TAAATGGGAA CCAGGTAGAG 2760
 CCACTCCGGG CAGCTGTAC CCATTAGAA CTCTTTTCCG CAGCTGAAGA AATGTTCACT 2820
 AACCTGTTTG ACGCTAATTA AACAGAGGCC TGCAAGAGT GGGCTAAAG TGGCATTGAG 2880
 TGATCTGTT CTGTAGACTT TTCTTCTTT TTTTAAACAA ATCCAAGGA TGTTCAGAA 2940
 AAGCTAGCCA CTGTTATTT GTTTGTTTA AAAAAAATA GAAAGAAAGA AAGAAAGAAA 3000

AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAGAA CTTTGTGATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTCACTC CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180
 TTTCTGTGTC TCTGGAAGTT GTTTAGAGGA AAGAAATCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCACTCTAG GAAACACAA TGGTTTATAGT 3300
 AGATAAGGGA TGCCCTACTAA TGCTTTTITA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGAITTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTTCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTA GCATTAAATT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGGTTGT GTGTGCTGTC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 TTATACITTC TAATAAATTT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GNMCTAMARM 3840
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGGG GGGCCACGT AGGTACGGCG ACCACGGCGG CCCAAACGGG ACCCCAGAAAG 3960
 GAAACCCCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCCCGGG 4020
 GGAAACCGCA GAGTGTGGCG TAAACCAAC CCGAAGAGAG AACTCAGAA CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A38 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNNG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGFTFFPCAS GIHCLIGRPR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNLGCIIDKSF ICDGQNNCQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPFPYSS DTESINQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PQQPGPQSGT AEPRDSEPSQ GTEBY

A39 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCTGTCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAAGAAAC TTCGTGCGA GGCTTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCGAG 120
 GACCGGGAGA GGGAGAGCGG GCGGAGGCT GCGGGGCTCC TGTGGGACCG CGCTGCGAGC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
 CCGCGGCGCG CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC CAGGACCCCT 300
 CGCTGCGCTC CTGACAGTTC CCGGGGAGG GTCCGCTTGC CAGTGAACCC TCCAGAGGCT 360
 TCCGAGCAGC AGCCCCGGG GCCCTCTGAC TGCACTCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACCGGGA TGGCTTAGGA 480
 GCTCCTGGAC CTAGGGCCCG GCGTCTGCGC CTCTGCGCG TCGCGGAGA GGGGAGTGCG 540
 CCGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCC GGGGTCGCG GGGGCCACGA 600
 CTCTCTCGAG ACGTCTCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGCTGCCA 660
 TGTGGGCGCG TCGCGCTCG TCCGTCTCCT CATCTTGAA CGCGCTTCC CTCTGCGAGC 720
 TGCTGCTGCG TCGCGCTCG GCGGCGGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGGC 780
 TGGCTGGAAG CGCAGGCGGT CTGGGCGATC GGCCTCCAGT GTCCGAGCG CTTGAGCGGC 840
 GCGGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTCGG ACCAGGGCGG CTGCGACAT GACCGCCAGC AGGCGCTCG GAGGCTGCG 960
 GGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGCTTAG GGGTACCCAA 1020
 GGAGACGGGG AGGTGCGGCC CCCACCGTGG AGGGCTTGGC AGCGGTGCTC CCTGAAGGC 1080
 TCCCGGAAAG GAAGGCGAGT CCTCAGGCTT TTCCCGGGGC TGCTGCCCGC TCCGAGAGCG 1140
 CGCGGATTCC CATCTCTTCC ACGCGGCGGC CCTCTCCCC TGCAGCGGCC CGCCTTGCCC 1200
 ATCTAGCTGC CGTTCCTCAT TGTGGCTCC GTGTTGTGCG CCTTTATCAT CTTGGGGTCC 1260
 CTGTTGGCAG CCTGTTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCA GCAGAGCCGA 1320
 GCGGAGGGGG GTAAACGCTT GATGGAGAAC ATCCCATGTA TCCCATGTGC CAGCACTTCC 1380
 CGGGGGTCTT CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG GCGCACTCC 1440
 GGGGCGCGGG CGCCCCAAC AAGGTACAG ACCAACTGTT GCTTGCAGGA AGGGACCATG 1500
 AACAACTGT ATGTCAACAT GCCCAAGAA TTCTCTGTGC TGAACGTGCA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAATATCTG CATCCCCAT ACGTGGGGA CACGGTGAC 1620
 CAGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCTGCGTAC 1680
 AGGCAGATTG AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 ACTGTATAAC CAGAGTCTAC TGGTGGGTTC CTTTACTGAA GCGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAGTCC GCACATGTCC GTGGTATTTA TGGCAGGATT CCTTTGGATG 1860
 GCTTCATTG CCCCCAGACT GTATGAAAA ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGAT ATCATGTATT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 TTGCTGATGG GTGTATTAACA AATGCTTAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100

5 TTGTTGTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTT 2160
 TTTTITTTT TTTTITTTT TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGGGATC TGGGCTCACT GCAACTTCAG CCTCTGQAT TCAGGCAACA CTCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCAT GGCTAATTTT TTGTATTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGTGCTCTC ACTCTCTGA CCTCAAGCAA 2400
 TCTGCTGTC TCAGCTCCC AAGTGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCTTTT TTTTCTTA ATGCATCCAA GGTAAAGGG AAGACGCAA TAACAGGACT 2520
 ATTCTAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATCCACA 2580
 10 GGCACACCTT AATTTCAITG TAAAAAGATA TATATATTT GTCTATTTT GTGCTTTTG 2640
 GGGCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTCA 2700
 TTAAGAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCTTC 2820
 TTGATTGAT CTAAATTTT TGGCTTAAAG GTGACATCTG AGAGGTAATG CATCTTTT 2880
 15 TATATTGAAA TCATAAACTA TCACCGCTG CTTCTGAG TTACTTTTAA TTTTGCTTG 2940
 TGGTATGGT TTGGCTTTC CTTCTGTTG GTTTCAGAG CCCCATGCT ATATAGTCT 3000
 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCTA GATCTGATA 3060
 AAAAAATTT TGTCTTAGT TATAAAAT CAAAGAAATG TGTACAAAG ATACTAGTA 3120
 TAGCTCTCA GCCATAACT GAGACTGGG ATGAAATTA AACAGATAC GATTACTTT 3180
 20 GCAGATCA AGGCTTTT TACTCTGTT ATCAAAATG CTTATTTT AGGCACTAAG 3240
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCTTT CTTCTCCAC ACTGTTCTG 3300
 ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCAATGT TCCAAATTA 3360
 CAAATTCAG TGAATTTT TGTGTTCT TACTTATAT AAAAAAGAT AACTTAAAG 3420
 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTAT TTGTAATTA ACAAATCGCT 3480
 25 GTATGGTATG GTCTTCTACA CATTATGTC TATAGATAT TATCGATCAT CTTTCTATT 3540
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660
 TGAATAATA AAAAAAATA AAAAAAATA

30 **A40 Protein sequence**
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 35 Transmembrane domains: 402-424
 Cellular localization: not determined

40 1 11 21 31 41 51
 | | | | |
 MLSGFLMSPS TQHRAYTPG GKLPWEASI GAHSTRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEKGNRGE PPAWIRAOQQ PRPPAGQAP GTAAGGAQDP RLRPRGRGR VRLEVPKPEA 120
 SGRQPRGSPD CIPRFPASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAEBSG 180
 45 PRGRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVV CGALAAPSP HPGTPLRSCS 240
 CCKLRCWRRG RGPSEGYCHG WLDAQGVWRI GFQCPERFDG GDATICCGSG ALRYCCSSAE 300
 ARLDQGGDDN DRQGGAGEPG RADKDGPRRL GRASCLRGQT GDGEGAPPPV RAWQRCSPEG 360
 SPKGQLLRA FPGLLPRARR RGFSSPRGG PSPLQRPALP IYVFLIVGS VFVAFIILGS 420
 LVAAACCCRL RPKQDPQSR APGGNRLMET IPMIPSASTS RGSSSRQSSST AASSSSSANS 480
 50 GARAPPTRSQ TNCCLEPGTM NNVIWNMPIT FSVLNCQQAT QIVPHGQGYL HPPVVGTVYQ 540
 HDSVPMTAVP PFMDQLQPGY RQIQSPFPHT NSEQKMPAV TV

A41 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 55 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGCTC CTGCTCTTA CTGTCACAG TTTCTTCAA CCTTGCCATT 120
 65 GCAATAAAAA AGGAAAAGAG GCCTCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 ATGGTTATTC ATCACTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
 CAAAATGAAG AATAACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAAATT ATCACTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
 70 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCTTC GGGATTATCC CCTATTGATA GAAACATGA AGAAGCATT AAGACTTATT 540
 CAGTCAGAGC TATAGAGAT GATAGAAAA AGCCTTCACT TCAAGAAAGT CAAATTTTAT 600
 GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
 75 TACTATTATA GTTTTAAATA TGTGTTGCA ATAGTCTTAT TAAATAAAT GTTTTAAATA 720
 TCTGAAAAA AAAAAAATA AAAAAAATA

A42 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 80 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

5
1 11 21 31 41 51
MMLHSALGLC LLLVTVSSNL AIAIRKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
PLMVIHLED CQYSQALKKV PAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120
FVDPSTLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
Probeset Accession #: NS1919
Nucleic Acid Accession #: AF189723
15 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
ATGATTCTCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
TCTCAGTTTA AAAATCCOCT TATTATGCTG CTCTGGCTT CTGCAGTCAT CAGTGTTTTA 240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCCT TGTACAGTT 300
25 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
CCAGAAATGCC ATTGTGTGCG TGAAGGAAAA TTGAGGCATA CACTTGCCCG AGACTTGGTT 420
CCAGGTGAGT CAGTTTGCCT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTC 480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540
AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
30 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTTCAT TGGAACAGGA 660
GAAAAATCTG AATTGGGGGA GGTTTTAAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTACTC CTTTGGTATA 780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840
ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCOCCTATGT GGTCACAGTG 900
35 ACGCTAGCTC TTGGTGTATG GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
ATTGTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGAG AACACTGAGC 1020
AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTACT 1080
GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTTGTTGATG GTGATGTTGT TCATGGATT 1140
TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
40 AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAA CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAAGTGTGA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTATGA AAGGTGCTTA CGAACAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGCAGACTC TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500
45 ATGGGCTCAG CGGACTCAG AGTTCCTGCT TTGGCTTCTG GTCCTGAACT GGGCAGCTG 1560
ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACAACACTCA TTGCCCTCAG AGTATCAATA AAAATGATTA CTGGAGATT CAGGAGACT 1680
GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCACAAA CTCCCAATC AGTCTCAGGA 1740
GAAGAAATAG ATGCAATGGA TGTTGAGCAG CTTCACAAA TAGTACCAA GGTTCAGTA 1800
50 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGTACA GAAGAACGGT 1860
TCAGTTGTAG CCATGACAGG AGATGGAATA AATGATGAGC TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
CTAGTGGATG ATGATTTTCA AACCAATATG TCTGCAATCG AAGAGGGTAA AGGGATTTAT 2040
AATAACATTA AAAATTCTGT TAGATTCCAG CTGAGCAGCA GTATAGCAGC ATTAACTTTA 2100
55 ATCTCATTTG CTACATTAAT GAACCTTCTT AATCTCTCTA ATGCCATGCA GATTTTGTGG 2160
ATCAATATTA TTATGGATGG ACCCCAGCTC CAGAGCCTTG GAGTGAAGAC AGTGATATAA 2220
GATGTCTATC TGAACCTTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTTGATA 2280
CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTCTGGCGGT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACACAA TGACCTTCAC ATGCTTTGTG 2400
60 TTTTGTGACA TGTTCAATGC ACTAAGTCC AGATCCAGCA CCAAGTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAAT GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGCACAATTA 2520
CTAGTTATTT ACTTTCCTCC GCTTCAGAAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTGTG TTTCTTGGG TCTCACTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
65 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
CTTGAAGTAT GA

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
Unigene number: Hs.106778
70 Probeset Accession #: NS1919
Protein Accession #: AAF27813
Signal sequence: none found
Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
75 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
Cellular Localization: not determined

80 1 11 21 31 41 51
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNSEFDIS EDEPLWKYI 60
SQFKNPLIM LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQBYRSEK SLEELSKLVP 120
PECHVREBK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSIDES SLTGETTPCS 180
KVTAQPPAAT NGDLASRSNI AFMGLTVRCG KAKGVVIGTG ENSBPGVEPK MQQABEAPKT 240
PLQKSNMDDLK QLSFPYSFGI IGIIMLVGWL LGKDILEMPT ISVBLAVALI PEGLPVIVTV 300

5	TLALGVMRMV	KIRAIVKKLP	IVETLGCCNV	ICSDKTGTLT	RNEMIVTHIP	TSDGLHAEVT	360
	GVGYNQFGEV	IVDGDVVHGF	YNPAVSRIE	AGCVCNDAVI	RNNTLMGKPT	EGALIALAMK	420
	MGLDGLQQDY	IRKAEYFFSS	EQKMWAVKCV	HRTQODRPEI	CFMKGAYEQV	IKYCTTYQSK	480
	GQTLTLTQQQ	RDVVQEKAR	MGSAGLRVLA	LASGPELGQL	TPLGLVGIID	PPRTGVKEAV	540
	TTLASGVSI	RMITGDSQET	AVAIASRLGL	YSKTSQSVSG	EEIDAMDVQQ	LSQIVPKVAV	600
	FYRASPRHKM	KIIKSLQKNG	SVVAMTGDGV	NDAVALKAAD	IGVAMGQTGT	DVCKEADMI	660
	LVDDDPQTIM	SAIEEGKGIY	NNIKMFVRFO	LSTSI AALT	ISLATLMNPP	NPLNAMQILW	720
	INIIMDGPPA	QSLGVEFVDK	DVIRKPPRNW	KDSILTKWLI	LKILVSSIII	VOGTLFVFWR	780
10	ELRDNVITPR	DTMTPTPCPV	PFDMFNALSS	RSQTKSVFEI	GLCSNRMFCY	AVLGSIMQQL	840
	LVIYFPPLQK	VFOQSSLSIL	DLFLFLGLTS	SVCIVABIIK	KVERSREKIQ	XHVSSTSSSF	900
	LEV						

A45 DNA sequence

15	Gene name:	ESTs
	Unigene number:	Hs.157601
	Probeset Accession #:	W07459
	Nucleic Acid Accession #:	AC005383
20	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGGTAGAAAG	TGAAGTACTT	60
25	TTTATTTCG	AGACCTGGGC	CGATGCCGCT	TTAAAAAAGC	CGAGGGGCTC	TATGCACCTC	120
	CTCTGGCGTA	GTTCCTCCGA	CCTCAGCCGG	GTCCGGTCTG	GCCGCCCTCT	CCCAGGAGAG	180
	ACAAACAGGT	GTCCACGCTG	GCAGCCGCGC	CCCGGGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TOGCGCTCT	CCTTCCGTTA	TATCAACATG	CCCCCTTTC	TGTTGTCTGA	GGCGCTCTGT	360
30	GTTCCTCTGT	TTTTCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
	GAAACCATCG	GGAAGATTTC	AGCTGCCAGC	AAAATGATGT	GGTCTCGGCG	TGCAGTGGAC	480
	ATCATGTTC	TGTTAGATGG	GTCTAACAGC	GTCCGGAAAG	GGAGCTTTGA	AAGGTCCAAG	540
	CACCTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCCAGT	TCAGTTCCAC	TCCTTCATCT	GAATTCCTCT	TGGATTCAAT	TTCAACCCAA	660
35	CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTCCTCAAG	GAGGGGCGAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCTGGAG	GCAGAAATGC	TTCTGTGCCC	780
	CAGATCCTCA	TCATGTCAC	TGATGGGAAG	TCCAGGGGG	ATGTGGCACT	GCCATCCAAG	840
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGG	TCAGGTTCCT	CAGGTGGGAG	900
	GAGCTGCATG	CACCTGGCAG	CGAGCCTAGA	GGGCAGCAGC	TGCTGTGGCG	TGAGCAGGTG	960
40	GAGGATGCCA	CCAAAGGCTT	CTTCAGCACC	CTCAGCAGCT	CGGCCATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAGGGTCCA	GGCTCACCCC	TGTGAGCACA	GGAGCGTGGG	GATGCTCCGG	1080
	GAGTTGCTCG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGCG	GGACCTTTGC	GGTGCTGGCT	1140
	GCACACTGTC	CCTTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCACTCTGC	CACCTGCTAC	1200
	AGGACCACCT	GCCAGGCCCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
45	CAGAAAGTGA	TGCAAGGCTA	CCAGTGCCTC	TGCCCGCTGG	CCTTTGGAGG	GGAGGCTAAC	1320
	TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	GTCCAGCTCC	TCTTCCTGCT	GGACAGCTCT	1380
	GCGGGCACCA	CTCTGAGCGG	CTTCTGCGG	GCCAAAGTCT	TOGTGAAGCG	GTTCGTGGCG	1440
	GCCGTGCTGA	GCAGGAGACT	TCGGGGCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
	CTGGTGGCGG	TGCTGTGGGG	GGAGTACCAG	GATGTGCTCG	ACCTGTGCTG	GAGCCTCGAT	1560
50	GGCATTCCTT	TCCGTGGTGG	CCCCACCTCG	ACGGGCAAGT	CCTTGCGGCA	GGCGGCAGAG	1620
	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTTG	1680
	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GCGGGCCGAG	CGGTGACGCG	AAGGGCGCGA	1740
	GAGCTGCTCC	TGCTGGGTGT	AGGCAGTGAG	GCCGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGCCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
55	GAGCTGCAGG	GGAAGCTGTG	CAGCCGCGAG	CGGCCAGGGT	GCCGACACCA	AGCCCTGGAC	1920
	CTCGTCTTCA	TGTTGGACAC	CTCTGCCTCA	GTAGGGCCCG	AGAAATTTGC	TCAGATGCAG	1980
	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGACGTGAC	ACAGGTCCGC	2040
	CTGGTGGTGT	ATGCGAGCCA	GGTGAGACT	GCCTTGGGCG	TGGACACCAA	ACCCACCCGG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
60	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGGCTTGTT	2220
	GTCCCCAAAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGGCG	CAGAGGATGC	AGCCGTTCCT	2280
	GCCCAAGAGC	TGAGGAACCA	TGGCATCTCT	GTCTTGGTGC	TGGGCGTGGG	GCCTGTCTTA	2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGATTTCCC	TGATCCAGGT	GGCAGCTTAC	2400
	GCCGACCTGC	GGTACCACCA	GGACGCTGTC	ATTGAGTGGC	TGTGTGGAGA	AGCCAAAGCA	2460
65	CCAGTCAACC	TCTGCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGCGT	CTGCAGAAAT	2520
	GGGAGCTACC	GCTGCAAGTG	TGGGATGGC	TGGAGGGGCC	CCCAGTGGCA	GAACCGTGAG	2580
	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTG	TTGAGAGGCC	CCTGAGGCAC	2640
	ATGGCTCCCG	TGCAGGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAAGGCCCTG	2700
	GGCACTGAAA	TGGTGCCTAC	CTTCTGGAAT	GTCTGTGCC	CAGGTCTCTA	GAATGTCTGC	2760
70	TTCCCGCCGT	GGCCAGGACC	ACTATTTCTA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCACCCACA	AACTATGTTG	TTGAAAAGTT	2880
	TTGATGTGTA	AGTAATAATC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTCTAT	2940
	CTGCCACCTT	TCCCTTGAGG	ATAAACAAAG	GGTCTGGAAG	ACTTAAATTT	AGCGGCTGTA	3000
	CGTCCCTTTG	CACACAATCA	ATGCTGCCCA	GAATGTTGTT	GACACAGTAA	TGCCAGCAG	3060
75	AGGCTTTTAC	TAGAGCATCC	TTTGGACGGC	GAAGGCCACG	GCCTTTCAAG	ATGGAAGACA	3120
	GCAGCTTTTC	CACCTCCCCA	GAGACATCTC	GGATGCATTT	GCAATGAGTC	TGAAAGGGGG	3180
	CTTGAGGGAC	GTGTTGTAAT	TCTTGGGAGC	TGCCCTTTGT	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT	3300
80	TGTGCTAGGG	CCGAGGTCTG	GAGGGCCACG	TAAATTCGTT	CTGAGTCTGT	AGCAGTGTCC	3360
	ACCTTGAAGG	TCTTC					

A46 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

10 1 11 21 31 41 51
 | | | | |
 MPPFLLEAV CVFLFSRVPP SLPLQSEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVGKGSFERS KHPAIVTCDG LDISPERVRV GAFQFSSTPH LEFPLDSPST QQEVKARIKR 120
 15 MVFKGGRTST ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKRGVTV 180
 PAVGVRRPWR EELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEW REFAGNAPCW RGSRRTLAVL AHCPCFYSWK RVFLTHPATC YRTTCGPGCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGSEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 RAKVFKRVF RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPLVNSL DGIPPRGGPT 420
 20 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVS 480
 EAVRALEEI TGSFKHVMVY SDPDLFNQI PELQGLCSR QRPQCRTQAL DLVPMLDISA 540
 SVGPENFAQM QSFVRSCALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVGA GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLRRNGI 660
 SVLVVGVGPV LSEGLRRLAG PRDSLIHVA YADLRHYQDV LIEWLCEGAK QPVNLCKPSP 720
 25 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETFLR HMAFVQEGSS 780
 RTPPSNYRES LGTEMVPTFW NVCAFGP

COLON

30 A47 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 35 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 | | | | |
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGTCACAG TTTCTTCCA CCTTGCCATT 120
 GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAGGCCATTA 240
 45 ATGTTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGGC 300
 CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420
 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTTAACAG ATTGTACACA 480
 TATGAGCTC GGGATTTACC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
 50 CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAGAAAGT CAAATTTCAT 600
 GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
 TTACTATTTA GTTTTITTA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTITAAA 720
 TCTGAAAAA AAAAAAAAAA AAAAAAAAAA

55 A48 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 60 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

65 1 11 21 31 41 51
 | | | | |
 MMLHSALGLC LLLVTSSNL AIAIKKEKRP PQLSRGNGD DITWQTYEE GLFYAQKSKK 60
 PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETDKNLS PDQYVPRIM 120
 70 FVDPSLTVRA DIAGRYNRL YTYEPRDLPL LIENMKKALR LIQSEL

A49 DNA SEQUENCE

75 Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 Probeset Accession #: AA478599
 Nucleic Acid Accession #: NM_005682
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 | | | | |
 CGGCAGCAGG GTCTCGCTCT GTCACACAGG CTGGAGTGCA GTGGTGATG CTTGGCTCAT 60
 CGTAACCTCC ACCTCCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120
 ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTGGGAGGA AAATGACTCC CCAGTCGCTG 180

5 CTGCAGACGA CACTGTTCTT GCTGAGTCTG CTCTTCTGG TCCAAGGTGC CCACGGCAGG 240
 GGCCACAGGG AAGACTTTTG CTCTGTCAGC CAGCGGAACC AGACACACAG GAGCAGCCTC 300
 CACTACAAAC CCACACACAGA CTTGCGCATC TCCATCGAGA ACTCCGAGAA GGCCCTCACA 360
 GTCCATGCCC CTTTCCCTGC AGCCCAACCT GCTTCCCGAT CCTTCCCTGA CCCAGGGGGC 420
 CTCTACCACT TCTGCTCTTA CTGGAACCGA CATGCTGGGA GATTACATCT TCTCTATGGC 480
 AAGCGTGACT TCTTGCTGAG TGACAAAGCC TTAGCCTCC TCTGCTTCCA GCACCAAGGAG 540
 GAGAGCCGTG CTCAGGGGCC CCGCTGTGTA GCCACTTCTG TCACCTCCCTG GTGGAGCCCT 600
 CAGAACATCA GCCTGCCAGG TGCCGCCAGC TTCACTTCTT CCTTCCACAG TCCTCCCCAC 660
 10 ACGGCCGCTC ACAAATGCCTC GGTGGACATG TGGAGCTCA AAAGGGACCT CCAGCTGCTC 720
 AGCCAGTTCC TGAAGCATCC CCAGAAGGCC TCAAGGAGGC CCTCGGCTGC CCCCJCACAG 780
 CAGCAGTTGC AGAGCCTGGA GTCGAAACTG ACCTCTGTGA GATTTCATGGG GGACATGGTG 840
 TCCTTCGAGG AGGACCGGAT CAACGCCACG GTATGGAAGC TCCAGCCAC AGCCGCGCTC 900
 CAGGACCTGC ACATCCATCT CCGGCGAGAG GAGGAGCAGA GCGAGATCAT GGAGTACTCG 960
 GTGCTGCTGC CTCGAACACT CTTCAGAGG ACGAAAGGCC GGAGCGGGGA GGCTGAGAAG 1020
 15 AGACTCCCTC TGGTGGACTT CAGCAGCCAA GCCCTGTTC AGGACAAGAA TTCCAGCCAA 1080
 GTCTCTGGTG AGAAGGTCTT GGGGATTGTG GTACAGAACA CCAAGTAGC CAACCTCAG 1140
 GAGCCCGTGG TGCTCACTTT CCAGCACCAG CTACAGCCGA AGAATGTGAC TCTGCAATGT 1200
 GTGTTCGTGG TTGAAGACCC CACATTGAGC AGCCCGGGGC ATTGGAGCAG TGCTGGGTGT 1260
 GAGACCGTCA GGAGAGAAAC CCAAACATCC TGCTTCTGCA ACCACTTGAC TACTTTTGCA 1320
 20 GTGCTGATGG TCTCTCGGT GGAGGTGGAC GCGGTGCACA AGCACTACCT GAGCCTCCTC 1380
 TCCTACGTGG GCTGTGCTGT CTCTGCCCTG GCGTGCCTTG TCACCATTCG CGCTACCTC 1440
 TGCTCCAGGG AGCCCTGCGG GTGCAGGAGG AAACCTCGGG ACTACACCAT CAAGGTGCAC 1500
 ATGAACCTGC TGCTGGCGGT CTCTCTGTCT GACACGAGCT TCCTGCTCAG CGAGCGGGTG 1560
 25 GCCCTGACAG CCGCTGAGGC TGGCTGCGGA GCGAGTGCCA TCTTCTGCA CTTCTCCCTG 1620
 CTCACCTGCC TTCTCTGGAT GGGCCTCGAG GGGTACAACC TCTACCGACT CGTGGTGGAG 1680
 GTCTTTGGCA CCTATGTCCC TGGCTACCTA CTCAAGCTGA GCGCCATGGG CTGGGGCTTC 1740
 CCCATCTTTC TGGTGAAGCT GGTGGCCCTG GTGGATGTGG ACAAATATGG CCCCATCATC 1800
 TTGGCTGTGC ATAGGACTCC AGAGGGCGTC ATCTACCTCT CCATGTGCTG GATCCGGGAC 1860
 30 TCCCTGGTCA GAGTGAATCA CAACCTGGGC CTCTTCAGCC TGGTGTCTT GTTCAACATG 1920
 GCCATGCTAG CCAACATGGT GGTGCAGATC CTGCGGCTGC GCGCCACAC CCAAAAGTGG 1980
 TCACATGTGC TGACACTGCT GGGCCTCAGC CTGGTCTTTC GCGTGCCTTG GGCCTTGATC 2040
 TTCTTCTCTT TTGCTTCTG CACCTTCCAG CTGTGCTGCC TCTACCTTT CAGCATCATC 2100
 AACTCCTTCC AAGGCTTCTT CATCTTCATC TGGTACTGGT CCATGCGGCT GCAGCGCCGG 2160
 35 GGTGGCCCTT CCGCTCTGAA GAGCAACTCA GACTGCGCCA GCGTCCCAT CAGCTCGGGC 2220
 AGCACTCTGT CCAGCGCAT CTAGGCCTCC AGCCACCTG CCCATGTGAT GAAGCAGAGA 2280
 TCGCGCCTCG TCGCACATG CCGTGTGCCC CCGAGCCAGG CCCAGCCCCA GGCCAGTCAG 2340
 CCGCAGACTT TGGAAAGGCC AACGACCATG GAGAGATGGG CCGTGGCAT GGTGGACGGA 2400
 CTCCCGGGGC TGGGCTTTT GAATGGCCTT TGGGACTAC TCGGCTCTCA CTCAGCTCCC 2460
 40 ACGGCACTCA GAAGTGGGCC GCGATGCTGC CTAGGGTACT GTCCCCACAT CTGTCCCAAC 2520
 CCAGCTGGAG GCCTGCTCTC TCCTTACAAC CCCTGGGCCC AGCCTCATTG CTGGGGGCA 2580
 GGCCTTGGAT CTTGAGGCTC TGGCACATCC TTAATCTGT GCCCTGCTT GGGACAGAAA 2640
 TGTGCTCCA GTTGTCTCTG CTCTGTGCT CACCTGAGG GCACTCTGCA TCCTCTGTCA 2700
 45 TTTAACTCT AGGTGGCACC CAGGGCGAAT GGGGCCCAGG GCAGACCTTC AGGGCCAGAG 2760
 CCTGTGCGGA GGAGAGGCC TTTGCCAGGA GCACAGCAGC AGCTCGCTTA CCTCTGAGCC 2820
 G

A50 Protein sequence

50 Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 Protein Accession #: NM_005682.1
 Signal sequence: 1-26
 GPS domain: 342-394
 Pfam domain: 7tm_2[400-665]
 55 Transmembrane domains: 410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
 Cellular Localization: plasma membrane

60 1 11 21 31 41 51
 MTPQSLQTT LFLSLFLV QGAHGRGHRE DFRPCSQRNQ THRSSLHYKP TPDLRISIEN 60
 SEALTIVHAP FPAAHFASRS FPDPRGLYHF CLYWNRHAGR LHLLYGRDFF LLSKASSLL 120
 CFQHQERSLA QGPPLATSV TSWWSPONIS LPSAASFTFS FHSPPHTAAH NASVDMCELK 180
 65 RDLQLLSQFL KHPQKASRRP SAAPASQQLQ SLESKLTSVR FMGDMVSFEE DRINATVWKL 240
 QPTAGLQDLH IHSRQEEBQS HIMEYSVLLP RTLPORTKGR SGAEKRLILL VDFSSQALPQ 300
 DKNSSQVLGE KVLGIWVQNT KVANLTFPVV LTFQHQLPK NVTLCQVFNV EDPTLSPGH 360
 WSSAGCETVR RETQTSFCN HLYTFVILMV SSVEVDVHK HYLSSLVYG CVVSALACLV 420
 70 TIAAYLCRSR PLPCRKPRD YTIKVHMLL LAVFLDTSF LLSEFVALTG SEAGCRASAI 480
 FLHFSLLTCL SWMGLBGYNL YRLVVEVPGT YVPGYLLKLS AMGWGPPIFL VTLVALVDVD 540
 NYGPILLAVH RTEGVITYPS MCHIRDSLVS YITMGLFSL VFLPNMAMLA TMVVQILRLR 600
 PHTQKWSHV TLLGLSLVLG LPWALIFFSF ASGTFLVLVL YLFSIITSFQ GFLPIIYWWS 660
 MRLQARGGPS PLKNSDCAR LPISSGSTSS SRI

A51 DNA SEQUENCE

75 Gene name: Hypothetical protein FLJ20063
 Unigene number: Hs.5940
 Probeset Accession #: AA053660
 Nucleic Acid Accession #: AA053660
 80 Coding sequence: 218-1360 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCCCCATGAC TTGTACAGC TACTTCACTG CTTCCCCCA ATTAGTACAC ATAGTTCCTC 60

5 CACAATTCTT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCTCTCA CAATTCTCTAT 120
 AACTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAAT TCATTAGCTA CCTCTGACAT 180
 AATCACGCTT TCATCTCCAA ATGATGGATT AATCACAATG GTTCTCTCTG AAACACAAAG 240
 TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGCCTC CCCTGCGAC 300
 CGCTTTATTG GAGACCAGCA CCGTAAACAG CACAGSTCCC AGCAATCCTT GCCAAGATGA 360
 TCCTGTGCA GATAATTGCT TATGTGTTAA GCTGCATAAT ACAAGTTTTT GCCTGTGTTT 420
 AGAAGGGTAT TACTACAAT CTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT 480
 TTCAGTGACA GTATCAGAAA CATTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA 540
 10 CTGTCATAGT GAAATTACTA GCTTGTTTAA AGATGTATTT GGCACATCTG TTTATGGACA 600
 GACTGTAATT CTCTCTGTAA GCACATCTCT GTCCACCAAGA TCTGAAATGC GTGCTGATGA 660
 CAGTGTGTTT GATGTAAACA TAGTAACAAT TTTGGCAGAA ACCACAAGTG ACAATGAGAA 720
 GACTGTGACT GAGAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA 780
 TGATTGACC CTTCGGTGTG ATTATTATGG CTGTAACCAG ACTGCGGATG ACTGCGCTCAA 840
 15 TGGTTTAGCA TCGAATTGCA AATCTGACCT GCAAAGGCCCT AACCCACAGA GCCCTTTCTG 900
 CGTTGCTTCC AGTCTCAAGT GTCCGTGATGC CTGCAACGCA CAGCACAAGC AATGCTTAAT 960
 AAGAGAGAGT GATGGGGGCC CTGAGTGTGC GTGCGTGGCC GGCTACCAGG AAGATGCTAA 1020
 TGGGAATGCG CAAAAGTGTG CATTGGGCTA CAGTGGACTC GACTGTAAAG ACAAAATTCA 1080
 GCTGATCCTC ACTATTGTGG GCACCATGCG TGGCATTGTC ATTCTCAGCA TGATAATTGC 1140
 20 ATTGATTGTC ACAGCAAGAT CAAATAACAA AOCGAAGCAT ATTGAAGAAG AGAACTTGAT 1200
 TGACGAAGAC TTTCAAAATC TAAATCTGCG GTGACAGGCG TTCAACCAATC TTGGAGCAGA 1260
 AGGGAGCGCT TTTCTAAGG TCAGGATAAC GGCTCCAGA GACAGCCAGA TGCAAAATCC 1320
 CTATTCAAGA CACAGCAGCA TGCCCCGCCCT TGAATATTAG AATCATAAGA ATGTGGAACC 1380
 CGCCATGGCC CCCAACCAAT GTACAAGCTA TTATTTAGAG TGTTTAGAAA GACTGATGGA 1440
 25 GAAGTGAGCA CCAGTAAAGA TCTGGCCTCC GGGGTTTTTC TTCCATCTGA CATCTGCCAG 1500
 CCTCTCTGAA TGGAAGTGTG GAATGTTTGC AOCGAATCCA GCTCACTTGC TAAATAAGAA 1560
 TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGTG AGAGAGGTGG TTTTCTTCAA 1620
 TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTTTTCT TAATCTTTT CCTGGTAGGG 1680
 CAACAAGAAC CATTTCCAAT CTAGAGGAAA GCTCCCCAGC ATTGCTTGTCT CCTGGGCAAA 1740
 30 CATTGCTCTT GAGTTAAGTG ACCTAATTCC CCTGGGAGAC ATACGCATCA ACTGTGGAGG 1800
 TCCGAGGGGA TGAGAAGGGA TACCCACCAT CTTTCAAGGG TCACAGCTC ACTCTCTGAC 1860
 AAGTCAGAA AGGGACACTG CTTCTATCCC TCCAATGGAG AGATTCTGGC AACCTTTGAA 1920
 CAGCCAGAG CTGCAACCT AGCCTCACC AAGAAGACTG GAAAGAGACA TATCTCTCAG 1980
 CTTTTTCAG AGCGGTGCT GGGAAATCCG GAACTTTTG ATGCTAATTA GAAGGCCTGG 2040
 35 ACTAAAATG TCCACTATGG GGTGCACTCT ACAGTTTTTG AAATGCTAGG AGGCAGAAAG 2100
 GGCAGAGAGT AAAAAACATG ACCTGGTAGA AGGAAGAGAG GCAAAGGAAA CTGGGTGGGG 2160
 AGGATCAATT AGAGAGGAGG CACCTGGGAT CCACCTTCTT CCTTAGTCC CCTCTCCAT 2220
 CAGCAAGGGA GCACCTTCTT AATCATGCC TCCCGAAGAC TGGCTGGGAG AAGGTTTAAA 2280
 40 AACAAAAAT CCAGGAGTAA GAGCCTTAGG TCAGTTTGAA ATTGGAGACA AACTGTCTGG 2340
 CAAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCG TCCAGCGCTC AGCGGTGAGG 2400
 TTTCTGAGGT GTGCCATTGG GGCTCAGCC TTCTCTGGTG ACAGAGGCTC AGCTGTGGCC 2460
 ACCAACACAC AACCAACAC ACACAAACC GGGGGCAACC ACATCCAGTA 2520
 CAAGCTTTTA CAAATGTTAT TAGTGTCTT TTTTATTTCT AATGCGCTGT CCTCTTAAA 2580
 45 GTTATTTTAT TTGTTATTAT TATTTGTTCT TGACTGTTAA TTGTGAATGG TAATGCAATA 2640
 AAGTGCCCTT GTTAGATGGT GAAAAAATA AAAAAAATA AAAAAAATA A

A52 Protein sequence:

50 Gene name: Hypothetical protein FLJ20063
 Unigene number: Hs.5940
 Probeset Accession #: AA053660
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 289-311
 55 EGF domain: 45-74
 SEA domain: 80-196
 Cellular Localization: plasma membrane

60 1 11 21 31 41 51
 MVPSETQSN ENSPITEDNQ SSQPPTGTAL LETSTLNTG PSNFCQDDPC ADNSLCVKLH 60
 NTSFCLCLEG YYNSSTCKK GKVPFKISV TVSETPDPPE KHSMAVQDLH SEITSLFRDV 120
 FGTSVYGQTV ILTVSTSLSP RSEMRADDPK VDVITVTLA ETSDNEKTIV TEKINKAIRS 180
 65 SSSNPLNYDL TLRCDYCGCN QTADDCLNGL ACDCSGLQR PNPSPQFVCA SSLKCFDACH 240
 AQHKQCLIKK SGGAPEACAV PGYQEDANGN CQKCAFYSG LDCKDKFQLI LTIIVGTIAGI 300
 VILSMIALI VTARENNKTK HIEEENLIDE DFQNLKLRST GPTNLGAEBS VPFKVRITAS 360
 RDSQMNPYS RHSSMNPFDY

A53 DNA SEQUENCE

70 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 75 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 ACOGGGCACC GGACGGCTCG GGTACTTTTC TTCTTAATTA GGTGATGCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180
 AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGGA AGCCCCCTTC 240

5 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCCCTGTTC ACCAGATGCA 300
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTCC CTCACTCCTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAAAG CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTTCG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCAATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 10 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCCCTCTG GCCACGTGCT TACCTTGCA GTCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCAAGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 15 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
 CTCACGCTGA ATGAAATGAT CCAGCCTGTG TGCCCTGCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAGG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTGCC TGAACCAACG CGCCGTCCCT TTGATTTCCT ACAAGATCTG CAACCCACAG 1320
 20 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCA GCTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620
 25 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
 TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCCTCCA TCTGATTCCA GCACAACCTT 1740
 CAGCTGCTT TTGTTTTTTT GTTTTTTTGA GGTGGAGTCT GCCTCTGTTG CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCGTGGTTCA AGCGATTCTC 1860
 TTGCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACACACCC CAACTAATTT 1920
 30 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAAACCCCTGA 1980
 CCTCAATGAA TGTGCTGTCT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
 ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTGT 2160
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 35 GCACCAGCCC AGAAGTGACG AACTGCAGTC ACTGCAGTT TTCTCTCTA GGGACCCAGAA 2280
 CCAAAACCCAC CCTTCTACTT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAACTTAGGA 2340
 ATGACTCGTT TAAGGCTAT TTTCAAGATT TCTTTGTAGC ATTTGGTGTCT TGACGTATTA 2400
 TTGCTCTTGG ATTCCAATA ATATGTTTCC TTCCCTCAA AAAAAAATAA 2460
 AAAAAAA

40 A54 Protein sequence:
 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 45 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

50
 1 11 21 31 41 51
 MGENDPFAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLLPLKFPF IIVIGIIALI 60
 55 LALAIGLGIH FDCSGKYRCR SSPKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVILQVP 120
 TAASWKTMS DWKGHYANV ACAQLGFPSY VSSDNLRVGS LEGQFREBFV SIDHLLPDDK 180
 VTALHHSVYV REGCASGHVV TLQCTACGHR ROYSSRIVGG NMSLLSQWFW QASLQFGGYH 240
 LCGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVERI VYHSKYKPKR 300
 LGMDIALMKL AGPLTFNEMI QPVCLPNESE NPPDGKVCMT SGWGATEDGA GDASFVLNHA 360
 60 AVPLISNLIK NHRDVYGGII SPSMLCAGYL TGGVDSQGGD SGGPLVCQER RLWLKLVGATS 420
 PGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

A55 DNA SEQUENCE
 Gene name: Putative G protein-coupled receptor GPCR150
 65 Unigene number: Hs.97101
 Probeset Accession #: AA215333
 Nucleic Acid Accession #: NM_014373
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 GTGGCTCGA GGTGGTGCA GGGCCGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG 60
 GCCTCCGGAG CGAGGTTCCG CTGGAAGGAA CCGCTCTCGC TTGCTCTTAC ACTTGCAGCA 120
 75 ATGTCTCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
 AAATAACATA ATTGAAGGCA GTAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
 GACCACTGG AGAGGACAGA AAATGAAGCA GTGTTTTATC ATGTGTAATT CAGCAGGTCT 300
 TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTTCA AGAACTGCTC TTTTCACTAC 360
 CAGTTACGTC AAACAAACCA GCCCTAGAC GTTAACTATC TGCTATTCTT GATCATACTT 420
 80 GGGAAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAAACAC CTGTCAAAAT 480
 TTTATGGAAT ATTTTGTGAT TTCACTAGCA TTCGTTGATC TTTTACTTTT GGTAAACATT 540
 TCCATTATAT TGTATTTCAG GGATTTTOTA CTTTAAAGCA TTAGGTTTCA TAAATACCAC 600
 ATCTGCCTAT TTACTCAAAAT TATTTCCCTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC 660
 CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TCTATTTAAG 720
 TGTCAAAAAT TATTTTATTT CTTTACAGTA ATTTTAAATT GGATTTCACT CTTGCTTAT 780

5 GTTTTGGGAG ACCCAGCCAT CTACCAAAGC CTGAAGGCAC AGAATGCTTA TTCTCGTCAC 840
 TGTCTTCTCT ATGTGAGCAT TCAGAGTTAC TGGCTGTGAT TTTTCATGGT GATGATTTTA 900
 TTTGTAGCTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
 ACTTCCCTATA TGAATGAAAC TATCTTATAT TTTCTTTT CATCCACTC CAGTTATACT 1020
 GTGAGATCTA AAAAAATATT CTATCCAAAG CTGATGTGCT GTTTCTCTAG TACTCGTTTA 1080
 CCATTGTGAC TACTTCAGGT AATCATTTGT TACTTAAAG TTCAGATTCC AGCATATATT 1140
 GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTT TCATTGTGAC AGTGTATTGG 1200
 TTTAATGTCT ACAAGCTTAA TTTAAAGAAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260
 10 TGGAAAGTCT GCTTCAATCC ACTTACAATT CCTAATCTTG AGCAAATTGA AAAGCCTATA 1320
 TCAATAATGA TTTGTTAATA TTATTAATTA AAGTTACAG CTGTCAATAG ATCATAATT 1380
 TATGAACAGA AAGAATCTAG GACATATTAA AAAATAAACT GAACATAAAC AACTTTTGCC 1440
 CCTGACTGA TAGCATTTCA GAATGTGTCT TTTGAAGGGC TATACCAAGT ATTAAATAGT 1500
 GTTTTATTTT AAAAAACAAA TAATTCCAAG AAGTTTTTAT AGTTATTTCAG GGACACTATA 1560
 15 TTACAAATAT TACTTTGTTA TTAACACAAA AAGTGATAAG AGTTAACATT TGGCTATACT 1620
 GATGTTTGTG TTACTCAAAA AAACACTGAG ATGCAAACTG TTATGTAAAT CTGAGATTTC 1680
 ACTGACAAC TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAT GTAGCAAGA 1740
 AAAAAAAA

20 A56 Protein sequence

Gene name: Putative G protein-coupled receptor GPCR150
 Unigene number: Hs.97101
 Protein Accession #: NP_055188
 Signal sequence: none found
 25 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297
 Cellular Localization: plasma membrane

30 1 11 21 31 41 51
 | | | | |
 MTALSSENC FQYQLRQTNQ PLDVNYLLPL IILGKILINI LTLGMRRIQT QNFMEYFCI 60
 SLAPVDLLLL VNISIILYFR DFVLLSIRFT KYHICLFTQI ISPTYGFLHY PVFLTACIDY 120
 CLNFSKTKL SFKCKRLYFP FTVILIWISV LAYVLGDPAI YQSLKAQNAV SRHCPYVSI 180
 QSYWLSFPMV MILPVAFITC WEEVTLVQA IRTSYMNET ILYPFSSHS SYTVRSKKIF 240
 35 LSKLVLCPLS TWLPVLLQV IIVLLKVQIP AYIEMNIPWL YPVNSFLIAT VYWFNCHKLN 300
 LKDIGLPLDP FVNWKCCPIP LTIPNLEQIE KPISIMIC

40 A57 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor (H.sapiens)
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | |
 GCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 50 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGA GCGAGGCCAG CGCGGACTTT GGGGCTGCTG GAGAGCCCGG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGCT GGGAGCTGCT GCGTGCAGCC 300
 TGTGCGACGC GGGCCCTGCC CCGTCTCTCC TCGGGGCCCC CCGTCCCTGC CCTGAAGTCC 360
 55 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCAACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAAGC AGCTGGAGCA GGAGAACTCG 480
 GCGCTCATTA AGCAGCTGTT TGAGGCTCCG CGCTTGAGCC AGCAGGACCG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTGTGGGGCC GCGTGGGCCC CCAGGGCCAG CCGTGCCTCT 600
 AGCCCTTCGA GGGTGGGGCG CCCATCGCAC CCAACCTCTC TGGCTGAGGA CCGCCGGCAG 660
 60 GCGCAGGCAC AGTCCGGGAG TGGGGGCTT CCGCGGCC TTGCGAGATG GCGTCCCGAG 720
 GCGTGCCTCC GCGTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGCTTGYTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTACTACTGG CCGCTGTTCAG 840
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCCCG TTTCCAGCGG TCGCGCCCTG 900
 GGTCCCATCT TCAGGGAAGG GCACGTGCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960
 65 AGAGGCGCG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGAGC GGAAGTAGAT GGAAGGGGTG GGGACGGCCT 1080
 GTAAGCGGGG GTGCTCTGCC TGGCTGGGGA GCCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
 CTGGCCAAGG CTGAGGGACC CTGGCTGCGA CGGATCGGCA CGCGGGGTGG GCGAGAGCTT 1200
 GGCGCTCATG TGCTCTCCAC AGACCTGGGG GTGATGGCCT TCCCTCTCTT GCGCGGGACG 1260
 70 TTGCCCCAGC TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCCAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGTCA TAGGCAAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
 CTGGGTCTCT GCTCACCCCC CTTTGCTCTC ACGCCAGGCC TGTCCCGAGG TTTCACTTGG 1440
 GAGAGGCCAC CTCCCTCAGC CAAGGAAAAA AGGAGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTGGGTGTGC ACTCCCTCAG CCGCTGCCCA GGCCACTCTC CGCTGTGTCT 1560
 75 GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACACA 1620
 GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680
 TCAGTGTGTG TGGGGCGCAG GGCCTCGGAT GCGGGGTGAG TCGTGGGGGG GCGCAGGGCC 1740
 CCGATGCGGG GGTGAGTGCG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACTTTGGT 1800
 ACACTGTCCC ACAGGCCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860
 80 CCTTCCGAGC CCGAGTCCA TGCTAACCTG CCAACAGCAA CCGCAAGAG CCACTTCCC 1920
 TGCTGCACTT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
 GCCTCTCTAC CCGTAAGATG GAGTGTGGCT TTCCAGGGGA CATAAGGATG TCAGGCTTGG 2040
 ACCTCTTGGG CAGGAAAGGG TGCAGTCTCT GAGGGCTGTG GCGCCACAGC CCGACACCCC 2100
 AGGTGGAAGT CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GAGGAAGCCC CCGCTCAGCA 2160
 GCGTGGGGTC TGCCACCGAG GGCCTCCCCA GGTCTGCCTT TGAGGGTGGC TGCCATGCCC 2220

5 TGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGACTTCA TCAGGAGACC GCCACATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340
 GAGACAGGCT GGCACTCCCG GAAAACATGC CTTTCAGCCT TGGTGTCCCG TGCAAGGTGA 2400
 AAAGAAATAG GTCCTCCCGG TTACAGCCTT GAAATCAGGC TAGTGAGTGG CCTGGAGAC 2460
 CACGAGGGGA GAATTTAAAG GCCCGGCTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGACCCTG CTTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGCGTC CTTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640
 GCGTGACAC TGTTGATGACA CCGCGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700
 10 CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760
 TTTTGTGTG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCACGC 2820
 CTGGAATCCG AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACAAAAAAAA AAAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCAGC CAGAAGCAAC AGATTGACTC 3000
 15 TAGACCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTCTCG GAAACATGAA AAAAAA

A58 DNA sequence

Gene name:

ESTs

Unigene number:

Hs.157601

Probeset Accession #:

W07459

Nucleic Acid Accession #:

AC005383

Coding Sequence:

328-2751 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
 TTTTATTTCG AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
 CCTGGCGGTA GTTCTCTCGA CCTCAGCCGG GTCCGGTCTGT GCGGCCCTCT CCCAGGAGAG 180
 30 ACAAAACAGT GTCCACAGTG GCAGCCGCGC CCGGGGCGCC CCTCTGTGA TCCCGTAGCG 240
 CCCCCTGGCC CGAGCCGCGC CCGGTCTGT GAGTAGAGCC GCCCGGCGAC CGAGCGCTGG 300
 TCGCGCTCTT CCTTCCGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GGCGGTCTGT 360
 GTTTTCTGT TTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAAGCAA 420
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGTCTGGC TGCAGTGGAC 480
 ATCATGTTCG GTTTAGATGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAAG 540
 35 CACTTTCGCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAGTTCAC TCCTCATCTG GAATTCCTCT TGGATTCAAT TTCAACCCAA 660
 CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
 CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCTCGGAG GCAGAAATGC TTCTGTGCC 780
 40 CAGATCTCTA TCATCGTAC TGATGGGAAG TCCAGGGGGG ATGTGGCACT GCCATCCAAG 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTGTGC TGAGCAGGTG 960
 GAGGATCCCA CCAACGGCCT CTTAGCAGCC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
 ACGCCAGACT GCAGGGTCTGA GGCTCACCCC TGTGAGCACA GGAACGCTGA GATGTTCCGG 1080
 45 GAGTTGCTG GAAATGCCCC ATGCTGGAGA GGATCGCGGC GGAACCTTGA GGTGTGCGCT 1140
 GCACACTGTG CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTGAC CACTGTCTAC 1200
 AGGACCACTT GCCCAGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
 CCAGAAGGAC TGGACGGCTA CCAGTGCCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGAACCTCC TCTTCTGCTG GGACAGCTCT 1380
 50 GCGGGCACCA CTCTGGAACG CTCTCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
 GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
 CTGTGTGGCG TGCCTGTGGG GAGGTACCAAG GATGTGCCCT ACCTGTCTG GAGCCTCGAT 1560
 GGCATTCCCT TCCGTGTGTG CCCACCCCTG ACGGGCACTG CCTTGGCGCA GGCGGCAGAG 1620
 CGTGGCTTGG GAGCGGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGTGTTTG 1680
 55 CTCACTCTGA CACACTCCGA GGATGAGGTT GCGGGCCAG CGGTCAAGC AAGGGCGCGA 1740
 GAGCTGTCTC TGCTGGGTGT AGGCAGTGAG GCCGTGCGGG CAGAGCTGGA GGAGATCACA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCTCAGG ATCTGTTCAA CCAATTCCT 1860
 GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1920
 CTGCTCTTCA TGTGGAACAC CTCTGCCCTA GTAGGGCCCG AGAATTTTCG TCAGATGCAG 1980
 60 AGCTTTGTGA GAAGCTGTGC CCTCCAGITT GAGGTGAACC CTGACGTGAC ACAGGTCCGC 2040
 CTGGTGTGTG ATGCGAGCCA GGTGCAGACT GCCTTCGGGC TGGACACCAA ACCACCCCG 2100
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160
 ACCGCCCTCG TGCACTCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220
 65 GTCCCAAGAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCGTTCT 2280
 GCCCAGAAAG TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGCGTGGG GCCTGTCTTA 2340
 AGTGAGGGTC TGCGGAGGCT TGCAGGTCCC CCGGATTCCC TGATCCAGT GGCAGCTTAC 2400
 GCGGACCTGC GGTACACCA GAGCTGTCTC ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG 2460
 CCAGTCAACC TCTGCAAAAC CAGCCGTGTC ATGAATGAGG GCAGCTGCGT CCTGCAAGAT 2520
 GGGAGCTACC GCTGCAAGTG TCGGATGGC TGGAGGGGCC CCACTGCGA GAACTGTGAG 2580
 70 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGAATC TTGAGACGCC CCTGAGGCAC 2640
 ATGGCTCCCG TGCAGGAGGG CAGCAGCGGT ACCCTCCCA GCAACTACAG AGAAGGCTG 2700
 GGCAGTGAAT TGTGCTCTAC CTCTGGAAT GTCTGTGCC CAGGCTCTTA GAATGTCTGC 2760
 TTCCCGCGGT GCCCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
 ATGTCTCTTA GAGACAAAG AGCAGCTGAT GTCAACCACA AACGATGTTG TTGAAAGTT 2880
 75 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGTGTTG CTTGTTGAG GCTATGTCT 2940
 CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTGAAAG ACTTAAATTT AGCGGCTGA 3000
 CGTTCCTTTG CACACAATCA ATGCTGCCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060
 AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCAAG GCGTTTCAAG ATGGAAGACA 3120
 CGAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTT GCATTGAGTC TGAAAGGGGG 3180
 80 CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAAGA GACTTGGAAA 3240
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300
 TGTGCAATGG CCCAGTCTG GAGGGCCAG TAAATCTGTT CTGAGTCTGT AGCAGTGTCC 3360
 ACCTTGAAGG TCTTC

A59 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKQWNC5AAV DIMFLLDGSN 60
    SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
    MVFKGGRRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS RQLKERGVTV 180
    FAVGVRFPPW EELHALASEP RGQHVLLAEQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240
    PCEHRTLEMV REPAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD 300
20  SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
    RAKVFVKRVV RAVLSSDSRA RVGVATYSRE LLVAVPVGEY QDVVDLVWSL DGIPFRGGPT 420
    LTGSLARQAA ERGFGSATRT QQDRPRRVVV LITESHSEDE VAGPARHARA RELLLLGVS 480
    EAVRAELSEI TGSFKHVMVY SDPQDLFNQI PELQKLCISR QRPQCRTQAL DLVFMLDTS 540
    SVGPNFAGM QSPVRSICALQ FEVNPVDVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
25  APYLGGSVSA GTALLHIYDK VMTVQRGARP GVPKAVVVL T GGRGAEDAAV PAQKLRRNGI 660
    SVLVVGVGVV LSEGLRRLAG PRDSLHVA A YADLRHQDV LIEMLCGEAK QPVNLCKPSP 720
    CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGNILETPLR HMAPVQEGSS 780
    RTPFSNYREG LGTEMVPTFW NVCAPGF
  
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TGGATGTCAA ACCCCTGCGC 60
    AAACCCCGTA TCCCATGGA GACCTTCAGA AAGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTCG CGAGTATCAT CATGTGGTT GTCCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCTCT CCGGCGAGCC TCTCCACTTC ATCCGAGGA AGCAGCTGTG TGACGGAGAG 240
    CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
45  GCACTGGCAG TCCGCTCTC CAAGGACGA TCCACACTGC AGGTGCTGGA CTGGCCACA 360
    GGAACCTGTT TCTCTGCTG TTTGCAAC TCCACAGAAG CTCTGCTGA GACAGCCTGT 420
    AGGCAGATCG GCTACAGCAG CAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
    GATCTGGATG TTGTTGAAT CACAGAAAC AGCCAGGAGC TTCGATGCG GAACCTCAAGT 540
    GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTG GAGAGCCTG 600
50  AAGACCCCCC GTGTGGTGGG TGGGAGGAG GCCTCTGTGG ATTCTTGCC TTGGCAGGTC 660
    AGCATCCAGT ACGACAACA GCACGCTCTG GGAGGGAGCA TCTCGGACC CCACTGGGTC 720
    CTCACGGCAG CCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGGGGCA 780
    GGCTCAGAGC AACTGGGCG CTTCCATCC CTGGCTGTGG CCAAGATCAT CATCATTTAA 840
    TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
55  ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
    GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
    GACATATCTG TGCAGGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
    GCGTACCAGG GGGAGTCAC OGAGAAGATG ATGTGTGCGA GCATCCCGGA AGGGGGTGTG 1140
    GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
60  GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCGA GCACCCAGG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
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A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_Spc domain: 204-429
 Cellular Localization: plasma membrane/ER

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1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIVV VLIKVILDKY 60
    YFLQGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVILDSAT 120
    GNVFSACFDN FTEALAEIAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELRMENSS 180
    GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPMQV SIQYDRQHVC GGSILDPHWV 240
    LTAACHFRKH TDVFNWVKRA GSDKLGSPFS LAVAKIIIE FNPMPYKNDI IALMKLQPP 300
    TFSGTVPIC LPFPDEELTP ATPLWIIWGG FTKQNGGRMS DILLQASQV IDSTRCNADD 360
    AYQGEVTEKM MCAGIPGEGV DTCQSDSGGP LMVQSDQWHV VGIVSWGYGC GGPSTPGVYT 420
    KVSAYLWIIY NVWKABL
  
```

A62 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
CCAAACAGAT TTGCAGATCA AGGAGAAACC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
CTGAGATCCT TGCCTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
CGGCTGTGCC TATTGCTGAG CTGCCTGGCG AAAACAGGAG TCCTGGGTGA TATCATCATG 180
AGACCCAGCT GTGCTCCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTAATTTCAGG 240
AAGCTGAGGA ACTGCTCTGA TGCCGAGCTC GAGTGTCACT CTTACGGAAG CCGAGCCCCAC 300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
CAGAGAAGCC AGCCGATATG GATTGGCCCTG CAGACCCAC AGAAGAGGCA GCAGTGGCAG 420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTGGAGCAG CAACGAATGC 540
AACAGGCCCC AACACTTCTT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
AACTCCTGCA CCAGCCCGCT CCTCTCTCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
TTCAGAGGGG AACCTAGCA AACTAAGAGT GATAAGGGCC CTAACACT GGTCTTTTAA 720
GGCTTAGAGA CAGAACTTT AGCATTGGGC CCAAGTAGTG CTCTAGCTC TAAATGTTG 780
CCCCGCCATC CCTTTCCACA GTATCCTTCT TCCCTCCTCC CTTGTCTCTG GCTGTCTCGA 840
CGAGTCTAGA AGAGTGCAATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAAT 900
AAAGATTGGA AGACAGAAGG AAGAAATCA GAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCTTCTC GCCCTCTCTC CATTGCTGTC ACCCAACCCC AGCCACTCAA CTCCTGCTTG 1020
TTTTCCTCTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

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A63 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MASRSMRLLL LLSCLAKTGV LGDIIMRPSG APGWFYHKSQ CYGYFRKLRL WSDAELECCS 60
YGNGAHLASI LSLKEASTIA EYISGYQRSG PIWIGLHDPQ KRQWQWIDG AMYLYRSWGS 120
KSMGGNKKCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP

```

A64 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

```

1      11      21      31      41      51
|      |      |      |      |      |
GCGGAACACC GGCCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCCTGTGGG ACCTCTGGCG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG CCGGGAGGCG 180
CGGAGCAGGA GCCCGGCCAG CGCTGGGGA AAGTATTTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAAT GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCGGGGG GCAGACGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAAG 540
AGACAGGCTG GTTGTGTGTT AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGA GAGCCCCATG AACATCTCCA 660
TCATCGTGAC CGACCAAGAT GACCAACAAG CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
GTGTCTTAGA GGGAGTCCCTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
AGGACCCACA CGACCTCATG TTCACAATTC ACCGAGCAC AGGCACCATC AGCGTCATCT 900
CCAGTGCGCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACATGCTTCC CATGTTTGAC CCCCAGAAAT ACGAGGCCCA TGTGCTGAG AATGCAATGG 1080
GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGAAGC CCCCACCTCA CCAGCGTGGC 1140
GTGCCAGCTA CTTTATCATG GGCGGTGAGC ACGGGGACCA TTTTACCATC ACCACCCACC 1200
CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCCCTT TGTGCTGAG CTCCCAACCT 1320
CCACGCCAC CATAGTGGTC CAGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAAGA CCTGACAAG GAGAATCAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500

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CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
GTGAGGATGA GCACTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
ATGGAAGCCC TCCACCACTT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
ACGTGCTGAA CATCAAGGAC AAGGACCTGT CTCCCACAC CTCCCCTTTC CAGGCCACGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACTTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGSCCAG TGTGTGCGAC TGCCATGGCC 1980
ATGTGGAAC CTGCCCTGGA CCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCGTGA CAACGTCTTC TACTATGGCG 2160
AAGAGGGGGG TGGGGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGCTCTG 2220
AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
TGTAACGCTC TAGGCACGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
AGGCGGCTAA CACAGACCCC ACAGCCCCGC CTAACGACAC CTCTTGGTGT TCGACTATG 2400
AGGGCAGCGG CTCGACGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
ACCAAGATTA CATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520
ACGTTGCGCG GGAGGAGCAG TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTGAGGC 2580
CACAGAGCAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTGA 2640
GGAAGTGGCC GTAGCAACTT GCGGAGACA GGTATGAGT CTGACGTTAG AGTGGTGTCT 2700
TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCG AGGGTTGCTT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
TGCTCAACCC TGTGTCTCTG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
CTGGAATGGA ACCTCTCTAG GCCTCCTGCT GCAACTTAAT TTTTATTTT AATGCTATCT 2940
TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAAG GCTGCTGGGC CCACTGGCCG 3000
TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060
ATACTGAGTG TGCTAGGTTT GCCCTTATT TTTTATTTTC CCGTTGGTGT TGCTATAGAT 3120
GAAGGGTGAG GACATCTGTG TATATGTACT AGAATTTTTT TATTAAGAA A

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A65 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

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1 11 21 31 41 51
MGLPRGPLAS LLLLQVCNLQ CAASEPCRAV FREAEVILEA GGAQEPEGQA LGKVFMGCPG 60
QEPALFSDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPPQORLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGNLLLN KPLDREELAK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIIHS EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TMDGDSGTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEP AVGHEVQRLT VTDLDAFNSP 360
AMRATYLMG GDDGDHFTIT THPESNQIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLK 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVG EGIPTEGPVC VYTAEDPEKE NQKISVRILR 480
DPAGNLAAMP DSGQVAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLTLLTLD 540
VNDHGFVPEP RQITICNQSP VRHVLNITDK DLSFPTSFPQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKIFL KDPTDYVHLS LSDHGNKEQL TVIRATVCDG HGVETCPGFP WKGGFILLPV 660
GAVLALLFL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFP YBEGGGGEDD QDYDITQLHR 720
GLEARPEVVL RNDVARTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF 780
DYEAGSGDAA SLSSLTSSAS DQDQDYDYLW EWGSRFKKLA DMYGGGEDD

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A66 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

70
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1 11 21 31 41 51
ATGATTCTCT TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
TCTCAGTTTA AAAATCCCTT TATTATGCTG CTTCTGGCTT CTGCAGTCAT CAGTGTTTGA 240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTATACAGT 300
GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
CCAGAAATGCC ATTGTGTGCG TGAAGAAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
CCAGGTGATA CAGTTTGCTT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTIT 480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540
AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATGAGG AAGTAACATT 600
GCCTTTGTTC GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTT TGGAACAGGA 660
GAAAAATCTG AATTGGGGGA GGTTTTAAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACATT CCTTTTACTC CTTTGGTATA 780
ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAGG ATATCTCTGA AATGTTTACT 840

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ATTAGTGTA  GTTTGGCTGT  AGCAGCAATT  CCTGAAGGTC  TCCCATTTGT  GGTCCAGTGT  900
ACGCTAGCTC  TTGGTGTAT  GAGAATGGTG  AAGAAAAGGG  CCATTGTGAA  AAAGCTGCCT  960
ATTGTTGAAA  CTCTGGGCTG  CTGTAATGTG  ATTTGTTTCT  ATAAAAGTGG  AACACTGACG  1020
AAGAATGAAA  TGACTGTTAC  TCACATATTT  ACTTCAGATG  GTCTGCTATG  TGAGGTTACT  1080
GGAGTTGGCT  ATAATCAATT  TGGGGAAGTG  ATTGTTGATG  GTGATGTTGT  TCATGGATTG  1140
TATAACCCAG  CTGTTAGCAG  AATTGTTGAG  GCGGGCTGTG  TGTGCAATGA  TGCTGTAAAT  1200
AGAAACAATA  CTCTAATGGG  GAAGCCAACA  GAAGGGGCGT  TAATTGCTCT  TGCAATGAAG  1260
ATGGGCTCTG  ATGGACTTCA  ACAAGACTAC  ATCAGAAAAG  CTGAATACCC  TTTTAGCTCT  1320
GAGCAAAAGT  GGATGGCTGT  TAAGTGTGTA  CACCGAACAC  AGCAGGACAG  ACCAGAGATT  1380
TGTTTTATGA  AAGGTGCTTA  CGAACCAAGT  ATTAAGTACT  GTACTACATA  CCAGAGCAAA  1440
GGGCGAGCCT  TGACACTTAC  TCAGCAGCAG  AGAGATGTGT  ACCAACAAAG  GAAGGCACGC  1500
ATGGGCTCAG  CGGGACTCAG  AGTTCTTGCT  TTGGCTTCTG  GTCCTGAACT  GGGACAGCTG  1560
ACATTCTTGT  GCTTGGTGGG  AATCATTGAT  CCACCTAGAA  CTGGTGTGAA  AGAAGCTGTT  1620
ACAACTACTA  TTGCTCAGG  AGTATCAATA  AAAATGATTA  CTGGAGATTG  ACAGGAGACT  1680
CGAGTTGCAA  TCGCCAGTGC  TCTGGGATTG  TATTCACAAA  CTTCCAGTCT  AGTCTCAGGA  1740
GAAGAAATAG  ATGCAATGGA  TGTTCAGCAG  CTTTCACAAA  TAGTACCAAA  GGTTCAGTA  1800
TTTTACAGAG  CTAGCCCAAG  GCACAAGATG  AAAATTATTA  AGTCGCTACA  GAAGAACGGT  1860
TCAGTTGTAG  CCATGACAGG  AGATGGAGTA  AATGATGCAG  TTGCTCTGAA  GGCTGCAGAC  1920
ATTGGAGTTG  CGATGGGCCA  GACTGGTACA  GATGTTTGCA  AAGAGGCAGC  AGACATGATC  1980
CTAGTGGATG  ATGATTTTCA  AACCATAATG  TCTGCAATCG  AAGAGGGTAA  AGGGATTAT  2040
AATAACATTA  AAAATTTCTG  TAGATTCCAG  CTGAGCAGCA  GTATAGCAGC  ATTAACTTTA  2100
ATCTCATGAG  TGTTCAATAT  GAACCTTCTT  AATCCTCTCA  ATGCCATGCA  GATTTTGTGG  2160
ATCAATATTA  TTATGGATGG  ACCCCAGCT  CAGAGCCTTG  GAGTAGAACC  AGTGGATAAA  2220
GATGTCATTC  GTAAACCTCC  TCGCACTGCG  AAGACAGCA  TTTTGACTAA  AAACCTTGATA  2280
CTTAAATATC  TTGTTTCATC  AATAATCATT  GTTTGTTGGA  CTTTGTGTTG  CTTCTGGGCT  2340
GAGCTACGAG  ACAATGTGAT  TACACCTCGA  GACACAACAA  TGACCTTCAC  ATGCTTTGTG  2400
TTTTTTGACA  TGTTCAATGC  ACTAAGTTCC  AGATCCGAGA  CCAAGTCTGT  GTTTGAGATT  2460
GGACTCTGCA  GTAATAGAAT  GTTTTGCTAT  GCAGTTCTTG  GATCCATCAT  GGGACAATTA  2520
CTAGTTATTT  ACTTTCCTCC  GCTTCAGAA  GTTTTTCAGA  CTGAGAGCCT  AAGCATACTG  2580
GATCTGTTGT  TTTCTTTTGG  TCTCAGCTCA  TCAGTGTGCA  TAGTGGCAGA  AATTATAAAG  2640
AAGGTTGAAA  GGAGCAGGGA  AAAGATCCAG  AAGCATGTTA  GTTCGACATC  ATCATCTTTT  2700
CTTGAAGTAT  GA
  
```

35 A67 Protein sequence:
 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Protein Accession #: AAF27813
 40 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

45
 50
 55
 60

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1 11 21 31 41 51
| | | | |
MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKYI 60
SQPKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQSEYSEK SLEELSKLVP 120
PECHCVREBK LEHTLARDLV PGDTVCLSVG DRVPADLRFP EAVDLSIDES SLTGETTPCS 180
KVTAQPAAAT NGDLASRENI AFMGTLVROG KAGGVVIGTG ENSEFGEVFK MMQAEAPKT 240
PLQKSMDLGL KQLSFYSFPI IGIIIMLVGLW LGKIDILEMPT ISVSLAVAAI PBGLPIVTV 300
TLALGVNRMV KKRATVKKLP IVETLGCNCV ICSDKTGLT KEMTVTHIF TSDGLHAETV 360
GVGVNQGEV IVDGVVHGF YNPAVSRIE AGCVCNDAVI RNNTLMGKPT EGALIALAMK 420
MGLDGLQDDY IRKAEYFPSS EQKMAVKCV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQKERAR MGSAGLRVLA LASGPGLQL TPLGLVGIID PPRTGVKEAV 540
TLIASGVSI KMITDGSQET AVALASRLGL YSKTSQSVSG EEDIDAMDVQQ LSQIVPKVAV 600
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMGQTGT DVCKEADMI 660
LVDDDFQTIM SAISBQKGIY NNIKNFVRFP LSTSIARLTL ISLATLMNFP NPLNAMQILW 720
INIIMDGPPA QSLGVFVVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTKSVPEI GLCSNRMPCY AVLGSIMGQL 840
LVYFPPLQK VFQTESLSIL DLLFLGLTSS SVCTIVAEIK KVERSRERIKI KHVSTSSSSF 900
LEV
  
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65 A68 DNA SEQUENCE
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719
 70 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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 80

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1 11 21 31 41 51
| | | | |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACGACGGGCC GGGACGGCCG CTTGCCCCCT 60
CTGCCACTCG GGGCCGCTGG GGGCCCGAGC CGGAGCGCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCAAGT GCGCTCACTG CGAGCTGCGG CGCGGCACAG CTTGCTGGCG CTTCTGGGAC 180
CCCTGTTCTT CTGCGCTCC GCGCTGGCGG ACTTCAGCCT GACAAACGAG GTGCACTCGA 240
GCTTCATCCA CCGCGCGCTC CGCAGCCAGG AGCGCGGGGA GATGCAAGCG GAGATCCTCT 300
CCATTTTGGG CTGCCCCCAG CGCCCGGCGC CGCACCCTCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT GCTGGACCTG TACAAGCCCA TGGCGGTGGA GGAGGGGCGG GGGCCCGGCG 420
GCCAGGGCTT CTCTTACCCC TACAAGCCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
GCTGCAAGA TAGCAATTTC CTCACGAGC CGCACATGGT CATGAGCTTC GTCAACCTCG 540
TGGAACATGA CAAGGAATTC TTCCACCCAC GCTACCAACA TCGAGAGTTC CGTGTGATC 600
TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCGGGATC TACAAGGACT 660
  
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5	ACATCCGGGA	ACGCTTCGAC	AATGAGACGT	TCCGGATCAG	CGTTTATCAG	GTGCTCCAGG	720
	AGCACTTTGGG	CAGGGAATCG	GATCTCTTCC	TGCTCGACAG	CGGTACCCTC	TGGGCTCTGG	780
	AGGAGGGCTG	GCTGGTGTTC	GACATCAAG	CCACCAGCAA	CCACTGGGTG	GTCAATCCGC	840
	GGCACAACCT	GGGCTGCGAG	CTCTGGGTGG	AGAAGCTGGA	TGGGCAGAGC	ATCAACCCCA	900
	AGTTGGCGGG	CCTGATTGGG	CGGCAAGGGC	CCCAGAACAA	GCAGCCCTTC	ATGCTGGCTT	960
	TCTTCAAGGC	CACGGAGGTC	CACCTCCGCA	GCAATCGGTC	CACGGGGAGC	AAACAGCGCA	1020
	GCCAGAACCG	CTCCAAGACG	CCCAAGAAC	AGGAAGCCCT	GGGATGGGCC	AACGTGGCAG	1080
	AGAACAGCAG	CAGGAGCCAG	AGGCAGGGCT	GTAAGAAGCA	CGAGCTGTAT	GTGAGCTTCC	1140
10	GAGACCTGGG	CTGGCAGGAC	TGGATCATCG	CGCTGAAGG	CTACGCGGCC	TACTACTGTG	1200
	AGGGGGAGTG	TGCCTTCCTT	CTGAACCTCT	ACATGAACGC	CACCAACCAC	GCCATCGTGC	1260
	AGAGCGTGGT	CCACTTCATC	AACCGGAAA	CGGTGCCCAA	GCCCTGCTGT	GCGCCCAAGC	1320
	AGCTCAATGC	CATCTCCGTC	CTCTACTTCG	ATGACAGCTC	CAACGTATC	CTGAAGAAAT	1380
	ACAGAAACAT	GGTGGTCCGG	GCCCTGGGCT	GCCACTAGCT	CCTCCGAGAA	TTGAGACCTT	1440
15	TTGGGGCCAA	TTTTTCTGG	ATCCTCCATT	GCTCGCTTGG	GCCAGGAACC	AGCAGACCAA	1500
	CTGCCTTTTG	TGAGACCTTC	CCCTCCCTAT	CCCCAACTTT	AAAGGTGTGA	GAGTATTAGG	1560
	AAACATGAGC	AGCATATGGC	TTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAAGA	1620
	TCCTCAATGC	TTGTCAGGCA	AAACCTAGCA	GGAAAAAATA	ACAACGCATA	AAGAAAAATG	1680
	GCCGGGCGAG	GTGATGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
20	TTATGAGCGC	CTAGCAGCCA	GGCCACCCAG	CCGTGGGAGG	AAGGGGGGCT	GGCAAGGGGT	1800
	GGGCACATTG	GTGCTGTGTC	GAAAGGAAAA	TTGACCCGGA	AGTTCTCTGA	ATAAATGTCA	1860
	CAATAAAACG	AATGAATG					

25	<u>A69 Protein sequence:</u>	
	Gene name:	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
	Unigene number:	Hs.170195
	Probeset Accession #:	BE616633
	Protein Accession #:	NP_001710.1
30	Signal sequence:	1-30
	Pfam domains:	TGFb_propeptide [37-281]
	Transmembrane domains:	none found
	Cellular Localization:	secreted

35	1	11	21	31	41	51	
	MHVRSLRAAA	PHSFVALWAP	LFLLRSALAD	FSLDNEVHSS	FIHRLRSQEE	RREMQREILS	60
	ILGLPHRRPR	HLQGGHNSAP	MFMLDLYNAM	AVEEGGGPGG	QGFSYPYKAV	FSTQGPPLAS	120
40	LQDSHFLTDA	DMVMFVNLV	EHDKEFFHPR	YHREFRFDL	SKIPEGEAVT	AAEFRIYKDY	180
	IRERFDNETP	RISVYQVLQE	HLGRESDLFL	LDSRTLWASE	EGWLVPDITA	TSNHWVVNPR	240
	HNLGLQLSVE	TLDGGQINPK	LAGLIGRHGP	QNKQPFMVAF	FKATEVHFPS	IRSTGSKQRS	300
	QNRSTPKPNQ	EAIRMANVAE	NSSSDQRQAC	KKHELYVSFR	DLGWQDWIIA	PEGYAAYYCE	360
	GECAFLPNYS	MAATNHAIVQ	TLVHFIPNET	VPKPCCAPTQ	LNAISVLVYD	DSSNVILKKY	420
45	RNMVVRACGC	H					

Cervical

50	<u>A70 DNA sequence</u>	
	Gene name:	bone morphogenetic protein receptor 1B (ALK-6)
	Unigene number:	Hs.87223
	Probeset Accession #:	AA250737
	Nucleic Acid Accession #:	NM_001203
	Coding sequence:	274-1782 (underlined sequences correspond to start and stop codons)

55	1	11	21	31	41	51	
	CGCGGGGCGC	GGAGTCGGCG	GGGCTCGCG	GGACGCGGGC	AGTGGGAGAG	CGCGGGGCGT	60
	GAGGACGCGG	GAGCCGGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
60	GTGAAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTTCAGACT	TCTGCTGATT	180
	CATAACCAT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTAAA	CTTACAAGCC	240
	TGCCATAAGT	GAGAAGCAAA	CTTCCTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAAATTA	300
	AAATGTGGGC	CCAAGAAAGA	GGATGTTGAG	AGTACAGCCC	CCACCCCGCG	TCCAAAAGGT	360
	TTGCGTTGTA	AATGCCAACCA	CCATTGTCCA	GAAGACTCAG	TCAACAAATAT	TTGCAGCACA	420
	GACGGATATT	GTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCCTGT	GGTCACTTCT	480
65	GGTTGCCTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTGGGG	ACACTCCCAT	TCCTCATCAA	540
	AGAAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAAGACCT	ACACCTTACA	600
	CTGCCTCCAT	TGAATAACAG	AGATTTTGT	GATGGACCTA	TACACCAAG	GGCTTTACTT	660
	ATATCTGTGA	CTGTCTGTAG	TTTGCTCTTG	GTCCTTATCA	TATTATTTTG	TTACTTCCGG	720
	TATAAAGAC	AAGAAACCA	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACTTAC	780
70	ATTCTCTCTG	GAGAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGG	840
	TCAGGCTCC	CTCTGCTGGT	CCAAAGGACT	ATAGCTAAGC	AGATTTCAGT	GGTGAACAG	900
	ATTGGAAGAG	CTGCTATGAG	GGAAAGTTGG	ATGGGAAAGT	GGCGTGGCGA	AAAGGTAGCT	960
	GTGAAGTGT	TCCTCACCA	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
	ACAGTGTGTA	TGAGGCATGA	AAACATTTTG	GGTTTCATTG	CTGCAGATAT	CAAGGGGACA	1080
75	GGGTCTCTGA	CCAGTTGTGA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
	TATCTGAAGT	CCACCACTTC	AGAAGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
	AGTGGCTTAT	GTCAATTACA	CACAGAAATC	TTTAGTACTC	AAGGCAAAAC	AGCAATTGCC	1260
	CATCGAGATC	TGAAGAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAAGCTG	CTGTATTGCT	1320
	GACCTGGGCG	TGGCTGTTAA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
80	ACTCGAGTTG	GCAACCAAGC	CTATATGCCT	CCAGAAGTGT	TGACGAGAG	CTTGAACAGA	1440
	AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCTTCAT	CCTTTGGGAG	1500
	GTTCGTAGGA	GATGTGTATC	AGGAGGTATA	GTGGAAGAA	ACCAGCTTCC	TTATCATGAC	1560
	CTAGTGCCCA	GTGACCCCTC	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAAGAAGTTA	1620

5 CGCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAACTC 1680
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
 ACACCTTGCCA AAATGTCAGA GTCCCAGGAC ATTAAACTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
 TAAGCATCCA CAGTACAAGC CTGGAACATC GTCTGTCTTC CCAGTGGGTT CAGACCTCAC 1920
 CTTTCAGGGA GCCACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTG GCGGAGAAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

10 A71 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / U89326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51
 MLRSAGKLN VGTKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCFTMIEED 60
 DSGLPVVTSG CLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECKNOLHPTL PPLKNRDFVD 120
 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPFRYS IGLEQDETYI PPGESLRDLI 180
 25 EQSQSSGSGS GLPLLQRTI AKQIQMWKQI KGKRYGEVWM GKWRGEXVAV RVFPPTTEAS 240
 WPRETEIYQT VLMRHNILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNHLV KKNGTCCIAH LGLAVKFIID 360
 TNEVDIPNPT RVGDTKRYMPP EVLDESILNRN HFQSYINADM YSFGILILEVE ARRCVSGGIV 420
 30 EEYOLPHYDL VPSDPSPYEDM REIVCIKKLR PSPFNWSSD ECLRMQMKLM TECWAHNPAS 480
 RLTLARVKKT LAKMSPESQDI KL

Bladder

A72 DNA SEQUENCE

35 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 ATGTTCACAG ATCTGTACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCTCAT CATAGCACTA 120
 45 CTGAGCCTCG CGAGTATCAT CATTGTGTTT GTCCCTCATCA AGGTGATCTT GGATAAATAC 180
 TACTTCTCTT CGCGGCGAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
 GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
 50 GGGAACTGGT TCTCTGCTG TTTGCAAC TTACAGAAAG CTCTCGCTGA GACAGCCTGT 420
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
 GATCTGGATG TTGTTGAAAT CACAGAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540
 GGGCCCTGTC TCTCAGGCTC CTGCTCTTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
 AAGACCCCCC GTGTGGTGGG TGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
 55 AGCATCCAGT ACAGCAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
 CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GTTGGGGGCA 780
 GGCTCAGACA AACTGGGCGA CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
 ACTTCTCTAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 60 GCCACCCAC TCTGATCAT TGGATGGGCG TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTACAGCA CACGGTGCAA TGCAGACGAT 1080
 GCGTACCAGG GGGAGTCAC CGAGAAGATG ATGTGTGTCG GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 GTGGGCTATG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
 65 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

70 A73 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 75 Tryp_SPc domain: 204-429
 Cellular Localization: plasma membrane/ER

80 1 11 21 31 41 51
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIVV VLIKVILDKY 60
 YFLQGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120

GNWPSACFDN FTEALAEATAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNRS 180
 GPCLSGSLVS LHLCLAGKSL KTRPVVGGE ASVDSWPNQV SIQYDKQHV GGSILDPHWV 240
 LTAHCFRKH TDVFNWVKRA GSKLGSFSP LAVAKIIIE FNPMPKND IALMLQFPL 300
 TFSGTVRPIC LPFFDELTLP ATPLWIIIGW FTKQNGKMS DILLQASVQV IDSTRNADD 360
 AYQGEVTERM MCAGIPEGGV DTCQDSGGP LMYQSDQHWV VGIVSWGYGC GGPSTPGVYT 420
 KVSAYLWMIY NVWKAEL

A74 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGA GCAGAGCCAG CGCCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
 CGGTCTACTC CCAAGGTACA AGAGGTGGCC CGGTCCCTGG GGGAGCTCTG GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCGGTCTCTC TCCGGGCCCC CCGTCCCTGC CTGACGTGCC 360
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGTC TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAGTCCG 480
 GCGCTCATTG AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG 540
 GATTCTACCT GATTCTAGTC CTTGTGGGCC CGGTGGGCCG CCAGGGCCAG CCTGGCACTC 600
 AGCCCTTCGA GGTGGGGGCG CCCATCGCAC CCACCCCTCTC TGGCTGGAGA CCCCAGGAG 660
 GCCCAGCCAC GGGCTGGGAG TGGGCGCCTT CCGTCCCGCC TTGCAGATG GGCTCCCGAG 720
 GCGTCCCGCC GCGTGGTCCC CGCACCGAGC GCTTGACTCC GTTTKGGCTC CTGGTTGTTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCGG CTACTACTGG CCGCTGTCTG 840
 TGGACAGTGG GGTACCCCTC CATGAGTTAG CGTCCCGCCG TTCCAGCGGG TGCCGCGCTG 900
 GGTCCACTCT TCAGGGAAGG GCATGCGCCA CGCCAGGCTG CACTTCCAAC AACGGGCAGC 960
 AGAGGGGCGG GGGCGGCTCC GACGCGGGTC CAAGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
 GTAAGCGGGG GGTGCTTGCC TGCGTGGGGA GCCCCAGGGA TAGCGGTCCG ACTTCAGGTT 1140
 CTGGCCAGAG CTGAGGAGCC CTGGCTGCAG CGGATCGGCA CGCCGGGTGG GCGAGAGCTT 1200
 GGCTCTGATG TGGCTCCACC AGACCCCTGG GTGATGGCCT TCCCGCTCTT GGGCGGGAGC 1260
 TTGCGCCAGG TTGATGCCA CACAACATCC TGTGAGCCTG GCTCCCGAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGTCA TAGGCAAGGC CTGTTTCCCC CCACTCAGGA TTTCAGAGC 1380
 CTGGGGTCTT GCTCACCCCC CTTTGCTCTC ACGCCAGGCC TGTCCCGAGG TTTCAGCTGG 1440
 GAGAGGCCAC CTCCTCAGC CAAGGAAAGC GAGAACCCCC AGGGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTGGGTGTC ACTCCCTCAG CCCTGCCCCA GGCCTACTCC CGCTGGTGCT 1560
 GAGGTGAGCA TGTGTGGGGG GGCCCTGCTC AGCCCAACTT GGAGGGTCCC AGTGTACCA 1620
 GAACAGGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CGATGCGGGG 1680
 TCAGTGTGTG TGGGGCGCAG GGCTCCCGAT GCGGGGTGAG TGGTGGGGG GCGCAGGGCC 1740
 CCGATGCGGG GGTGAGTGGG TGGGGGGGCG AGGGCCCCCT CGTGTCCAGG GCCTTTGGT 1800
 ACCTGTGCCC ACAGGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAATC 1860
 CTTCCGAGG CCGAGCTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACTTCCC 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1980
 GCCCTCTTAC CTGAGAGATG GAGGTGGGCT TTCCAGGGGA CATAAGGATG TCAGGCTTGG 2040
 ACCTCCTGGG CAGGAAAGGG TGCAGGTCTT GAGGGCCTGT GCGCCACAGC CCGAGCACCC 2100
 AGGTGAGCTC CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GGAGAAGCCC CCGCTCAGCA 2160
 GGCTGGGGTC TGGCCACGAG GGCTCCCCCA CGTCTGCCTT TGAGGGTGCC TGCCATGCCC 2220
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGACTTCA TCAGGAGACC GCCCACATAG AGCTGAGACC CGCAGCTGAA GCGGAAATGT 2340
 GAGACAGGCT GGCACCTCCG GAAGAACTGC CTTTCAAGCT TGGTGTCCG TGCAAGGTGA 2400
 AAAGAAATAG GTCTCCCAAG TTTACAGCTT GAATCAGGC TAGTGAGTGG CCGTGGAGAC 2460
 CACGAGGGGA GAATTAAAG GCCCGGCTG GCAGGGCTTA GTGGCTGGC AGAGGCACAT 2520
 GCAGACCCCT CCGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGGCTC CTGGGCTCT ATCCGGGAGG TGCCAGTAGC GTGTGCAAGT ACATACAGT 2640
 GCGTGACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700
 CAGAAGTGTC CCAAGTTGAG AATCTGCCCC AGAGGAACAC ACCCAACCA GGCCTCAGGA 2760
 TTTTGTGTTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGGTGGT TGGTTCAAGC 2820
 CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAAGC CAGTGAGAGA 2880
 CCCCATCTCT ACAARAAAAA AAAAGAAAGG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

A75 DNA SEQUENCE

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Nucleic Acid Accession #: AB035089
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GGGCATGTCG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA 60
 CAGTTCTAGT AAAAGGGGGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGAAGG 120
 CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180
 TTGGTTTGAA AGCATTTAGT AAATATGATG TCTGTCCCTG GCAGTGTTTG CAGAGTAGGA 240

	AGGAGGAAGG	GAGGCAAGAG	ATAATATCAT	TTTCTCTGTG	CTCCAACGTG	ACTTACATAT	300
	GAGACTATTT	CCCTCTCTGC	TTTTCAAACC	TTACTGGAGT	TGTTTTCCCT	CATGAAAACC	360
	AAGAAAGGAA	AGCTAGTTAG	TCTTGTCTCG	AGGTGTGTCA	ATGTATACAT	ATCTATATCT	420
5	GTAGACAGAA	TCCTTGGGAA	TACAGTAATT	GACATATATT	CTGTTATTTG	ATGCTTGAAG	480
	AATCTCCTCC	ACTAACCACT	TTCCCTATAG	ATTGCCACAA	GCACATAATA	AGAAACAATA	540
	AATAAAATGT	TCTCTTGACT	TTGTACTTTA	ACAAATGCTGA	GAAAACCTTA	CAGCCTTCAT	600
	AAGGAAGTGA	GCTCCAGGAA	AATCTAGGAG	ATAATTTCTA	ACCAATCTAT	AAAGGCATTA	660
	GTAATGACAG	GATATTTCTT	GAAAGTGTAA	TTTCCCATTG	AGGATTTGTT	TTTAATTTCT	720
	GGATTCCTGG	AGCCAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
10	CAAGTGTTC	TATGCAAAAA	CTTCTTGGAA	TTTCTGAGTT	CTCTGTGSCA	ATATATGACA	840
	TCAGGATATG	TCCAGTCTCA	CACACCAGGA	TATGTCTCTT	CTAGCCTGTC	TATCACATGC	900
	TAGGAGAACT	ATTTAGGAAC	AGAAAAAAAT	GCCTGAAATG	ATTTCTCATT	TGAACCTATC	960
	CAAGCTTTCT	CTAAATTTAA	GCAAACTCCT	GGTCATTTTC	AGTTAGTACC	TTTCTTAAG	1020
15	TTCAACCTTC	AGGGCAAAAC	TCGGTGCTTC	AGACGTTTAG	CCATAGTCTG	AAATCTCTCT	1080
	CCATAGATTG	GTCCCTGTGA	ACCCCGGTTT	GTCTCAGCTT	GTATCCCTGT	TTTTTTCTTC	1140
	CCTCCATTCG	CAGGATGAGC	TTGTGTCTTC	TGTCTATGTA	GACATTAGAT	TCCTTTCTCT	1200
	TGGTAACTCC	GTAATCTCAT	CCTACTCCAA	TAGAGGAAGG	TCCATTTTTC	TCTTATAGCG	1260
	CTGGATCGAG	ACTCAGCTGA	GAAGACCATT	ATTCAATTTT	GGAATTTCTT	ATCTCAGATA	1320
20	TTTCTCTCTC	TTTCTTTTTC	TTCTATCTTT	GGATTTTTC	TCCATCAACG	CCCATTTAGT	1380
	CTATTCCCGG	ACTTCAATCA	GGGAACCTAT	ACCTCTTAAA	CTCATTCAGA	GACTCAAAAC	1440
	ATATATATTG	ATACAGGAGA	CCTAAGAAGA	GCATGTCTTG	GGGGTTGAGG	AAACAGGCAG	1500
	GTGAGAAACT	TCCAGATTGG	AAACACAGCT	TCCTTTCTCC	CATCCAGCCC	CTACTTTTCT	1560
	CCTATGTGTT	TCTGGCACTT	TGTTGTAGAT	AAATCTCCCT	TGACTTTGTT	ATGTGCTGAG	1620
25	AAAACAACCT	ACGGCTGTGT	GTTAAAAAGG	GCCCATGACA	ATACCAAGTG	TTGGGGAGAA	1680
	TGTGGAGAAA	TCAGAACTCT	ATTACGGGTC	GGTTGGAATG	CACACTTGTG	CAGAAATCTA	1740
	TGGAGAGAG	TCTGGCACTT	CCTCAAAATG	TAAACCTGGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCACTTAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAACATCAT	TATTCATAT	AGTAAAGGGA	TGGAACAAC	ACAAATGTCC	1920
30	ATCAACTTAT	GATTAAAGAA	AATCTGTCT	ATTATAGAAA	TGGAATATTA	TTGACCCACA	1980
	AAAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAA	TAACACTAGA	2040
	TTAAAGAAGC	CAGTCAACAA	AGGACTTACT	GTATGATTCC	ATTACCTGTA	AAATGTTTGA	2100
	ATAGGCAAACT	CATAGAAAAC	AGGAGGTAGA	TTCTGTGTTT	CCAGGGTCTC	CAGGAAGGGA	2160
	AGATGAAGT	ACAAGATTTC	TTTTGGAGGT	AGTGAATTTG	TTGTGGAATG	AGATCATGAT	2220
35	GATGATAGCA	CAACTTTGTG	AATATAATAA	AATCATTGAA	TTGTACAGTT	GAATTTATGG	2280
	TATATAAATT	ATATGTTAAT	AAAAAGGGGG	TCCACAAAAC	AAACAGCCCC	CCACTCTGGT	2340
	TGTGAGGAG	ATATTGGATT	AAATGGCCTT	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	TTACAAGATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	CCGAGGTGCT	2460
	AAACAGAAGG	ACCATTGAGA	AATGTTGTGA	TCCTGACAGG	TCAAGCAATT	TATTTTTCGG	2520
40	CTTCATTTT	AAATGTAATA	TTAGAAAGCT	GCCATTTAAA	ATGGCCCGTC	TGTTTCAATT	2580
	GCTCTTCTCA	GTGTGAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAAATGG	GCTTAGAGTT	CCACGTGATT	2700
	GGGAGGAGCT	CAATACTACA	GTAGGAGGCA	AAAGTTATT	TTACATGTTG	GCTGCAAGAG	2760
45	AAGATGAGGA	AGAAGCAAAA	GAAGAAACCC	CTGATAAAC	CATCGGATCT	CCTGAGGCTT	2820
	ATTAACATTC	ATGAGAATAG	CACAAGAAAG	ACCGGCCCTC	ATGATTCAAT	TACCTCTACC	2880
	TGGGTCCCTC	CAATAACATG	TGGAAATCT	GGTAGATACA	ATTCAGTTG	AGATTTGGGT	2940
	GGGAACACAG	CCAAACCAT	TCACTCAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AACAGAAAAC	CATCTGGGAT	GGTTGTAAGG	GGCACAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CAAAGCTGAG	CACCTAGGAG	AAGGCAATAG	AATCCTATTC	TCCATAGTAT	GCTATAAGAT	3120
50	ACTGAAGTAC	ACTTCTTCTC	TATCTCTTTG	GACTTTAGAAT	TAGCACTACA	TTCTTGTGTA	3180
	TACAGAAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAAA	CTTTGAGAAC	TGAAAAACAG	3240
	GAAATGTAA	CTTTTATGTT	CTTTGGTATT	CGAAGTATGC	CTAAAAGACA	ATGCAAAATC	3300
	CAAGAAAAAG	ATGGTGGGTT	TTTTGTTTGT	TTGGTTTGTG	TTTTGTTTGA	CAGCTGGAGT	3360
	AGAATACAAA	GGGATGGAGT	TGAAACAAAT	GAGAGGAAAT	TGGAATTTCT	AACTTATTCT	3420
55	CATTGGCATT	AGAAAGGCAC	CTACATGTAT	TTACATGAG	CCGGTGACTG	CTGACTTGCA	3480
	TTCTTATTTT	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GTAGAACTGT	AAATCCTGTCC	3540
	TTTGTATATA	ATTTTCTAT	TCATAAAGG	GAGTGTATGC	CCGCTTGTGA	AATCTGAAGT	3600
	TGAGTAACTT	CAATACTATA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	GGATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	GCCCACCTCT	GCTTCTCTTA	3720
60	GGAAACACAG	TAAAGGCTTC	AAGCCTCTCC	AGCTTAAATA	CATGAATTAT	TTTTGAGAA	3780
	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGCTGATT	ATATTTTACT	3840
	TATCTGCCA	GAGCAAAAT	AAAATACTTA	TTTCACTGTA	TTTGTCTTTT	ATCTAAATTT	3900
	CTTAGTTCCA	AGTAAACCAA	GGCACTTTTA	GGAAACACAGA	GGGAGAGTGC	CTTGACAGCA	3960
	GAGAGTCTTG	AAGGAGATGT	CAGGGAAGCA	TCTTAACAGC	TGGTTGAGTG	TGATCCACAG	4020
65	AGGTCTCCTG	TAGCATTCTA	TTGTAAGGCC	ATCCTACCTA	GCTCTAGTGT	AAACAGCAAT	4080
	GAAAGAAAAG	TAAAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTGT	4140
	TAAAGCCTCT	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTT	4260
	TTTAAGAAAA	TTGTACTACA	AAATACCAAT	CCATTTATTA	AAGTCATTCT	GACAGGAATC	4320
70	TGATGCTTTT	CCAGGAGTTC	CAGATCACAT	CGAGTTCACC	ATGAATTCAC	TCAGTGAAGC	4380
	CAACACCAAG	TTCATGTTTG	ATCTGTTCCA	ACAGTTCAGA	AAATCAAAAG	AGAAACACAT	4440
	CTTCTATTCC	CCTATCAGCA	TCACATCAGC	ATTAGGGATG	GTCCCTCTAG	GAGCCAAAGA	4500
	CAACACTTGA	CAACAAATTA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
	TTTTTCTCTG	GTTCCGTGGG	CTAGCAGGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
	AGCACAGGGG	GCTGTGCAGG	AATCCCATTA	ACTGTGAGAC	CAGTCACTTA	AACAGATCTT	4680
75	TTGAGTAAAG	TTTCTTGTG	CCGCTTCCAG	TCTCTTCCAG	TTCTTCTACT	TTGATCAAGT	4740
	CACAGAGAAC	ACCCAGAGAA	AAGCTGCAAC	ATATCATGTG	AGTCACAGAG	CAGCTCTGAT	4800
	CAGCTTTAGA	TCCCTGAACA	GCTCATAGTT	TAAACCTGGA	ACTTCACAAA	AACTAAGAAA	4860
	AGGCCAGTTT	TAGGAAAAT	CTTGACACAA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
80	TTCATGGCAC	ATAATTATTA	TTCTTCATTT	CTGCTTACT	AAAAGACAGT	CAGCACTGTA	4980
	CCTCAGAGCA	TAGGCTGGA	TCAGGATAGG	CTGGGTTCCG	ACTCCAGCTT	TGCTCTTCAC	5040
	AAATGATGAA	TAAAGAGCAG	ACACAACCTG	TGGAGTCCCT	AGTGACCTCA	TCCAGAGAAA	5100
	CTAAGGGTAA	GAAAAATCT	GACTCAATAC	ATGCAAAATG	ATGCAAAATG	TTACCAACAGT	5160
	GCCTTGCCCA	TAAAGTTCAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	ATAATTATAC	5220
	TAATCATAAT	AATGTGAAAA	TAAATTAATT	TTCAATGAGT	CATTAATGAG	ATTCAGAGGA	5280

	ATAAGCACAA	GTCCAAAGTAT	ATTTTGGAAA	ATGATTGCTA	TGGAATATAT	TGGTTTAGAG	5340
	CCTTAATAGT	GC AAAATGTCT	TTGCTGGAA	GTAGAAAGTT	CTAGATTATA	ACAGGCTTAG	5400
	GTTCAAAAC	TGGCACTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCCATTCTC	5460
5	TGAGCTTTCT	TGTGTTTCATC	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
	TTAGCCATGG	ACCTGGCATA	CACCTCTCTT	ACGTGCAGAG	AATGACCATC	ATGAGGAAAG	5580
	AGCCACAGAT	CAGTCAATGT	GTCCCTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640
	CCTGGCATAA	TCTATTTAAA	ATATCCAAAC	TTCAACATAC	TCGTATCCTT	GATGACTGTT	5700
	AGAAGTGAAA	TATGGTCTCT	GCCCATAAAG	AGCTGAGAGT	TTAACTGGGA	AGCTAAACCT	5760
	AACCTTTTAA	AGCAACAAGG	AGAAAATCTA	CTGGTAGACA	GCGCTGCATC	TTTAGTTTCA	5820
10	AAGAGAAAAG	ATTGCAGTAC	GTTAGAGCAA	GAAGAAATTT	CTGGAAGAAG	TCAAATATAA	5880
	GGTGGATTTT	GAAGGGTATT	TGAGGTGAAA	TACACCAATT	ATCAGGGAAT	AACATCAAAG	5940
	GTCCTCAATG	AGACTACCCAG	CATTTAGGGA	CTGATCTAAC	AGACTTAGCA	TGGGTTTAGT	6000
	ATTTACATTT	ATACAGCAAT	TGAATGATCT	CCTTTTTTGA	TGTTTGAAGG	TTGATAGGTC	6060
	AGGAAATGTT	CATCAACAGT	TTCAAAGCT	TCTGACTGAA	TTCAACAAAT	CCACTGATGC	6120
15	ATATGAGCTG	AAGATCGCCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAAT	TTTTACAGGT	6180
	AATTTACCTT	GGCCTACCCA	CATTTCAATT	GCATCCTGAT	GTCTGTGTCT	CTGAGTGGCC	6240
	AAATGGGAAG	AAGCAAGGCA	GATGAGCCTG	GCCGACCCAG	GTGGAGAGCA	TTTACTCAGA	6300
	GTGCATTAGC	TCCATTCCCA	CAACTCTCCC	CCACTGAGAT	GTCCAGACCC	CCAAACGATAC	6360
20	ATCACTGAAG	TGTGATTTTA	GGGATAATCT	TGTGATAAAA	GAGGAGGTTG	TGTAATAGAG	6420
	TGAGTAAGAG	TAATAAGTAA	TAAGATACCA	TCGATAAACT	GGCACTGACT	CAGTCACATA	6480
	CGATACATCT	TGGTGGGAAA	TGTATGACTA	ATGGGATATT	ATTGGAATGG	GCAGGCTTGG	6540
	GTGAGTTCTT	GAGAAATAGT	GAGGAAAGTAC	CAGGAAATAT	TGAATGCACA	GAGTGAAGA	6600
	CAAAAAA	CATCAGAAAC	ATCATGGTTA	AAATTAATGG	AGAGAGTCT	GAGAGCAAT	6660
	GAATCTCTCT	CAGGGAAGCC	TGCTCTGCAG	TTTGCAAAAC	ACAGCCTCTT	CTGCTTCTGC	6720
25	CTTTTGCCAA	GATGATATTG	ACCTTCAGTG	ACCTCTTTCT	TGTGCCAGCC	CACATTCCCC	6780
	TTTTGCATTG	CCTACATGAC	ACCTGTATAA	AAATATCCAT	GGACAGGAGA	TACTGCATCT	6840
	ATTCAGGCTG	TGGATTTCAG	TTACTGTTGT	TACAAATAAG	TAAATTTGGT	AATATATAGT	6900
	TACATAAATT	ACTCTTAATT	CCTACTTCTT	CCTTCATATC	TCAAAGGAAT	ATTTAGATGC	6960
30	CATCAAGAAA	TTTTACCAAG	CCAGTGTGGA	ATCTACTGAT	TTTGCAAAAT	CTCCAGAAGA	7020
	AAGTGAAGAG	AAGATTAACT	CCTGGGTGGA	AAGTCAAAAG	AATGGTAGGA	GAGCCACCCA	7080
	TTATAGAAAC	ACCTTTGAGA	AACTTATGCC	AGTGAGCCTT	GTGCTTGACA	CTGCATGGGG	7140
	GAACAGGTGT	GGGATTTGAG	ATGGGTTTGC	AGGGAGGGCT	GAAGAGGGCA	CTCCAGATGA	7200
	AGGATTTGTC	CAAAATGAATA	TGAAGAGAGC	CTAGGGGAGC	CAAGGAGGAA	ATCACAGGAA	7260
35	GCCAAATGAA	TGGAAACACA	TCTGGAGAA	TATTTGCTTA	TGGCCCTGCA	TGCAATAGC	7320
	TTTGTTGATC	CCCTGTCTCC	GCTCAGACCT	ATTTTGAGAT	CATATCCTTT	ACTTTAAATC	7380
	AGACTCAAAAT	TTTTATGATG	AATATTTAAT	AGAAAACATT	AGAAAGCGTC	TCTCTCTCC	7440
	TTTACTAATT	GGGAAACAG	CAGCTCTCTG	GTAAATCACC	CTTTTGTCTC	TGAGCTGGAG	7500
	CTGCCCTGAT	CACATCTGTA	GCCAAATGTT	TCTGCAGGGA	TTATCAGAGC	TCTCTTCCCC	7560
40	ATCAAGGGCA	AAGAGCTTGA	CAAAGTCTCC	ATCTACAGA	CATCTTCTCT	ACCTCCACCC	7620
	TCTCATTTACA	GGCCAAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCCG	7680
	GAAGTAGTGT	CTGACAGCAC	AGGACATGCG	TTTCATATTA	CAGAGCTCAA	GTCACTCATC	7740
	CTAAATATTC	CTCAGGGGCT	CCTTCTCTG	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
	AAGTAGGAAG	AGGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAATACA	7860
45	GTTTATCAGT	ATTTCCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTAACTCC	7920
	TTCTCTATCA	CAGAAGTGA	TGTCTCCATC	AAGGTAACT	TTATAAGACT	GGAGCCTTGA	7980
	AGAAAGCTGC	ATCTGTGAAA	CCACTGGTCA	GTGAGTCTAA	CAATTCAGAA	ATCAAAGTCA	8040
	GTGAGTCTCA	AGCAGGGATT	TGGGTCAATA	ATTAAAGATC	AGTCAGGAAC	ATTTGCAAA	8100
	CATCTTCCAG	ACAAGCCATT	TGTAGCTTGT	GTAAAGACT	CTTTTATTCT	TTCCCTTGCA	8160
50	GA AAAAATA	AAAACCTATT	TCTGTATGGG	ACTATTGGCA	ATGATACGAC	ACTGTTCTCT	8220
	GTGAAGCTAA	TCTATTTCAA	AGGGCAGTGG	GAGAATAAAT	TTAAAAAGAA	AAACACTAAA	8280
	GAGGAAAAAT	TTTGGCCAAA	CAAGGTATTG	TCTATATTTT	ATTATATATG	TGTAATATGT	8340
	TAATACATGG	AATGTTAAAC	ATTTCTGATG	GAATGTAAAC	TGATAAGTAA	AAAAATAAAA	8400
	TTGTTTCTGT	CTGTATTATT	GTGTTTATAC	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
55	GA AAAAATA	TGTTTCTAAC	TCTATGAAAT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	TGTTGCTATC	TCAATATATG	TATCTTTTTT	GTCTTGTGTT	TCAAGTGTAA	TTTGTGGAC	8580
	ACATGATTTT	ATTGCAAGAT	ACATACAAAT	CTGTACAGAT	GATGAGGCAA	TACAATTCCT	8640
	TTAATTTTGC	CTTGCTGGAG	GATGTACAGG	CCAAGGTCCT	GGAAATACCA	TACAAAGGCA	8700
	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	ATGAAATCGA	TGCTCTGCAG	AAGGTAAAGAA	8760
60	CTTGCACTCA	CAACTCTTCC	TCTACTGCCC	GGACATTTTT	CCAAAGATAC	CAAGTTTAAA	8820
	CAAGGTAAAA	GCTTATGACC	GAGTTGCCCT	AAAATGATGA	AAAATTCATA	ATGAGGAATG	8880
	ATGACTCACC	TTCAATATTAC	AAATATTGTA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940
	GT TTTTGT	GT TTTTGT	TTTATTATT	ATTATTATA	TACTTTAAGC	TTTAGGGTAC	9000
	ATGTGCACAA	TGTGCAGGTT	AGTTACATAT	GTATACATGT	GCCATGCTGG	TGTGCTGCAC	9060
65	CCATTAACAT	ATCATTTAGC	GTTAGGTATA	TCTCCTAATG	CTATCCCTCC	CCCCCTCCCC	9120
	CACCCACAAA	CAGTCTCCAG	AGTGTGATGT	TACCTTCCCTG	TGTCCAGTGG	TTCTCATTTG	9180
	TCAATTTCCA	TCTATGATTT	AATTTCCATCT	ATGGCTTAGT	TAATGATTAA	TTTATTAGAG	9240
	TTACATGCAAT	TGGATATCAA	TTTGATGATA	TTATTATGCA	GCAATTTAAA	CTTGACTGGG	9300
	AGAAATATAT	ACCAATGTGA	GGAAAGTTTA	CAATAGGCC	GAGTAGAAAA	GGGAATACAA	9360
70	ATTTAGGAAT	TTAGGGAAT	ACAATTTAAT	AATTGCAATG	TGTACTAAAT	AATGTATACA	9420
	GA AAAATATG	ATGAGCCTAT	TAAAAATTGA	CACATGTAGT	AGGCTGTGGG	CACAAAGAAAT	9480
	AGTGATACAT	ACAGTTCAAT	GTGTACAAAA	TAATGTAAATC	ATATTTTACA	TGTGTATCAT	9540
	ACAGTTGTAT	ACATACATAT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
	ACATACATGT	ATATACATAT	ACATATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
75	TTTTACCTAT	TAGAATAATA	ATGCTATTTA	AAGTGAACCT	TCTGTATTTT	ACATTTATTG	9720
	CCAAATTAAC	GAATCTCCAC	ATAGTCAATT	CTTGTGTAAG	GTGTATTAGA	GATCGACAGT	9780
	TAGTCATATC	AGTTTCTTTT	TTCCATTGTT	ATAGCTTGAA	GAGAACTCA	CTGCTGAGAA	9840
	ATTGATGGAA	TGGACAAGTT	TGCAGAAAT	GAGAGAGACA	TGTGTGATT	TACACTTACC	9900
	TGGTTCAAA	ATGGAAGAGA	GCTATGACCT	CAAGGACACG	TTGAGAACCA	TGGGAATGGT	9960
80	GAATATCTTC	AATGGGAGTG	CAGACCTCTC	AGGCATGACC	TGAGGCCACG	GTCTCTCAGT	10020
	ATCTAAGTCT	CTACACAAGG	CCTTTGTGGA	GGTCACTGAG	GAGGGAGTGG	AAGCTGCAGC	10080
	TGCCACCGCT	GTAGTAGTAG	TGGAATTATC	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTGT	10140
	TAATCACCTC	TTCCTATTCT	TCATAAGGCA	AAATAAGACC	AACAGCATCC	TCTTCTATGG	10200
	CAGATTCTCA	TCCCATAGAA	TGCAATTAGT	CTGTCACCTC	ATTTAGAAAA	TGTTCACTCA	10260
	GAGGTGTTCT	GGTAACTGAA	TTGCTGGCAA	CAACAGATTC	TCTTGGCTCA	TATTTCTTTT	10320

5 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTTA ATGATTAATA TAGCATGCCT 10380
 TTCTCTCTTT CTCTTAATAA GCCACATAT AAATGTACTT TTCCTTCCAG AAAAATTTC 10440
 CTTGAGGAAA AATGTCCAAG ATAAGATGAA TCATTTAATA CGTGTCTCTT TAAATTTGAA 10500
 ATATAATTCT GTTCTGACC GTTTTAAAT GAACCAACC AAATCATACT TTCTCTTCAA 10560
 ATTTAGCAAC CTAGAAACAC ACATTTCTTT GAATTAGGT GATACCTAAA TCCTTCTTAT 10620
 GTTCTAAAT TTTGTGATTC TATAAACAC ATCATCAATA AAATAATGAC ATAAATCAT 10680
 TTTTGTCTTA CCTGTCTTCT CTCTGAAAAG GGCAAGTGT CAGTTACACA TAGGAAAGAT 10740
 AATTAGAGA TATATTAATC ATATATAAAG GAAATTTAAA AACAGAGTAG TTCATGATGA 10800
 10 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACCACA TAGGAACCTC 10860
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 15 AGAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGAAGAATA TCTTGTCTT 11160
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 TCAAATGGAT TTGCTGGCA GGCACCTGAA GATATTAGTC TAAATCTCAG AACAGATA 11280
 TGATCTGAAG CTTAAATTT GTGATATTCA ATATAAATAC TTAGAGTCA TTGGGATAAA 11340
 TATGTTAGTT GTAGCTAAAA GCAGAAATAA GATACTAGGG AGAAGGATA AAGTTAGTAA 11400
 20 AAAGAAGAT CTAGAATTGA CCTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460
 CATTTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTTACTCC CATAGATTCT 11520
 TCCC

25 A76 Protein sequence:
 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Protein Accession #: BAB21525
 30 Signal sequence: none found
 Transmembrane domains: none found
 Serine Proteinase Inhibitor domain: 13-390
 Cellular Localization: secreted

35 1 11 21 31 41 51
 MNSLSEANTK FMFDLFQQR KSKENNIFYS FISITSALGM VILGAKDNTA QQISKVLHFD 60
 QVTENTTEKA ATYHVDKSGN VHHQFQKLLT EFNKSTDAYE LKIANKLFG E KTYQFLQEYL 120
 40 DAIKKFYQTS VESTDPANAP EESRKKINSW VESQTNEKIK NLFPGDTIGN DTLVLVNAI 180
 YFKGQWENK KENTKEEKF WPNKNTYKSV QMMRQYNSFN FALLEDVQAK VLEIPYKGD 240
 LSMIVLLPNE IDGLQLEEK LTAEKLMWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
 TMGMVNIIFG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAATAVV VVELSSPSTN 360
 EEFCCNHPPF PFIRQNKINS ILPYGRFPSP

45 A77 DNA SEQUENCE
 Gene name: hypothetical protein FLJ13459
 Unigene number: none found
 Probeset Accession #: XM_047266
 Nucleic Acid Accession #: XM_047266
 50 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 55 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAAGTG CTGGGATTAC AGGTGTGAGC 60
 CACCATGCCA GGCCTCTTAA ACCTCTTCAA GTCTGTTTTC TCATCTGCAA AACAGAGGTA 120
 ATAAGATCAG TATCTCTTAA ATGGAAGCAC CTGGACTACA TTTTTCAT TCATGTTAT 180
 CATAAATGAG GACTAACCTG TCTCCCGTTG GAGTGTGGA ACCTAGACCT CATGTCTTCA 240
 TGAGGTATC ACTGCCCCAG GCCCAGCTGT GTCCCTACAC CAGCCCCAGC TGAAGCATCT 300
 60 TCTTTTCTG CCTGTAGAGA TGGTTACAAAT GCTTGGGCTG ATGCATTCTG GCCTTCGCAG 360
 ATCTTGGCG GGTGTGCGCA ACGCTGTGGC CTCCCTGCCC CTGAATACCG AGCGGTGCT 420
 GTCAGGTGG GCAGCAAAAT CTTCTGACA CCACCGGAGA CCCTGCCCCC AGGGATCTCT 480
 TCACATGTGG ATTGACATCT TTCTCTAAGA TGTGCTGCT CCACCCCCAG TTGACATCAA 540
 GCCTGGCAG CCAATCAGCT ATGAGCTCAG AGTTGTATC TGAACACCG AGGATGTGCT 600
 65 TCTGGATGAC GAGAATCCAC TCACCGGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGAGCTT CACTTCAACT CCTTGACTGG 720
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTTGAC TACCTGCCCA CGGAGCGGGA 780
 GGTGAGCGTC TGGCGCAGGT CTGGACCTTT TGCCCTGGAG GAGGCGGAGT TCCGCGAGCC 840
 TGCAGTCTG GTCTGTCAGG TCTGGACTA TGACCGCATC TCTGCCAATG ACTTCTTGG 900
 70 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCCCC AGCTCTGCTC 960
 TGTGCACTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTGGCT GCGCGGCTCT 1020
 GAGGGGCTGG TGGCGGTAG TGAAGCTGAA GGAGGCGAG GACGTGGAGC GGGAGCGCGA 1080
 GGAGGCTCAG GCTGGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GCGCAGAGA 1140
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCCTC ACGGCGAAG TGGAGGCAGA 1200
 75 GTTGTGAGCT CTGACTGTGG AGGAGGCCGA GAAACGGCCA GTGGGGAAGG GCGGGAAGCA 1260
 GCCAGAGCCT CTGGAGAAAC CCAGCCGCC CAAACTTCC TTCAACTGGT TTGTGAACCC 1320
 GCTGAAGACC TTTGCTTCT TCATCTGGCG CCGGTACTGG CGCACCTTGG TGCTGCTGCT 1380
 ACTGTTGCTG CTCACGCTCT TCCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG 1440
 CCAGGTATC TTCCGTCCCC TCCACAAGTG ACTCTGCTG ACCTTGGACA CTCACCCAGG 1500
 80 GTGCCAACCC TTCAATGCCT GCTCCTGGAA GTCTTTCTTA CCCATGTGAG CTACCCAGAG 1560
 GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG

A78 Protein sequence:
 Gene name: hypothetical protein FLJ13459

Unigene number: none found
 Probeset Accession #: XM_047266
 Protein Accession #: XP_047266
 Signal sequence: none found
 Transmembrane domains: 291-313
 C2 domain: 27-86
 Cellular Localization: plasma membrane / ER

10 1 11 21 31 41 51
 MWIDIPPDV PAPPVVDIKP RQPISEYELRV VIWNTEVDVL DDENPLTGEM SSDIYVKSUV 60
 KGLEHDKQST DVHFNLSLTGE GNFNWRPFVR FDYLPTEREV SVWRRSGPPA LSEAEFRQPA 120
 VLVLQVWDYD RISANDPLGS LELQLPDMVR GARGPELCSV QLARNGAGPR CNLPRCRLR 180
 15 GHWFPVVKLKE AEDVEREAQE AQAGKKRKRQ RRRKORPEDL EPTDMGNNVY ILTGKVEAEF 240
 KLLTVEBAEK RPVGKGRKQP EPLEKPSRPK TSNWPFVNPL KTFVFFIWRR YWRTLVLALL 300
 VLLTVFLLLV FYTIPGQISQ VIFRPLHK

20 A79 DNA SEQUENCE

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Nucleic Acid Accession #: AL137708
 25 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120
 AGACTGGGGG GCTGCAGAGG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
 ATGGCCTGGG CTGGGCCCCG GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240
 CTCTGTGTGG CAAAGCAGGG GAGGCGCCAA TGTGAGGAA CAGAGTCTCC TGGTGGCTG 300
 35 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCCTG 360
 GGGTCAACGT AGGCCCATG TAGCACCTCT GTTCCCCTGC CTGTAGGTGA CAGGAGCCAG 420
 CCCAGCCAGG TGTGCTCCTT CCCAGGCCCT TAGGCAGGGG GGTACAGGGG CCAGCAGCTG 480
 CGCCCGCCCC ACCTTCTCTT CCACCCACAT GCGAAGGGT GGCAGGCGAC GCAGGTGGAC 540
 GAGTCCAGCG AGCGGCTGAG TCAGTGTGTG TGAATGTTT TGGCCGCTCC CAGCTGCACC 600
 40 CTGCCCCTAC CTGCCACCAC CTCACCTTCA TCCTCAGGGG CTGCGGCCCT GAGCCCCCTG 660
 CAGGAATGCA CCTTTAGCCC AGGCCCTGCT AGTGAGCTCC GCCCAGCAGC AGCCCTGCTC 720
 CTCGCCCAT GACCTGCGAG ACCCTCTGCG GCTTCCAAGT TCCTGGGGGC TGCAATGAAC 780
 ATGCTCCACC TGATGCGCTG GCAAAACCAT GTGGGCCCCA GCTGTGTGTC GTGCTGGGGT 840
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 45 AGGCAGGGCC CAGGGTCCAG GGCCCGAGAG AGAGAAGCAG GAGGGAGAGG AGCTTCCTGG 960
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 AGGCTGCGAG GGCCCTGCCT GCTTGGCTGG GGCTGGGGGC TGCTGGGAGG TGGCTGGGAG 1080
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 50 CTTCCTGCTG CACAGAACCC TCGCCCTGCG CCACCCCGTG CTGCCTCCTT GCCCTGGCAG 1200
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 55 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500
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 60 GGGAGATTCA GCGCCAGGGA TGGTTTAACC CCCACAGAGG CAGGGCGTGG AGGACCTTCC 1800
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 GGGCCGAGG GAGCCACAGC GGGTCTCTGA GGAAGGCAGG GGTACCCCA GATGCCAAGT 1920
 TTTGGGTGGG TTTGGCGGGT CTCACAGAGC GAAGCGAAGC ATTTGTGCTT GTTGGGTGGC 1980
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 65 CTCTGATGAG GCATGATGTC AGCACCACTT GCGCCTTGTC CCAACTCACT CCAGGTGCAA 2100
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 70 GTGGGCTGTA GGCAGGCAGC GGCCTGAGG CCTGGGGGCA CGGTGGACCC CTATGCCCGG 2400
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 75 AGGCGGAGCT GGCAGGGGCC ACCCTGCAGG TGCACTTTT CAATTCAGG CGCTTCTCGG 2700
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 80 TGAAGCCCCC CTTCCTGCC ACAGCCCGAG CAGGTGGGG AGCTGTGCTT CTCTCTCGG 3000
 TACGTGCCCA GCTGAGCGG GTGGTGTCTG AGGCTCGAGG CCTGGGTCCA 3060
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 CTGCCGCTCC GAATGAGCC CGTAGGCAAG GTGCACCTGG GTGCCCGGGC CTCGGGGCAG 3300

CCCCGACG ACTGGGCGA CATGCTGGC CACGCCGGC GGCCCATTCG CCAGCGGCAC 3360
 CCCCTGGGC CAGCCAGGGA GGTGGACCGC ATGCTGGGCC TGCAGCCCCG CCTTCGCCTG 3420
 CGCTCGCCCT TGCCCACTC CTGAATGCAC CACATGCCCT TGTCTCCCGG CTGAGCCCG 3480
 GCACTGGCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

A80 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Protein Accession #: CAB70885
 Signal sequence: none found
 Transmembrane domains: 69-85
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MGHPVPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWL QLSTDALSLA 60
 STPGPRNALI AGALAAGVLL VSCLLCAACC CCRHRKPKPR DKESVGLGSA RGTTHLVR 120
 SGLLTQSRG GLKSLQSPG QRGEFSPRDG LTPTEAGR

A81 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51
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 CCTCCGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGGC 180
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 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAAT GGCAAGGGTC 420
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 ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGCTTCTGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTGTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660
 TCATCGTGAC CGACCAAGAT GACCAACAAG CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
 GTGTCTTAGA GGGAGTCTTA CAGGTACTT CTGTGATGCA GGTGACGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGTGGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
 AGGACCCGTA CGACCTCATG TTCACAATT ACCTGAGCAC AGGCACCAT AGGCTCATCT 900
 CCAGTGGCCT GGACCGGGAA AAGTCCCTGT AGTACACACT GACCATCCAG GCCACAGAGC 960
 TGGATGGGGA CGGCTCCACG ACCACGGCAG TGGCAGTAGT GGAGATCCCT GATGCCAATG 1020
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 GTGCCACCTG CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
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 CCTCCAAAGT CGTTGAGGTC CAGGAGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAAG CCTGACAGAG GAGAATCAAA AGATCAGCTA CCGCATCCCT AGAGACCCAG 1500
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCA AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGGCC TCCACCACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCGTCAGA TCACCATCTG CAACCAAGC CCTGTGCGCC 1740
 ACGTGTGAA CATCAGGAC AAGGACCTGT TCCCCACAC CTCCCTTTC CAGGCCACG 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
 ACCATGGCAA CAAGAGCAG CTGAOGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGAAAC CTGCCCTGGA CCCTGGAAGG GAGTTTCTAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTTCTCT CTGCTGTGTC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CTCTCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCGCG CCTTGGTG TGCGACTATG 2400
 AGGGCAGCGG CTCGACGCGG GGTTCCTTGA GCTCCCTCAC CTCTCCGCG TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GGAGGACGAC TAGGCGGCTT GCCTGCAAGG CTGGGGACCA AACCTCAGGC 2580
 CACAGAGCAT CTCACAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTGG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GGCGAGACA GGCATATGAG CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTAGGATGCG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
 CACCTGGGCC AGGGTTGCTT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAACCC TGTGTCTCTG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATT TCGGTTTCCA GACCCCAATG CCGCCATTC GATGATGAT CTGCGTTTCT 3060
 ATACTAGTG TGCTAGGTT GCCCTTAT TTTTATTTT CCGTGTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAACTTTT TATTAAAGAA A

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)

Cellular localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MGLPRGPLAS LLLLQVCNWLQ CAASEPCRAV FREAEVTLEA GGADQEPGQA LGKVFMGCPG 60
    QEPALFSTDN DDFTVRNGET VOERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
    KGPPFQRLAQ LKSNKORDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREELAK 180
    YELFGHVAISE NGASVEDPHN ISIIVTDQND HKPKFTQDTP RGSVLEGVLP GTSVMQVTAT 240
    DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
    TDMGDGSGTT TAVAVVEILD ANDNAPMPDP QKYEAHVPEV AVGHEVQRLT VTDLDAPNPS 360
    AWRATYLIWG GDDGDHFTIT THPESNQGIL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
    PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
    DPAGWLAMPD DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLLTLID 540
    VNDHGPVPFP RQITICNQSP VRHVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNBEGD 600
    TVVLSLKKPL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILFVL 660
    GAVLALLFL LVLVLLVRKK RKIKESPLLLP EDDTRDNVFP YGEGGGGEDD QDYDITQLHR 720
    GLEARPEVVL RNDVAPTIIP TFMVYRPRPAN FDEIGNPIIE NLKAANTDPT APPYDTLLVF 780
    DYEAGSGDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGGEDD
  
```

A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
40  AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGTGG CTGTGGCCTC 60
    GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTTACACTTC GCCATGAGTT TCCTGATCGA 120
    CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTITGGA TTTGGGTGGC TTTTCTTCAT 180
    GCGCCAAATG TTTAAAGACT ATGAGATAAG TCAGTATGTT GTACAGGTGA TCTTCTCCGT 240
    GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
    GAATAGCAGC TCCCGTTATT TTCACTGGAA AATGAACCTG TGGCTAATTC TGTCTGATCT 360
    GGTTTTCATG GTGCCTTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
    TAAACAACGA CTGCTTTTTT CCGTCTCTCT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
    ACTAGAGAGT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
    CATCAGCCGG GTTGTGTGTA TTGAGTGAC TCTCATGGCT CTCTTCTCTG GATTTGGTGC 600
    TGTCAACTGC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
    TCTAGCCCTG GAACGGCGAC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
    GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGAGG GTGCATAACA AACCATCAGC 780
    TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
    TATTCAACAG GAAGTGGATG CTTTGGGAAG ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
    TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATATT 960
    TAATTTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
    CAATATTGTT TTTGATCGAG TTGGGAAAAA GGATCTCTGC ACAAGAGGCA TTGAGATCAC 1080
    TGTGAATTAT CTGGAATCC AATTGTAGT GAAGTTTGGG TCCCAACACA TTTCTTCTAT 1140
    TCTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200
    CTTTATGCC ATCTCTAGCA GTAAGTCTCT CAATGTCAAT GTCTCTCTAT TAGCAGAT 1260
    AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320
    CCGCACCAAT ATCACTGAAG TCCTTGGAGA ACTGCAGTTC AACTTCTATC ACCGTGGGTT 1380
    TGATGTGATC TTCTTGGTCA GCGCTCTCTC TAGCATACTC TTCTCTATT TGGCTCACAA 1440
    ACAGGCACCA GAGAAGCAAA TGGCACCTTG AACTTAAAGC TACTACAGAC TGTTAGAGGC 1500
    CAGTGGTTTC AAAATTTAGA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
    ATAAACAAC AAAATGCTAT GTTAGCATTT TTCACTTCA TAGCATACTC CTTCCCCCTC 1620
    AGGTGATACT ATGACCATGA GTAGCATCAG CCGAACATG AGAGGGAGAA CTAACTCAG 1680
    ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CCGAGAGGAG 1740
    CCAAGAAACT AAAGGTGAAA AATACACTG AACTCTGGG CAAGACATGT CTATGGTAGC 1800
    TGAGCCAAAC ACGTAGGATT TCCGTTTTAA GGTTCAATG GAAAAGGTTA TAGCTTTGCC 1860
    TTGAGATTGA CTCATTAATA TCAGAGACTG T
  
```

A84 Protein sequence

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Protein Accession #: NP_057418.1
 Signal sequence: none found
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
  
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5 MSFLIDSSIM ITSQILFFGF GWLFFMRQLF KDYEIRQYVV QVIFSVTPAF SCTMFELIIF 60
 EILGVINSSS RYFHWKMNLC VILLILVFMV PFYIGYFIVS NIRLLHKQRL LPSCLLWLT 120
 MYFFWKLQDP PPIILSPKHGI LSIEQLISRV GVIGVTLMAL LSGPGAVNCP YTYMSYPLRN 180
 VTDITLILE RRLLOTMDMI ISKKRMAMA RRTMPQKGEV HNKPSGPNMG IKSVITTSASG 240
 SENLTLIQE VDALEELSRO LPLETADLYA TKERIBYSKT PKGYFNPLG YFFSIYCVWK 300
 IFMATINIVF DRVGKIDPVT RGIETVNYL GIQFDVKFWS QHISFILVGI IIVTSIRGLL 360
 ITLTKFFYAI SSSKSSNVIV LLLAQIMGY FVSSVLLIRM SMPLEYRTII TEVLGELQFN 420
 10 FYHRWFDVIF LVSALESSILF LYLAKHQAPE KQMAP
 A85 DNA SEQUENCE:
 Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 15 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 GGAATTCCTT TTTT TTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG 60
 CAATGGGACA ATCTCAGCTT ACTGCAACCT CCGCTCCCG GGTTCAGCG ATTCTCCTGC 120
 CTCAGCCTCT CAAGTAGCTG GGATTACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180
 25 CTTTCTTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
 ACCTCAGGTG ATCCACTTGC CTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAACATG 300
 TGCCTGGCTG ATCTTTTTT TGTGTTGGA TTTTGAAGC AGGCTCTCC TTGTCGCCC 360
 AGGCTGGAGT GCAGTGGTGC GATCTGGCT CACTATAACC TCCACTCCTT GGTTTCAAGT 420
 GATCCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGACCA CCACACCCGG 480
 30 CTAATTTATT TATTTTATT AGAGACAGGG TTTCACCATG TTGGCCAGGC TGTCTCAAA 540
 CTCTGGACT CAAGGGATCC GCTGCTCC ACTTCCCAA GTCCCGAGT TACAGGTGTG 600
 AGTCACCATG CCTGACCTTA TAATCTTAA GTCAATTTT CTGGTCCATT TCTTCTCTAG 660
 GGTCTCACA ACAATCTGC ATTAGGCGGT ACAATAATCC TTAACCTCAT GATTACAAA 720
 AGGAAGATGA AGTGATTCAT GATTAGAAA GGGGAAGTAG TAAGCCACT GCACACTCCT 780
 35 GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAA 840
 TTTGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA 900
 ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960
 TGCAGTTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT 1020
 CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080
 40 AACTAAGCTT CTAATAAAA TCTGCTGATA CTACAGATAA CTGGGAAC GTTAACCAA 1140
 TTATGATGAT GCAAAACAAC CCAGAGGACT GGTGAGTTT GTTGCTCAA CTAGAGAAA 1200
 ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCGTAC AGTCAAGCAA 1260
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAATGAGAG TTTTGCTAGA ATTCAGTGA 1320
 GATTGTCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTACTAC TTTCAAATGG 1380
 45 CCAGAGCAA CTGCAAGAAA TTTGCTTTG TTTTATATC TTTTGCAAA TTTGAATCTG 1440
 CACAAGGTA TGTCAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG 1500
 TACCACTAGA AATGCTGGA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560
 TTTTCAAGAA GGAAAGAGAG AATTATCAG CATCTACGGT ATTAACCTGC CAAGAATCAT 1620
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 50 CTACTAAGC CAGTTTCTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740
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 CAGTTAAGCT TCTAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCA GTTGTACCTT 1860
 GTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGGTTGTG CCGGATCTA 1920
 AACCAGTGG AATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTC AAATAGTCAT 1980
 55 TCAAGGAAC CTGCTGTGCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATA 2040
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 AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTCA GTTCAAAAC 2280
 60 AGTCACCAAC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGTT AAGACACCA 2340
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 65 GTTCAAGCAA GGTATTCTAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
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 70 TTCAACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACCACTT AACTTTCTGA 2940
 TAGTTGATGG AATGCTAAG CTAAATTGAT TTGGGATTGC AAACCAATG CAACAGATA 3000
 CAACAAGTGT TGTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060
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 GTGATGTTGT GTCTTAGGA TGTATTTGT ACTATATGAC TTAGGGGAAA ACACCATTTT 3180
 75 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCTTAAT CATGAATATG 3240
 AATTTCCCGA TATTCCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTGTT TAAAAAGGG 3300
 ACCCAAAACA GAGGATATCC ATCTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360
 CTACCCAGT TAACCAAGAT GCCAAGGGAA CCACTGAAGA AATGAATAT GTTCTGGGCC 3420
 AACTGTGTGG TCTGAATCTT CCTAATCCA TTTTGAAGC TGCTAAACT TTATATGAAC 3480
 80 ACTATAGTGG TGGTGAAGT CATAACTCTT CATCTCCAA GACTTTTGA AAAAAAGGG 3540
 GAAAAAATG ATTTGCAAGT ATCGTAATG TCAGATAGGA GGTATAAAT ATATTGGACT 3600
 GTTATCTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660
 ATCAGCAAAA AAAATCAAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCA 3720
 TTAGGCACT GTATATATTG TAGACTGTTT TTCTCTGTTT TATGCTCTG TGAATCTAC 3780
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTTG 3840

TAAATAAAGT TTTGTGGCTA AAATGA

A86 Protein sequence:

5 Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 10 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51
 15 MNKVRDIKNN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MHANNPEDNL SLLKLEKNS 60
 VPLSDALLNK LIGRYSAIE ALPPDKYQON ESPARIQVRF AELKAIQEPD DARDYFQMAR 120
 ANCKKPAFVH ISPAQFELSQ GNVKSKQLL QRAVERGAVP LEMLEIALRN LNLQKKQLLS 180
 EEKKRLSAS TVLTAQESFS GSLGHLQNRN NSCDNRGQTT KARFLYGENM PPQDAEIGYR 240
 NSLRQNTTK QSCPFGRVFV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPKSKP 300
 20 SGNDSCLELN LKSVQNSHPK EPLVSDKSS ELIITDSITL KNTKESLLA KLEBTKBYQE 360
 FEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFE QPVFVSVKQS 420
 PPISTSKWFD PKSICKTPSS NTLDDYMSCF RTPVVKNDFF PACQLSTPYG QPACFQQQKH 480
 QILATPLQNL QVLASSANE CISVKGRIVS ILKQIGSGGS SKVPQVLNEK KQIYAIKYVN 540
 LEADNQTLN SYRNEIAYLN KLQGHSDXII RLYDYEITDQ YIYVMVECGN IDLNSWLKKK 600
 25 KSIDPWERKS YWKNMLEAVH TIHQHGIVHS DLKPANFLIV DGMKLKIDFG IANQMOPDIT 660
 SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYGKTPFQK 720
 IINQISKLHA IIDPNHEIEF PDIEPKLDQ VLKCCLEKRP KQRISIPELL AHPYVQIQTH 780
 FVNQMAKGTG EBMKVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRKG 840
 K

A87 DNA SEQUENCE

35 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 GGGGCGACGG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCCCT 60
 CTGCCACCTG GGGCCCGTCC GGGCCCGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
 CGATGCACTG GCGCTCACTG CGAGCTGCGG CGCCGACAGC CTTCGTGGCG CTCTGGGCAC 180
 CCTGTCTCT GCTGGGCTCC GCGCTGCGG ACTTCAGCCT GGACAAACAG GTGCACTCGA 240
 45 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGCGGGGA GATGCAGCGC GAGATCCTCT 300
 CCATTTTGGG CTGCCCCAC CGCCCGCGCC CGCACTTCCA GGGCAAGCAC AACTCGGCAC 360
 CATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGGC 420
 GCGAGGGCTT CTCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CTCTGGGCA 480
 GCGTCAAGA TAGCCATTTC CTACCGAGC CGGACATGGT CATGAGCTTC GTCAACCTCG 540
 50 TGGAAACATG CAAGGAATTC TTCCACCCAC GCTACCCACA TCGAGAGTTC CGGTTTGATC 600
 TTTCAGAGT CCCAGAGGGC GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
 ACATCGGGA AGCGCTCGAC AATGAGAAGT TCCGATCAG CGTTTATCAG GTGCTCCAGG 720
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 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAGCAA CCCTGGGTG GTCAATCCGC 840
 55 GGCACACCTT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
 AGTTGGCGGG CTGATTGGG CGGCACGGGC CCCAGAACA GAGCCCTTC ATGTTGGCTT 960
 TCTTCAAGCG CAGGAGGCTC CACTTCCGCA GCATCCGCTC CACGGGAGC AAACAGCGCA 1020
 GCCAGAACCG CTCAAGACG CCCAAGAAC AGGAAGCCCT CGCGATGGCC AACGTGGCAG 1080
 AGAACAGCAG CAGCAGCCAG AGGCAGGCGT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
 60 GAGACCTGGG CTGGCAGGAC TGGATCATCG GGCCTGAAGG CTACGCGGCC TACTACTGTG 1200
 AGGGGGAGTG TGCTTCCCT CTGAATCTCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
 AGACGCTGGT CCACCTTATC AACCCGAAAA CGGTGCCCAA GCGCTGCTGT GCGCCCAAGC 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTCC ATGACAGCTC CAACGTTCATC CTGAAGAAAT 1380
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 65 TTGGGGCCAA GTTTTCTCG ATCTCTCAAT GCTCGCTTGG GCCAGGAACC AGCAGACCAA 1500
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 TCCTACAGCG TGTCAGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
 GCGGGGCGAG GTCATTGGCT GGGAAAGTCT AGCCATGCAC GGAAGTGTGT CCAGAGGTAA 1740
 70 TTATGAGCGC CTACCAAGCA GGCACCCAG CGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
 GGGCATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
 CAATAAAGCG AATGAATG

A88 Protein sequence:

75 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 80 Pfam domains: TGF β propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

```

1      11      21      31      41      51
5      MHVRSRLRAAA PHSPFVALWAP LFLRLRSALAD PSLDNEVHSS FIHRRRLRSQB RREMOREILS 60
      ILQLPHRPRP HLQKQKNSAP MFMLDLYNAM AVEEGGPGG QGFSYPYKAV PSTQGPPLAS 120
      LQDSHLFTDA DMVMSFVNLV EHDKEFPFPHR YHREPRFDL SKIPEGEAVT AAEFRIYKDY 180
      IRERFDNETP RISVYQVLQE HLGRESDLPL LDSRTLWASE EGWLVDITA TSNHWVNVNR 240
      HNLGLQLSVB TLDQGSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
      QNRSKTPKNQ EALRMANVAB NSSSDQRQAC KKHLYVSPR DLGWQDWIIA PEGYAAYCE 360
10     GECAPPLNSY MNATNHAIVQ TLVHPTINFET VPKPCCAPTQ LNAISVLYFD DSSNVILKRY 420
      RNMVVRACGC H

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A89 DNA SEQUENCE:

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15     Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
      Unigene number: Hs.27373
      Probeset Accession #: F13036
      Nucleic Acid Accession #: AC012478
      Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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25     CGCGAGTGGC GGCCACCGCC CGGCCCGGGG CCGCGGAACA CCACCCGGTT TGGGTCTGGG 180
      GCGGCGGGCG GCAGCGGCAG CTCACGTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240
      ATTTCCATCC CCTCCGCGCA CCTACCCACC CTCAAGGCAG CCGTGATCGT GCGGTTCCGC 300
      TTACCAACC TCCTCATCGC CTGCTGCTG CTGCGCTCT TCAGGTGGG AAAGAGGTTA 360
      AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGG AATGGCGCCA 420
30     CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
      TCCTTGCCGG CTGCACGAGT ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTT 540
      GTGCCCCACC CCTTCATCCT CGACATTGAC CTTCAGCAA GATGCACTGG AAGGCTCTAT 600
      GGTGAATCA GACCTGGTAA AACCTGTTTC CCAGCTGGT GGCATCCTGT GGAAAGTTGG 660
      TCAGCTGCAA CTTGGGCTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCT CGGAGGTGTT 720
35     GAAACCAAAA CGAACGTTAT GTATAAAACC CCAGCTCCAT CGTGCCTGTC AGGCATCTGC 780
      TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
      TTGGGTCATC CCTTTAAAGT GCGCCCTACT TCTACTCCCG ATGGTTTTCG ACAACTGCAG 900
      CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCATCT 960
      GCCAGGTGCT TGCCACTGGT CTTGGCAGAA ATGGCGGCTG CTGAAAAGTA CCTTCCAAAT 1020
40     CCTTGGTGCG CACTCAGCGC CACAGGCTCT CCAATAAAAA CCTTTACAC ACAAAACCATG 1080
      AGTACCTTGG GCTTGATGAT TTTCTGTGGT GCGCGCCAGC GGGGCACCTT TTGTGAAGAC 1140
      AGAGCAGTGA CTAAGGTTCT CCAGGTTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
      GGCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
      ACCCATCTCT TCAGTTGGC TCGTTTCAGT GCGCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
45     AGGGTGTTTC GCGGTCCCGC GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCAACT 1380
      TGCCCTTTGG TTTTGAAGAT TCTGTTGAGG CGCATCTCTC ACCTTGACCT CTCTACAAA 1440
      ATCTGTCTCC CCGTGTGTGC CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
      GTCTTGCGT CATTTGAGCA GAGCCCAACA AAGCAGCTG CTGCCACGG GGAGCCTGTC 1560
      AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
50     GCGAACCTGC AGACAATTCC AGATACCCAA GCGCAGGAAG GCGCAGTGA GATGTCTACT 1680
      CACCCCTGAG GAGACTTGGG TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
      GATGGCAGAT CGCAGAAGAT GGTCTGATG TCTGAGGAAG GCGCACCTAG TTTGACAGGA 1800
      TGTGAGAGGC TCACAGTTTC CCATCACTTC TCCAGCATTC CCAAGTCTG GTCTCTCCTT 1860
      TCCCCCGCAG AGCCCTGTGT TCTGTCCAGG CCCTGA

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A90 Protein sequence:

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55     Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
      Unigene number: Hs.27373
      Probeset Accession #: F13036
      Protein Accession #: PGENESH predicted
      Signal sequence: 1-27
      Transmembrane domains: 94-115, 448-469
      Cellular Localization: not determined

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65     1      11      21      31      41      51
      MRVPLPAPL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNITRFGSG 60
      AAGSGSSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAPA FTLLLIACLL LRVPRSGKRL 120
70     KKTRKYDIIT TPAERVEMAP LNEEDDED ED STVPDIKYRV SLPAALRRQL PGQTLTLTV 180
      VPPFFILID LPARCSGRPD GGIRPGKTCF PAWHHPVESW SAATWGVKDW TWKPSCVGGV 240
      ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPP FGHPPKVPTT STPHGFRQLQ 300
      LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAAESDLFN PMWHFSATGS PIKTLTYQTM 360
      STLGLDVFCG AGQGRTFCEB RAVTKVLQGS SPSKQLRWKP ALESQFPFHL RLLRECPPLS 420
75     THPVRLARD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
      ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEPV KRGPSSGLTR HTPCGWGITH 540
      ANLQITPDQ GQEGPREDDT HPGGDLGVA NFYLEEBGPQ DGRQCKWVLM SEEGPPSLTG 600
      CERLTGSHHF SSHSKWSWPL SPRQPLFLSR P

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EWING**A91 DNA SEQUENCE**

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      Gene name:      G protein-coupled receptor 64
      Unigene number: Hs.184942

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Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5
 10
 15
 20
 25
 30
 35
 40
 45
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 55
 60
 65
 70
 75
 80

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1      11      21      31      41      51
|      |      |      |      |      |
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CTGCGGTGCA GGATGGT1TT CTCTGTACAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
GTTTTACTGA CGTTCAAGAT ATTCTTTGTC ATCATTTGTC TTCAATGCTG TCTGGTAACA 180
TCCCTGGGAG AAGATACTGA TAATTCAGT TTGTACCCAC CACCTGTCTAA ATTATCTGTT 240
GTCAGTTTTC CCCCCTCTCT CAATGAGGTT GAAACAACAA GCCTCAATGA TGTTACTTTA 300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
GCTTCAGCG TCAAACCCCA GAGAAATATC TGCAATTTGT CATCTATTG CAATGACTCA 420
GCATTTTITA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCAGAAAT 480
CAACATATAA CGAATGGCAC CTTAACCTGGA GTCTGTCTCT TAAGTGAATT AAAACGCTCA 540
GAGCTCAACA AAACCTCTGA AACCTTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAAC TGAATAATAC AATGAATGCA 660
TGTGCTGCAA TAGCCGCTTT GGAAGAAGTA AAGATTGCGA CAATGGAAAC CTGCTGCTGT 720
TCTGTACAGG TAGCCCTGCC TTCTCTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
CAGGATCCCA TGTGCTGTCT TGCTGACCAT CCAGCTGGCC CACCATTTTT TTCCAGCCAA 840
TCCATCTCAG TTGTGCTGCT GGCCACTGTG CTTTCCAGG TCCCAGAAAG TACCTCTTTT 900
GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
CAACCCCTTT CACCAGAGCC TTCAGCTCCC ATAGCTTCCA GCGCTGCCAT TGACATGCCC 1020
CCACAGTCTG AAACGATCTC TTCCCTATG CCCCAGACCC ATGTCTCCGG CACCCACCTT 1080
CCTGTGAAAG CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140
AGCGCACTTC CTGTGACAGC AGACATCGTC AACACACGCA GTATTCTGA TCTTGAGAAC 1200
CAAGTGTGCG AGATGGAGAA GGCTCTGTCC TTGGGACAGC TGGAGCTTAA CCTGCGAGGA 1260
GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCCTCCG CTGACATGCT GGCCCTCTGT 1320
GCTCAAGAT TGCTGAAAGT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAAACAG 1380
ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TTCAACACAA CTACCTTTGT GGCCCAAGAC CCGTCAAAAT CTCAGGTTTC TCTGGAAACC 1500
CAAGCTCCTG AGAACAGTAT TGGCACAATT ACTCTTCCCT CATGCTGTAT GAAATAATTA 1560
CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTITGTA AACACCTGCT 1620
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GTGCTAAACC TGACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
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GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGAGAGAT GAATGAAACC 1860
ATCTGTACCT GTAGCCATCT AACAAAGCTT GCGGTTCTGC TGGACCTATC TAGGACATCT 1920
GTGCTGCTGT CTCAAATGAT GGCTCTGAGC TTCATTACAT ATATTGGTTG TGGGCTTTCA 1980
TCAATTTTTC TGTCACTGAC TCTGTAAACC TACATAGCTT TTGAAAAGAT COGGAGGGAT 2040
TACCCCTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CTTGCTCTTC 2100
CTCTGAGACT GGTGATTTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160
TTTCTTCACT ATTTTCTCTT GGTCTCATT ACATGGATGG GCCTAGAAGC ATTCATATG 2220
TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCG3AA AATACATCCT TAAATCTGTC 2280
ATTGTGCGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT 2340
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ATCAACACAA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTTCTGTGT GATATTTTGT 2460
CTGAACGTCA GCATGTTTCA TGTGTCCTCT GTTCAGCTCT GTGAAATTA AAAGAAGAAG 2520
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ATGGCTCTCA GAAGGACTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
CTTTCTCTTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180
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AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
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ATACACTAAG AATGACTCCT ATAAAGAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
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AAATCCTAAA GCTCCTTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
TCAAGAAATA ATGATCCAG CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTTAGC 3780
TCATACAGTG CCTTTGAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCGA CACAGCCCTA 3840
TGGGTCAATG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCACTC ACCCTCTTGG 3900
GTGACAGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCATCCC CTGACCGCAT 3960
CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
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ATACACTGCC GCTTCTCAAA TCCCCAGAGC CTTTAGGAA AGGAGAGTAG ACTAGGATTC 4140
CTTCTCTTAA AAAGGTACAT ATATATGAAA AAAAATCATA TTGCGTTCT TTAAGAGGCA 4200
ACTGATGTGT ACATTGTGGA TTGTATGAC TGGTACACT TGGCCAGCC AGAGCTATAA 4260
TTGTTTITTA AATGTGTCTT GAAGAAATGA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
GGGAACCTGC CTACACTGCT ATTTGTGCTA CATGTATGGA GCCTTGATTG CTCCTAGTTA 4380
TATACAGGAT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCTTC AAGTACATCC 4440
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ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
CTGACTGTGC TTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTTGA TTTATATGTT 4620

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AAATCAAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

A92 Protein sequence

5 Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 15 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60
 PSSNEVETTS LNDVTLSELL SNETEKTIT IVKTFNAGV KPORNICNLS SICNDSAFFR 120
 GEIMFYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYP IMCATAEAS 180
 TLNCTPTIKL NMTNACAAI AALERVKIRP MEHCCSVRI PCPSSPEELG KLQCDLQDPI 240
 VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSPAEPP DYSFVTHNVP SPIGRIQPLS 300
 PQPSAPIASS PAIDMPQSE TISSPMPTQTH VSGTPPPVA KSFSPTVSNAP ANVNTTSAPP 360
 20 VQTDIVNTSS ISDLENQVLQ MEKALSLSGL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL 420
 LKVVDDIGLQ LNFSTTISL TSPSLALAVI RVNASSPNTT TPVAQDPANL QVSLETAPE 480
 NSIGTITLPS SLMMNLPAHD MELASRVQFN PFETPALFQD PSLENLSLIS YVISSSVANL 540
 TVRNLTNRVT VTLKHINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600
 SHLTSFGVLL DLSTSVLPA QMMALTFFITY IGCGLSSIPL SVTLVITYIAF EKIRRDYPSK 660
 25 ILIQLCAALL LNLVFLDLS NIALYKMQGL CISVAVFLHY FLLVSFTWMG LEAPHMYLAL 720
 VKVNTYIRK YILKFCIVGH GVPAAVVVII LTISPDIYGL GSYGKFPNGS PDDFCWINNN 780
 AVFYITVVGG PCVIFLLNVS MFIIVLVQLC RIKKKQLGA QRKTSIQDLR SIAGLTPLIG 840
 ITWGFAPFPAW GPVNVTFMYL FAIFNTLQGF FIFIPYCVAK ENVRKQWRY LCCGKLRLAE 900
 30 NSDWSKTATN GLKQKTQVNG VSSSSNSLQS SSNSTNSTL LVNNDCSVHA SGNNGASTER 960
 NGVSFSVQNG DVCLHDPGK QHMFNEKEDS CNGKGRMALR RSKGRSLHF IEQM

Fibrosis

A93 DNA SEQUENCE

35 Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 CGCAGAGGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCTCCCC AGGCCGCGAG 60
 CGCCCTCGCC GCGGTGCCTG GCCTCCCCTC CCAGACTGCA GGGACAGCAC CGGTAACTG 120
 45 CGATGTGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
 GGGTCCGCGC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAG CGGTGCGAGA 240
 ATGCTCTGCG CCGTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCGGTGGTGC AGGTGGTTTC 300
 GGGAAACGCG CCAGTGCAAG GCATCACGGG TTGTTAGCAT CGGCACTGCA GCGTGGGTC 360
 TGTCACTATG GAACTAAACT GGCCTGCTCG TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
 50 TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
 AGATGCTTTC CAGGATACAC CGGGAAAACC TGCACTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGCG CATGCCAACA CAGATGTGTG AATACACAG GAAGCTACAA GTGCTTTTGC 600
 CTCACTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAAGGC CACAGTGCCT GTGTCCATCC 720
 TCAGGACTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
 55 GGTAAAGTGA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGGAAG CTACTACTGC 840
 AAATGTCACT TTGTTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGGATAG CCATACGTGC AGCCAOCATG CCAATTGCTT CAATACCCAA 960
 GGGTCCCTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTGG GTGTTCTGCT 1020
 60 ATCCCTGAAA ATTCTGTGAA GGAAGTCCCT AGAGCACCTG GTACCATCAA AGACAGAATC 1080
 AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAATTAAT AAATGTTACC 1140
 CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTTG AGCCCTTCAA CTATGAAGAG 1200
 ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
 GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCTGGA AGAATGACAT AGAGGAGCGA 1320
 65 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGTGAATT CGGCCTGATT 1380
 CTGCTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTATAA TATCTCGTTT 1440
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 GGTCAACAAG AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAAGC 1620
 70 AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCCCGAGACA AAGTCGGGAA ACTTCAAGTG 1680
 TTTGTGAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCAAGAGTGA GGATGAAAAG 1740
 TGAAGAAGAG GGAATATTCG GTTGATATCA GGAAGTATG CTACCAAAAG CATCATTTT 1800
 GAAGCAGAAC GTGGCAGGGG CAAAACCGCG GAAATCGCAG TGGATGGCGT CTTGCTTGTT 1860
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
 75 TTGACTTTGT ATGTGAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
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 TCTTGATATA GATATGCCAA TATTGCTTAT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
 TTTCTGAATC TTTCCACATT ATATTATAA ATATGGAAT GTCACTTTAT CTCCCTCTCT 2160
 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
 80 TAGAAAAAAA AGCAGAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
 TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
 TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
15  MPLPMSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60
    CEATCEPGCK FGECVGPNNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRVC NTHGSYKCFPC 120
    LSGHMLMFDPA TCVNSRTCAM INCQYSCEDT EEPQCLCPS SGLRLAPNGR DCLDIDECAS 180
    GKVICPVNRR CVNTFGSYTC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240
    GSPKCKCKQQ YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KLLAHKNSM KKKAKIKNVT 300
    PEPTRTPPK VNLQPPNYEE IVSRGNSHG GKKGNEERMK EGLEDEKREE KALKNDIER 360
    SLRGDVFPFK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGCD WKQDREDDFD 420
    WNPADRDNAI GPYMAVPALA GHEKDIIRLK LLLFDLQPOS NPLCLFDYRL AGDKVKGKLV 480
    FVKNSNNALA WEKTTSEDEK WRTGKIQLYQ GTDATKSIIF EAERGKGKTG EIAVDGVLLV 540
    SGLCPDSLLS VDD
  
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GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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    CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGGAAACAAC TCACCAATGA 120
    GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180
    GTGTGACGGG CTGCCGTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
    GTGGAAATGT GGCCCAACCT TCTTCCCCTG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300
    CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
    AAACCGCTCG CTTTGCTCCA CGCCCGGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
    GAGCTTCATC TCGGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
    AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAAC AACTTGTGTA 540
    TTACCCAGCG ATCACCCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGCG TGGTGGTGGC 600
    CCTGCTGSCA CTGGTCTTGC ACCACGACGG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
    GCACCGGCTG CAGCACCGTG TGCTGCTGTC CGGCTGGTGG TCTCTGAGCC ACCCCACCA 720
    CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
    GAATCGCTGG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840
    TGCGTGGTAT GACCTTCCTC CACCCGCCCTA CTTCTCTGAC ACGGAACTCT TGAACCAAGC 900
    CGACCTGCCG CCTACCGCTC CCCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
    CAGCAGCGCT CTGAGCGTGG AAGACACCAAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
    GGGCACTGCT GAGCCCGAGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAGTCCC 1080
    AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATT TCACCAATTG 1140
    TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
    AACTATCTCT GCATTCCOCT CCTCCCGGAC ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
    TGACATGATC TGTGTGGGT CTTTCTGTG AGGTCACTCT TCCCTTGGGA CCCGAGATCA 1320
    CACCTCATTT TTTCACTTA TTCTGTTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380
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    CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500
    ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCCCC CAAAAAATT CCATTGTAGC 1560
    ATCAAAACCT GCTTTGCACA ATCCTATTG ATGCCCCAG TTCAAGAGAG TCAGTGGCCA 1620
    AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTGGC AAGCTTATT TTGTTTGTG 1680
    AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTG CCCAAGAAAG 1740
    CTCATTCTGA GAGCTTTCCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
    GAGCCCCCTC CATGAGTTTA TCCAGTTTCT CAGCTCCTAA AATGCAAGCT GCCAAGACCC 1860
    TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCACT CTCCAGCTG 1920
    ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
    GTATGTCCTT GTGGCCACAC CCCAGCCTGT CTGTCTATT CATGCAGCCT CAACACTGGC 2040
    CTCCAAAGTT CCTTAACACA TTGCAAAGTC CTTTTTACCT GTGCATTGG ACTTGAGGAC 2100
    ACTGTTTCT ATCAGAGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCTGAGCTC 2160
    CTGCACTGTG CAGGCTCTCT TCCCAAGGT CCAATACCA GCACCTTAG TTAGAGTTAG 2220
    GGTCAAGGTC AGGCTCTTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
    AGACAAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
    TGAACAGTGT TGTTTGTTT TCCCTTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400
    AGCTGTCTCT TTTTTTGTG TCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAGAGAGATC 2460
    ACACCTTGGC CCGCTGAGC CCGTGTATA CAAGTCACTC CAGACTAAC TGTGTGCCAG 2520
    ACATTGTGTC ATTGTGTCAC TTTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580
    AGAGGAGACT CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
    TTTCTGTGTG CCAGTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG TATAAACGTT 2700
    AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGTGAA CCAGGTAGAG 2760
    CCACTCCGGG CAGCTGTAC CATTTCAGAA CTTCTTCCG CAGCTGAAGA AATGTTTCA 2820
    AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTTCAG 2880
  
```

5	TGATCCTGTT	CTGTAGACTT	TTCTTTCTTT	TTTTAACCAA	ATCCAAAGGA	TGTTACAGAA	2940
	AAGCTAGCCA	CTGGTATTTT	GTTTTGTTTA	AAAAAAAAAA	GAAAGAAAGA	AAGAAAGAAA	3000
	AACGGAAAGG	AACCTAGCTG	CCTGTATCTT	TCATTTTTAA	AATAGCACTT	GAGTTATTTT	3060
	CTGAGTAATC	CAATAAAGAA	CTTTTGATGA	CAGCCAGAAAT	GTGTTAGAAC	TCTGGCTGAA	3120
	CATTTCATCT	CCTGTGAGTC	AGAAGGGCTT	TATTTCTCCC	TTTGAATGGG	CCCTTCTCTC	3180
	TTTCTGGTGC	TCTGGAAGTT	GTTTAGAGGA	AAGAATTCTA	ATTTTAATTA	ATTGCGCAGT	3240
	GAGTTAATCT	CACTCGCTTT	TCTGCTTCCA	GGCATCTTAG	GAAAAACAAA	TGGTTTTAGT	3300
	AGATAAGGGA	TGCCTACTAA	TGCTTTTTTA	AAACAAACAG	GGACATTTT	ATTATAGATT	3360
10	TGATTTTTTT	AATGAATGTT	TTTAAAAATA	TATAAATAGG	ACACCAAAGC	GGCAGGGTTT	3420
	TTTTTGGGGG	GAGGGGGTTT	GTTTTCCAAC	TCAAGATGGC	ACATTATGGG	CCAGCAATAT	3480
	TTTTTAATTC	ATTTCAACCA	GGAAGCTTTT	TTATACATTG	CCTAAATCTA	CGCCAACCGA	3540
	AAAAATAGTCT	CATCTCTTTT	TTTCTCAAAAT	GAGATCCGTG	TTTTIATTTA	GCATTAAATT	3600
	AGTTACACTG	TGATGACTGG	CCTATTACCT	GACTCAGCTC	CCTCTACCTT	GAAATTGACA	3660
15	TTTTTAAAAA	ATGCAACTAA	GTGGTTAATA	GTGTGTGACG	CTCAAAGTTA	ATGTAAACTG	3720
	GAAAGGTTGT	GTGTGCTTGC	TTTTTGTGTT	TTGGTTAGGC	TTGGTTTGTG	TTTTTAATTT	3780
	TTATACATCT	TATAAAATTT	GCAGTTTCAT	TCTTCTGTTT	TGTGCAAAAG	GWMTAMARM	3840
	AAMMAAAAC	AWYWTGGGG	GGGCTTGGGC	CTCGGAAAAA	GTTTTTAACA	CCACTTCGGG	3900
	TGGGGCGGCG	GGGCCCCAGT	AGGTACGGCG	ACCACGCGGG	CCCAACCGGG	ACCCAGAGAG	3960
20	GAAACCTCGG	CCAAGAAAAA	GGTGGCGAGA	ATTCTCCACA	CCAGAAAAAA	ACGCGCCGGG	4020
	GGAAACCGCA	GAGTGTTCGG	TAAACCAAC	CCGAAGAGAG	AACTCAGAA	CACACAAGCG	4080
	GGACTCAACC	AGGAGGACCC	AAGGGAACCC	GATAGAGTAC	G		

25	<u>A96 Protein sequence:</u>	
	Gene name:	ESTs
	Unigene number:	Hs.293616
	Probeset Accession #:	AW043782
	Protein Accession #:	none found
30	Signal sequence:	1-17
	Transmembrane domains:	169-191
35	LDLa domains:	28-66, 70-108, 112-149
	Cellular Localization:	plasma membrane

35	1	11	21	31	41	51	
	MWLLGPLCLL	LSSAAESQLL	PGNNFTNECN	IPGNFMCNSG	RCIPGAWQCD	GLPDCFDKSD	60
	EKECPKAKSK	CGPTFFPCAS	GIHCIIGRFR	CNGFEDCPDG	SDEENCTANP	LLCSTARYHC	120
40	KNGLCIDKSF	ICDQNNQCQD	NSDESCSSSS	QEPGSGQVFP	TSENQLVYYP	SITYAIIGSS	180
	VIPVLVALL	ALVLHQRKR	NNLMTLPVHR	LQHPVLLSRL	VVLDPHPRHN	VTVNVNNGIQ	240
	YVASQAEQNA	SEVGSPPSYS	EALLDQRFAN	YDLPPPPYSS	DTESLNQADL	PPYRSRSGSA	300
	NSASSQAASS	LLSVEDTSHS	PQPGPQEGT	AEPRDSEPSQ	GTEEV		

45 LUNG

	<u>A97 DNA SEQUENCE</u>	
	Gene name:	putative GPCR, Weakly similar to dJ365012.1
50	Unigene number:	Hs.256897
	Probeset Accession #:	BE001836
	Nucleic Acid Accession #:	BE001836
	Coding sequence:	1-2955 (underlined sequences correspond to start and stop codons)

55	1	11	21	31	41	51	
	ATGGCGGTCA	AATCTTTTTT	CTTCAACACT	GGGAATGATG	GGCTAGACCC	AGACCCAATC	60
	ATGTTAAGTA	TGATAGGGAT	CAGTGGCCCA	GCTGGTGTGG	AAGACAAGTG	GGTCATACTG	120
	GGTTTAGGCC	CACATAGCAC	TAAAGGTCTT	CAACATGCAA	TTAGAAGCTC	AAATGTTGAC	180
60	GGGAATATTG	TTCACTCTAA	AAAAGATGTT	TCTATTAGAA	TTTACTTACT	CTTTCAATGA	240
	AACATAGATG	CTTCTCTTTT	CCTGATTAGT	GATGGCCATC	AGTTAACCCA	AGTGCACTCA	300
	GAGAAGTCAA	ATTCTGACAC	AATCCAGCAA	GTAACATAAA	AAACTGATGG	CCCAGTCGAA	360
	GAATATCAGC	TGCTGCTTCA	GGTGACCTAT	AGAGATTCCA	AGGAGAAAAG	AGATTGAGA	420
	AATTTTCTGA	AGCTCTTGAA	GCCTCCATTA	TTATGGTCAC	ATGGGCTAAT	TAGAATTATC	480
65	AGAGCAAAAG	CTACCACAGA	CTGCAACAGC	CTGAATGGAG	TCCTGCACTG	TACCTGTGAA	540
	GACAGCTACA	CCTGGTTTCC	TCCTCTATGC	CTTGATCCCC	AGAACTGCTA	CCTTCAACAG	600
	GCTGGAGCAC	TCCCAAGCTG	TGAATGTCTAT	CTCAACAACC	TCAGCCAGAG	TGTCAATTTC	660
	TGTGAGAGAA	CAAAGATTGG	GGGCACTTTC	AAAATTAATG	AAAGGTTTAC	AAATGACCTT	720
	TTGAATTCAT	CTTCTGCTAT	ATACTCCAAA	TATGCAATG	GAATTGAAAT	TCAACTTAAA	780
70	AAAGCATATG	AAAGAATTCA	AGGTTTGTAG	TCGGTTGAGG	TCACCAATTT	TCGAAATGGA	840
	AGCATGCTTG	CTGGGTATGA	AGTTGTTGGC	TCAGCAGTGG	CATCTGAAC	GCTGTGAGCC	900
	ATTGAACATG	TTGCCGAGAA	GGCTAAGACA	GCCCTTCACA	AGCTGTTTCC	ATTAGAAGAC	960
	GGCTCTTTCA	GAGTGTTCGG	AAAAGCCCG	TGTAATGACA	TTGTCTTTGG	ATTGCGGTCC	1020
	AAGGATGATG	AATATACCTT	GCCCTGTCAG	AGTGGCTACA	GGGGAAACAT	CACAGCCCAAG	1080
75	TGTGAGTCTT	CTGGGTGGCA	GCTCATCAGG	GAGACTTGTG	TGCTCTCTCT	GCTTGAAGAA	1140
	CTGAACAGAA	ATTTCAATAT	GATTGTAGGC	AATGCCACTG	AGGCAGCTGT	GTCATCCTTC	1200
	GTGCAAAATC	TTTCTGTGAT	CATTGCGCAA	AACCCATCAA	CCACAGTGGG	GAATCTGGCT	1260
	TCGGTGTGTT	CGATTCTGAG	CAATATTCCA	TCTCTGTGAC	TGGCCAGCCA	TTTCAGGGTG	1320
	TCCAATTCAA	CAATGGAGGA	TGTTCATCAGT	ATAGCTGACA	ATATCCTTAA	TTTCAGCTCA	1380
80	GTAACCAACT	GGACAGTCTT	ACTGCGGGAA	GAAAAGTATG	CCAGCTCAGG	GTTACTAGAG	1440
	ACATTAGAAA	ACATCAGCAC	TCTGGTGCCT	CCGACAGCTC	TTCTCTGAAA	TTTTTCTGGG	1500
	AAATTCAATG	GAATGGAAAG	GATTCCAGTG	AACAAAAGCC	AACTCAAAG	GGGTTACAGC	1560
	TATCAGATTA	AAATGTGTCC	CCAAAATACA	TCTATTCCCA	TCAGAGGCCG	TGTGTTAATT	1620
	GGGTGAGACC	AAATCCAGAG	ATCCCTTCCA	GAAACTATTA	TCAGCATGGC	CTCGTTGACT	1680
	CTGGGGAACA	TTCACCCGT	TTCAAAAAT	GGAATGCTC	AGGTCAATGG	ACCTGTGATA	1740

5 TCCACGGTTA TTCAAACTA TTCCATAAAT GAAGTTTTCC TATTTTTTTC CAAGATAGAG 1800
 TCAAACTCGA GCCAGCCTCA TTGTGTGTTT TGGGATTTCG GTCAATTGCA GTGGAACGAT 1860
 GCAGGCTGCC ACCTAGTGAA TGAACCTCAA GACATCGTGA CGTGCCAATG TACTCACTTG 1920
 ACCTCCTTCT CCATATTGAT GTCACTCTTT GTCCCTCTA CAATCTTCCC CGTTGTAAAA 1980
 TGGATCACCT ATGTGGGACT GGGTATCTCC ATTGGAAGTC TCATTTTATG CCTGATCATC 2040
 GAGGCTTTGT TTGGGAAGCA GATTAAAAAA AGCCAAACCT CTCACACAG TCGTATTTGC 2100
 ATGGTGAAAC TAGCCCTGTC CCTCTTGATT GCTGATGTCT GGTTTATTGT TGGTGCCACA 2160
 GTGGACACCA CGGTGAACCC TTCTGGAGTC TGCACAGTGT CTGTGTTCTT TACACACTTC 2220
 10 TTCTACCTCT CTTTGTCTT CTGGATGCTC ATGCTTGGCA TCCTGCTGGC TTACCGGATC 2280
 ATCCTCTGT TCCATCATAT GGCCCGACAT TTGATGATGG CTGTGAGATT TTGCTCGGGT 2340
 TATGGGTGCC CTCTCATTAT ATCTGTCAAT ACCATTGCTG TCACGCAACC TAGCAATACC 2400
 TACAAAAGGA AAGATGTGTG TTGGCTTAAC TGGTCCAATG GAAGCAAAAC ACTCTGGCT 2460
 TTTGTGTGCC CTGCACTGGC TATTGTGGCT GTGAACCTCG TTGTGGTGTCT GCTAGTTCTC 2520
 15 ACAAAGCTCT GGAGGCGGAC TGTGGGGAA AGACTGAGTC GGGATGACAA GGCCACCATC 2580
 ATCCGCTGG GGAAGAGCCT CCTCATTCTG ACCCTCTGCG TAGGGCTCAC CTGGGGCTTT 2640
 GGAATAGGAA CAATAGTGA CAGCCAGAAT CTGGCTTGGC ATGTATTATT TGCTTTACTC 2700
 AATGCATTCC AGGGAATTTT TATCTTATGC TTGGGAATAC TCTTGGACAG TAAGCTGCGA 2760
 CAACCTCTGT TCAACAAGTT GTCTGCCCTA AGTCTTGGGA AGCAACACAGA AAAGCAAAAC 2820
 20 TCATCAGATT TATCTGCCAA ACCCAAATTC TCAAGCCTT TCAACCACT GCAAAACAAA 2880
 GGCCATTATG CATTTTCTCA TACTGGAGAT TCCTCCGACA ACATCATGCT AACTCAGTTT 2940
 GTCTCAAAATG AATAA

A98 PROTEIN SEQUENCE

25 Gene name: putative GPCR, Weakly similar to dJ365012.1
 Unigene number: Hs.256897
 Protein Accession #: none found
 Signal sequence: 1-17
 Pfam domain: 7tm_2 [561-820]
 30 Transmembrane domains: 545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
 Cellular Localization: plasma membrane

35 1 MHALLLCPSV 11 LNASGLSL 21 QSPVEYQLL 31 LQVTRYDSKE 41 KRDLRNPLKL 51 LKPPLLWSHG 60
 LIRIIRAKAT TDCNSLNGVL QCTCEDSYTW FPPSCLDPQN CYLHTAGALP SCECHLNLS 120
 QSVNFCBERK IWTGPKNER PTNDLLNSSL AIYSKYANGI EIQLKKAYER IQGFSVQVT 180
 QFRNGSIVAG YEVVGSSSAS ELLSAIEHVA EKAKTALHKL FPLEDGSFRV FGKAQCNDIV 240
 40 PGFGSKDDEY TLPCCSSGYRO NITAKCESSG NQVIRETCVL SLLEELNKNF SMIVGNATEA 300
 AVSSFVQNLS VIIQNPSTT VGNLASVSI LSNISLSLA SHFRVSNSTM EDVISIADNI 360
 LNSASTVNT VLLREEKYAS SRLLETLENI STLVEPTALP LNFSRKFDW KGIPVNXSQL 420
 KRGSYQIKM CPQNTSIPR GRVLIGSDQF QRSLEPTIIS MASLTGLNLI PVSXKNGNAQV 480
 NGPVIISTVIQ NYSINEVFLP FSKIESNLSQ PHCVFWDPSH LQWMDAGCHL VNEDQDIVTC 540
 45 CQTHLTSFSI LMSPPFVSTI FVVVKWITYV GLGISIGSLI LCLIIIEALFW KQIKKSQTS 600
 TRRICMVNIA LSLLIADVWF IVGATVDTTV NPSGVCTAAV PFTHFFYLSL FFWMLMLGIL 660
 LAYRIILVPH BMAIGLMMV GPCLGYGCPL IISVITIAVT QPSNTYKRKD VCVLWNSNGS 720
 KPLLAFFVPA LAIVAVNFVV VLLVLTKLWR PTVGERLSRD DRATIIIRVGK SLLILTPLLG 780
 LTWFGIGITI VDSQNLAMHV IFALLNAFQV RTVTITYCTIV K

A99 DNA SEQUENCE

55 Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

60 1 AGCACCTGGG 11 AAAAGGCAGA 21 CCGTGTGAGG 31 GGGCCTGTGG 41 CCCCAGCGTG 51 CTGTGGCCTC 60
 GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTACACTTC GCCATGAGTT TCCTGATCGA 120
 CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTGTGGA TTGSGGTGGC TTTTCTTCAT 180
 65 GCGCCAATTG TTTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCTTCTCOGT 240
 GACGTTTGCA TTTTCTTGCA CCATGTTTGA GCTCATCATC TTGAAATCT TAGGAGTATT 300
 GAATAGCAGC TCCCGTTATT TTTACTGGAA AATGAACCTG TGCCTAATTC TGCTGATCCT 360
 GGTTTTCATG GTGCCPTTTT ACATTGGCTA TTTTATTGTG AGCAATATCC GACTACTGCA 420
 TAAACAACGA CTGCTTTTTT OCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGSA 480
 70 ACTAGGAGAT CCCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
 CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGCTC CTCTTCTCTG GATTGTGTTG 600
 TGTCAACTGC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
 TGTAGCCCTG GAACGGGAGC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAAG 720
 GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGAA GTGCATAACA AACCATCAGG 780
 75 TTTCTGGGGA ATGATAAAAA GTGTTACCA TFCAGCATCA GGAAGTGAAA ATCTTACTCT 840
 TATTCAACAG GAAGTGGATG CTTTGGGAAG ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
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 CAATATTGTT TTGATCGAG TTGGGAAAAC GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
 80 TGTGAATTAT CTGGGAATCC AATTGTATGT GAAGTTTGG TCCCAACACA TTTCTTCAT 1140
 TCTTGTGGA ATAATCATGT TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200
 CTTTATGTC ATCTCTAGCA GTAAAGTCTC CAATGTCAIT GTCTGCTAT TAGCACAGAT 1260
 AATGGGCATG TACTTGTCT CCTCTGTGCT GCTGATCCGA ATGATATGCT CTTTAGAATA 1320
 CCGCACATA ATCACTGAAG TCCTGGAGA ACTGCAGTTC AACTCTTATC ACCGTGTGTT 1380
 TGATGTGATC TTCTGTGTC GCGCTCTCTC TAGCATATC TTCCTCTATT TGGCTACAA 1440

	ACAGGCACCA	GAGAAGCAAA	TGGCACCTTG	AACTTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAATTAGA	TATAAGAGG	GGGAAAATG	GAACCAAGGC	CTGACATTTT	1560
	ATAAACAAAC	AAAATGCTAT	GGTAGCATT	TTCACTTTCA	TAGCATACTC	CTTCCCCCTC	1620
5	AGGTGATAC	ATGACCATGA	GTAGCATCAG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGGAGAGGAG	1740
	CCAAGAAACT	AAAGGTGAAA	AATACACTGG	AACTCTGGGG	CAAGACATGT	CTATGCTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTTAA	GGTTCACATG	GAAAAGGTTA	TAGCTTTGCC	1860
	TTGAGATTGA	CTCATTAATA	TCAGAGACTG	T			
10	<u>A100 Protein sequence</u>						
	Gene name: putative G-protein coupled receptor						
	Unigene number: Hs.16085						
	Protein Accession #: NP_057418.1						
	Signal sequence: none found						
15	Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446						
	Cellular Localization: plasma membrane						
20	1	11	21	31	41	51	
	MSFLIDSSIM	ITSQILFPFG	GWLFFMRQLF	KDYAIRQYVV	QVIFSVTFAP	SCTMFELIIF	60
	EILGLVNSSS	RYPHWKNLNC	VILLILVFMV	PFYIGYPIVS	NIRLLHKQRL	LPSCLLNLTF	120
	MYFFWKLQDP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGPGAVNCP	YTMSYPLRN	180
	VTDTDLALE	RRLQLTMDMI	ISKKKRMAMA	RRTMPQKGEV	HNKPSGFWGM	IKSVTTSASG	240
25	SENLTLIQGE	VDALBELSRQ	LFLLETADLYA	TKERIEYSKT	PKGKYPNPLG	YFSTIYCVWK	300
	IFMATINIVF	DRVGKTDVPT	RGIEITVNYL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
	ITLTKFPYAI	SSSKSSNVIV	LLLAQIMGMY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
	FYERWFDVIF	LVSALSSILF	LYLAHKQAPE	KQMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]						
	Unigene number: Hs.19322						
	Probeset Accession #: AA088458						
	Nucleic Acid Accession #: AA088458						
35	Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)						
40	1	11	21	31	41	51	
	GCCCTTGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
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	CGCGGGGGCC	GGGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCCGC	180
	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTCC	CCAAGGTACA	AGAGGTGGCC	CGGTGCTGCT	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCTCTGCC	CCCGTCTCTC	TCCGGGGCCC	CCTGCCCTGC	CCTGACGTCC	360
	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGGACT	420
45	CTCACCAGGG	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAAGTCG	480
	GGCTCATTA	AGCAGCTGTT	TGAGGCCCGC	GCCTGAGGCC	AGCAGGACCG	GGGACCTCTG	540
	GATTCCACCT	TCATCTAGTC	CTTGTGGGCC	GGGTGGGCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTCGA	GGGTGGGGCC	CCCATCGCAC	CCACCTCTCT	TGGCTGGAGA	CCCCCGGCGA	660
50	GGCCAGGGCA	AGTCCCGGAG	TGGGGCGCTT	CCTGCCGGCC	TTGCCAGATG	GGCTCCCCAG	720
	GGCTGCCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTCTTGGGCTC	CTGGTTGYTG	780
	ACATGGGCTG	GGGGCTCTCT	TGAGTCCGCA	TAGTCCGCGA	CTACTACTGG	CGGCTGTCTG	840
	TGAGACAGTG	GGTACCCCTC	CATGAGTTAG	CGTCCCCCCC	TTTCCAGCGG	TGCCGCTCTG	900
	GGTCCCATCT	TCAGGGAAAG	GCATCTGCCA	CGCCAGGCTG	CACCTTCAAC	AACGGGCGAG	960
55	AGAGGGCGCG	GGGTGGGCTC	GACGCGGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TCGGACGGAC	GGAAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAGCGGGG	GGTGCCTGCC	TGGCTGGGGA	GCCCAGGGGA	TAGCGGTCCG	ACTTCAGGTT	1140
	CTGGCCAAAG	CTGAGGGACC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GGGAGAGCTT	1200
	GGCTCGCATG	TGGCTCCAC	AGACCCCTGG	GTGATGGCCT	TCCCCCTCTT	GGCCGGGAGC	1260
60	TTGCCCGGAG	CCAGGTCCCA	CACAACATCC	TGTGAGCCTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCACGTCA	TAGGCAAAAG	CTGTTTCCCC	CGACTCAGGA	TTTCCAAGGC	1380
	CTGGGGTCTC	GCTCACCCCC	CTTTGCTCTC	ACGCCCAAGC	TGTCCCCAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAAC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCCTGCCCA	GGCCCACTCC	CGCTGGTGCT	1560
65	GGAGTACGCA	CTGGTGGGGG	GGCCCTGCTC	AGCCCAACCT	GGAGGGTCCC	AGTGTACCCA	1620
	GAACCAAGGG	CACGGCAACA	GCATCGATGG	GTTCTGCAGC	CCAGGGCCCC	CGATGCGGGG	1680
	TCAGTGTGTG	TGGGGGCGAG	GGCCTCCGAT	CGCGGGTCAG	TGCGTGGGGG	GGCAGGGGCC	1740
	CCCGATGCGG	GGTCAAGTGG	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCATTTGGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGTCTCAGAG	GAGGGGGCCT	GGCAGGCAGC	GTGGCAACTC	1860
70	CCTTCCGGAG	CCAGGTCCCA	TGCTAACCTG	CCCAAGCAGAA	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCGAG	GACAGGCCCA	AGTCAGCCCA	GCATGCAGCT	1980
	GGCTCTCTAC	CCTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCTCTG	2040
	ACCTCTCTGG	CAGGAAAGGG	TGCAGGTCTT	GAGGGGCTGT	GGCCCAAGGC	CCGAGCACCC	2100
	AGGTGGACTG	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCCGTCAGCA	2160
75	GGCTGGGGTG	TGCCCAACCA	GGCCTCCCCA	CGTCTGCCTT	TGAGGGTGCC	TGCCATGCCC	2220
	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCCG	2280
	GGTGAATTTA	TCAGGAGAGC	GCCCCACATG	AGCTGGAGCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCAGCTCCG	GAAAAACTGC	CTTTCAGCCT	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCCCAAG	TTTACAGCTT	GAAATCAGGC	TAGTGAAGTG	CCCTGGAGAC	2460
80	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGG	AGAGGCACAT	2520
	GCAGACCCCT	CCTGGAGCTCT	GCCCTAGGAC	GCTGGGGGGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGGGTC	CCTGGGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACACGT	2640
	GGGTGCACAC	TGTGATGACA	CCCGAAATG	TCTCAGGATG	TTGAAATGTE	TCTTTGGGGG	2700
	CAGAGTGTGC	CCCAAGTTAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTTGTGTTG	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CCGGGCGTGG	TGGTTCAGCG	2820

5 CTGGAATCCC AGCACTTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACAARAAAAA AAAAGAAAG AAAGAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTITT ATATATCTAA 3060
 AGAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A102 DNA SEQUENCE

10 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

15
 1 11 21 31 41 51
 | | | | |
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 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA ACACCTGTGG CTACTATCTC TTCCGTGGTG 120
 20 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGGG CCTTGATGAT TTGAAAATAA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTGG CTGACAGAT CCGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 25 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTGACTGTC 420
 TCAGGGAAGT ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAAAATG TGCTGTGCTC CACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 30 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCCCTCG GCCACGTGGT TACCTTGACG TGCACAGCCT GTGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTGCC AGGGCTACCA CCGTGTGCGG GGTCTGTGTA TCAGGCCCTT GTGGATCATC 960
 35 ACTGCTGAC ACTGTGTTTA TGACTTGATC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
 CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGAAGCC 1260
 40 TCCCTGTGCC TGAACACAGC GGCCTGCCCT TTGATTTCCT ACAAGATCTG CAACACAGG 1320
 GACGTGTAGC GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCCCTGGTG GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCAAG CTTTGGCATC GGTCTGCGAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCGGTG TCACCTCCTT CCTGGACTGG ATCCAGGAGC AGATGGAGAG AGACCTAAAA 1560
 45 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
 TTCGGCACC AGTAGCAGGC CGAAGAGAGG CACCCCTCCA TCTGATTCCA GCACAACTT 1740
 CAAGCTGCTT TTTGTTTTTT GTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 AGTGACGTGG CGAATCCCTT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
 50 TTGCTCTAGC TTCCCGAGTA GCTGGGACCA CAGTGCCCGG CCACCAACC CAACTAATTT 1920
 TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCCCTGT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
 ACBCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAG AAAAGAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
 55 ACAGATAAG CAGTTATGTG ACCTCAGTGG CAAGGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAAGTT TTCATCTCTA GGGACAGAA 2280
 CCRAACCCAC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCTAT TTTCAATGAT TCTTTGTAGC ATTTGCTGCT TGACGTATTA 2400
 60 TTGTCTTTG ATTTCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAA

A103 Protein sequence:

65 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 70 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APPSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFPF IIVIGIILI 60
 LALAIGLGIH FDCSGKYRCR SSPKCIELIA RCDGVSDCKD GEDBYRCVRV GQNAVILQVF 120
 TAASWRTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSVIV REGCAGSHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPF QASLQFQGYH 240
 80 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYRPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA 360
 AVPLISNKIC NHRVYVGGII SPSMLCAGYL TGGVDSQCGD SGGPLVCQER RLWKLVGATS 420
 PGIGCAEVNK PGVYTRVTSF LDWIHQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 ATGCACACCG TGGCTACGTC CGGACCCAAAC GCGTCCTGGG GGGCACCGGC CAAAGCCTCC 60

GGCTGCCCGG GCTGTGGCGC CAACGCTCTG GACGGCCCGG TCCTCTGCGC GCGGGCCGTG 120

GACGCTGCGC TCGTGGCCGT CTCTCTGCGC GCGCTGATGC TGCTGGCGCT GGTGGGGAAC 180

TCGCTGGTCA TCTACGTCT CTGCGGCCAC AAGCGATGTC GGACGCTGAC CAACTTCTAC 240

15 ATGCGCAACC TGGCGGCCAC GGACGTGACC TTCCTCTGTG GCTGCGTCCC CTTACGCGCC 300

CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360

ATCCAGCAGG TCTCGGTGCA GCGCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420

TGGTACGTGA CGGTGTTCCT GTTGGCGCGC CTGCACCGCC GCACGCGCGC CTGGCGCTG 480

GCTGTACGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCGGCT GCTCGCCCTG 540

20 CACGCGCTGT CACCGGGGCC GCGCGCTTAC TGCAGTGAGG CCTTCCCCAG CCGCGCCCTG 600

GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC 660

TGCGCCTGTG ATCGCGCCAT GCTGCGCCAC CTGGGCGGGG TCGCGGTGCG CCGCGCGCCC 720

CGCGATAGCG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCGCT GCGGGCCAAG 780

GTCTCGCGCC TGGTGGCGGC GGTGGTCTCT CTCTTGGCGC CTGCTGTGGG CCGCATCCAG 840

25 CTGTTCTCTG TGTGTCAGGC GCTGGGCCCC GCGGGCTCCT GGCACCCACG CAGCTACGCC 900

GCCTAGCGCG TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCCG GCTGAACCCG 960

CTGCTCTAGC CCTTCTCTGG CTGCACTTTC CGACAGGCGT TCGCGCGGCT CTGCCCCCTG 1020

GCGCGCGCGC GCGCGCGCGC CCGCGCGCGC CCGGAGCCCT CGGACCCCGC AGCCCCACAC 1080

GCGGAGCTGC ACGCGCTGGG GTCCCAACCG GCGCCGCCCA GGGCGCAGAA GCCAGGGAGC 1140

30 AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCT TCTCTGA

A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

1 11 21 31 41 51

45 MHTVATSGPN ASWGAPANAS GCPGCGANAS DGFVPSPRAV DAWLVPLFFA ALMLLGLVGN 60

SLVIYVICHK KPMRTVTNPF IANLAATDVT FLCCCVPTFA LLYPLPGWVL GDFMCKFVNY 120

IQQVSVQATC ATLTAMSVDR WYVTVPFLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180

HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240

ADSALGGQVL AERAGAVRAK VSRVAAVVL LFAACWGPIQ LFLVLQALGP AGSWHPRSYA 300

50 AYALKTWAKH MSYSNSALNP LLYAFLGSHF RQAFRRVPCP APRRRPRPRR PGPSDPAAPH 360

AEHLRLGSHF APARAQKPGS SGLAARGLCV LGEDNAFL

A106 DNA SEQUENCE

Gene name:

integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM_002214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

60 CCCAGAGCCG CCTCCCCCTG TTGCTGGCAT CCGAGCTTCT CTCCTTGGCC AGCCAGGACG 60

CTGCGGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAGCTGCG AACTAATGGT 120

GTGGGCTTCC TCGCCACCTT GTGGAAGCAA CTGGCTGATG TGATGCGCCA CAGACTTTTT 180

65 TCCCCCTGAC CTGCGCGGCG TACCTTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240

TAGGGTGGTT TCCCCCCCAG CTCGGGCTTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300

CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCCTTTCTT 360

TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGGCC GCCGGGGCCT 420

70 TGGCGGTGCA AGGAGGTGCT TCTCGGGGAG ACCGCGGGAC CCGCGGTGCC GAGCGGGGAG 480

GGCGGTAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540

CGGAGCCGCG GGGTCCGCTT GCTAGGCTTG CGGAAAACGT CCTAGCGACA CTCGCCCGCG 600

GGCCCGAGG TCGCCCGGGA GGCGAGCCCC GCGTCCGGAA GGCAGCCAGG CCGCGGGGCG 660

GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGGC TTTTTTTACC GCTGCATTGT 720

75 TCTGCTGCA AAGGACCGG CGAGGTCCCG CCTGTTCTCT CTGGGACGCC TGGGTGTTTT 780

CACCTGTGCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCACTTTCA AATGCAGCAT 840

CTGTGTCAGG GTGCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTC 900

TTTCAGGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTT CAATTTAATA AGCAAGGCT 960

GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCACTGTTT AATACCCACT GAAATGGA 1020

TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080

80 ATTTTATGCT GAAAGTTTAT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140

ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAAATAAA TTCCGTGTGA AACGATTAT 1200

CTAGAAAAAT ATCAATTTTT TCCCGTGAAT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260

AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320

ACAAATTAGA CTGATGCTCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAA 1380

TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAACATA GATACACCAG 1440

5 AAGGAGGTTT TGACGCCATG CTTGAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560
 GCAAATTTGGC AGGCAATAGT GTGCCCAATG ACGGAAACCTG TCATCTGAAA AACAAAGTCT 1620
 ACGTCAAAATG GACAAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
 ACAACAACAT TAATGTATC TTTGCACTTC AAGGAAACAA ATTTCATTGG TATAAGGATC 1740
 TTCTACCCCT CTGCGCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACTCA 1800
 ATAATTGGT AGTGGAAAGCC TATCAGAAGC TCATTTTCAG AGTGAAAGTT CAGGTGGAAA 1860
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
 CAGGCATGGA AGGATGCAGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
 10 TTACAATGAA AAAATGTGAT GTCACAGGAG GAAAAAACTA TGCAATAATC AAACCTATTG 2040
 GTTTTAATGA AACCCGCTAAA ATTCAATATC ACAGAAACTG CAGCTGTGAG TGTGAGGACA 2100
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCAGT 2160
 GTGATGAGAA TAAATGTCTAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220
 15 ACAAGGATCA GCCTGTTTGC AGTGGTCGAG GAGTTTGTGT TTGTGGGAAA TGTTCAATGTC 2280
 ACAAAATTAA GCTTGAAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340
 CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
 GCCTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
 TCAATTCAAA GGGCCAAGTG TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
 20 GCACCGATCC CAGGAGCATC GCGCGCTTCT GTGAACACTG CCCCACTGT TATACAGCT 2580
 GCAAGGAAAA CTGGAATGTG ATGCAATGCC TTCACTCTCA CAATTGTGCT CAGGCTATAC 2640
 TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACACA GCATTATGTC GACCAAACTT 2700
 CAGAATGTTT TCCAGGCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
 TCTTGATGG GTTGCTTAAA GTCTGTATCA TTAGACAGGT GATACTACAA TGGAAATGTA 2820
 25 ATAAATTAAG GTCTCTATCA GATTACAGAG GTTCAGCTC AAAAAAGGAT AAGTTGATT 2880
 TGCAAGATGT TGGCACAAGA GCAGTCACCT ACCGAGGTGA GAAGCCTGAA GAAATAAAAA 2940
 TGGATATCAG CAAATTAATG GCTCATGAAA CTTTCAGGTG CACTTCTTAA AAAAAAGATT 3000
 TTAACACTT AATGGGAAAC TGGAAATGTT AATAATTGCT CCTAAAGATT ATAAATTTAA 3060
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT ACACTCGAAC 3120
 30 GAAGACTGAC AAGTATCTCT ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
 AAAATGTGTC TTAATCTGCT TTGAGACTAG TGTGTTGTA GCATTTTACT GTAATATATA 3240
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
 TACCTGTTAT CCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCAATTGTT 3360
 CACTACAAGG GTACAGTAAT CCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
 35 TATATTCTAA GGTTCCTCAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
 ATGAATAAAT GATTGCTGTT TCACCTCTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
 AAAGATTATT GCTTTTAAAA GTGTGTAGTT TTATGATGAT GTGTTTATGG TTTGCTTATT 3600
 TTTGCAAGAT GATACATAAT TCCAGCATTC TCTCCTCTTT GCTTTTATGT TTTGTTTCT 3660
 TTTTACAGG ATAAGTTTAT GTATGTCA CA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
 40 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAAGCT 3780
 GAATGTTAA

A107 Protein sequence:

45 Gene name: Integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Protein Accession #: NP_002205.1
 Signal sequence: 1-39
 50 Transmembrane domains: 682-704
 EGF domain: 552-584
 INB domain: 54-469
 Cellular Localization: plasma membrane

55
 1 11 21 31 41 51
 | | | | |
 MCGSALAFFT AAFVCLQND RGPASFLWAA WVPSLVGLGL QGEDNRCASS NAASCARCLA 60
 LGPECGWCVQ EDFISGGRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
 60 GEVSIQLRPG AEANFMLKVH PLKKYPVDLY YLVDVBSAMH NNIEKLSNVG NDLRKRMAFF 180
 SRDFRLGPGS YVDKTVSPYI SIHFERIHQ CSDYNLDQMP PHGYIHVLSL TENITEPEKA 240
 VHRQKISGNI DTPGGFDAM LQAAVCBESI GWRKEAKRL LVMTDQTSHL ALDSKLAGIV 300
 VPNDGNCHLK NNYYVKSTTM EHPSLGQLSE KLIDNNINVI FAVQGGKQPHW YKDLLPLPG 360
 65 TIAGEIESKA ANLNLVVEA YKLISEVKV QVENQVQGIY FNITAICPDG SRKPGMEGCR 420
 NVTISNDEVLP NVTVMKKCD VTGGKNYAI KPIGFNETAK IBIHRNCSCQ CEDNRGPKGK 480
 CVDETFLDSC CPQDENKCH FDEQPSSES CKSHKQDQPV SGRGVCVCGK CSCHKIKLKG 540
 VYGYKCEKDD FSCFYVHGNL CAGHGECEAG RCQCFSGWEG DRQCPSAAA QHCNVSKGQV 600
 CSRGTCVCG RCECTDPRSI GRPCEHCPTC YTACKENWNC MQCLHPHNLS QAILDQCKTS 660
 70 CALMEQOHYV DQTECFSSP SYLRIFPIIF IVTFILGLLK VLIIRQVILQ WNSNKIKSSS 720
 DYRVASAKKD KLILQSVCTR AVTYRREKPE BIKMDISKLN ABETPRCNF

A108 DNA sequence

75 Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 | | | | |
 ATGCTGCTCG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAGAGAAC TTCGCTGGGA GGCTTCCATC GGTCCGCACA CCTCCGAGG GCGAGGCAGC 120
 GACCGGGAGA GCGAGAGCCG GCGGAGGCT GCGGGGCTCC TGTGGGACCG CGCTGACGCC 180
 GGGGAGGGGG AGAAGGGGAA CCGGGGCGAG CCGCCGCTCT GGATCCGCGC CCAGCAGCAG 240

5	CGCGGGCCGC	CGCCAGCTGG	GCAGGCTCCC	GGGACTGCGG	CTGGGGGCGC	GCAGGACCTT	300
	CGCCTGCGTC	CTGGACGTTT	CGGGGGGAGG	GTCCGGTTGC	CAGTGAAACC	TCCAGAGGCT	360
	TCGGGACGAC	AGCCCCGGGG	GCCTTCTGAC	TGCATCCCGA	GATTTCCATC	AGCGAGTGCA	420
	ACTCATAAAG	CAGTCCCTAA	GGGGACCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCCTGGAC	CTAGGGCCCG	CGCTCGTCGC	CTCCTGGGCG	TGCGGCGAGA	GGGGAGTGGC	540
	CGCGCGGAA	AGCGCGCGGG	GACAGTCAGT	GACGAGGCC	GGGGTGCSCC	GGGGCCAAGA	600
	CTTCTCGGAG	ACCGTCTGTC	GCTCTCTGGA	GACGCGCTGT	CGCGGCCAG	GGTGGTGCCA	660
	TGTGGGGCGC	TGCGCGCTCG	TCCGCTCTCT	CATCCTGGAA	CGCCGCTTCG	CTCCTGCAGC	720
10	TGCTGCTGGC	TGCGCTGCTG	CGCGCGGGGG	CGAGGGCCCA	GCGCGAGTA	CTGCCACGGC	780
	TGGCTGGACG	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCGAGCG	CTTGGACGGC	840
	GCGGACGCCA	CCATCTGCTG	CGGCAGCTGC	GCGTTGCGCT	ACTGCTGCTC	CAGCGCCGAG	900
	GCGCGCCTGG	ACCAGGGCGG	CTGCGACAAT	GACCGCCAGC	AGGCGCTGG	CGAGCCTGGC	960
	CGGGCGGACA	AAGACGGGCC	CGGACGGCTC	GGCAGGGCTT	CATGCTTAG	GGGTACCCAA	1020
15	GGAGACGGCG	TGCGCTGCGC	CCCAACCGTG	AGGCGCTGGC	AGCGGTGCTC	CCCTGAAGGC	1080
	TCCCGGAAAG	GAGGCGAGCT	CCTCAGGGCT	TTCCCGGGGC	TGCTGCCCGG	TGCCAGACGC	1140
	CGGGGATTCC	CATCTTCTCC	ACGCGGCGGC	CCCTCTCCCC	TGCAGCGGCC	CGCCTTGCCC	1200
	ATCTACGTGC	CGTTCCTCAT	TGTTGGCTCC	TGTTTGTGCG	CCTTTATCAT	CTTGGGTCC	1260
	CTGCTGGCAG	CGTGTGCTG	CAGATGTCTC	CGGCCTAAGC	AGGATCCCCA	GCAGAGCCGA	1320
20	GCCCGAGGCG	GTACCGGCTT	GATGGAGACC	ATCCCATGA	TCCCGAGTGC	CAGCACCTCC	1380
	CGGGGGTCTG	CCTCACGCCA	GTCCAGCACA	GCTGCCAGTT	CCAGCTCCAG	CGCCAACTCC	1440
	GGGGCCCGGG	CGCCCCCAAC	AAGGTACACG	ACCAACTGTT	GCTTGCCGGA	AGGGACCATC	1500
	AACRAAGTGT	ATGTCAACAT	GCCCACGAAT	TTCTCTGTGC	TGAACTGTCA	CGAGGCCACC	1560
	CAGATTGTGC	CACATCAAGG	GCAATATCTG	CATCCCCCAT	ACGTGGGGTA	CACGGTGACG	1620
25	CACGAGCTCG	TGCGCTGCGC	AGCTGTGCCA	CCTTTCATGG	AGCGCTTGCA	CTCTGGCTAC	1680
	AGGCAGATTC	AGTCCCCCTT	CCCTCACACC	AACAGTGAAC	AGAAGATGTA	CCGACGCGTG	1740
	ACTGTATAAC	CGAGAGTCAC	TGGTGGGTTT	CTTTACTGAA	GGGAGACGAA	GGCAGGGGTG	1800
	GATTCTCGAG	GTGGGAAGTCC	GCACATGTGC	GTGGTATTTA	TGGCAGGATT	CCTTTGGATG	1860
	GCTTCATTTC	CCCCCAGACT	GTATGAAATC	ATCTCGAAT	TAGCATTTCT	GGATATGTTT	1920
30	CATCCAGGAT	ATCATTTGAT	TATGATGGAA	AACCGGCTTC	AGCTGGAGAT	GACTGTGATG	1980
	TGCTGATGCG	GTGTATAACA	AATGCTTGAG	TCCGAAGTGC	CCTTGAGATA	TGTTTGACGA	2040
	AAGAATTTTA	TAAACTGATA	AATTAAGGAT	TTTTATTATG	TGTTTATTAT	TATTTCTTTT	2100
	TGTTTGTGAG	CTGCACAGGA	TCAAAATGCC	TGTTATCTCC	CTTTTACTGG	GACTTTTTTT	2160
	TTTTTTTTTT	TTTTTTTTTA	TCAGACAGGG	TCTTGCTCTG	TTGCCACGGC	TGGAGTGACG	2220
35	TGGTGGGATC	TGCGCTCACT	GCAACTTCAG	CCTCCTGGAT	TCAGGCAACA	CTCCTGCCTC	2280
	AGCCTCCACC	GTGGCTGGGA	TTACAGGTGC	CTGCCCCCAT	GGCTAATTTT	TGTTATTTTT	2340
	TGTAGAGATG	GGGTTTCCAC	ATGTTGGCTG	GGCTGGTCTC	ACTCTCTCGA	CCTCAAGCAA	2400
	TCTGCGCTGC	TCAGCCTCCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	GCCCCAGCC	2460
	TGAGCCTTTT	TTTTTTTCTA	ATGCATCCAA	GGTTAAGGGG	AAGACGCAAA	TAACAGGACT	2520
40	ATTCTAAAG	GAAACCTGTT	TGAACTCTGT	GAGATCAGTC	ATCAGTCTCA	GTATTCACA	2580
	GGCACACCTT	AATTTCAITG	TAAAAAGATA	TATATATTTT	GTCTATTTTT	GTGCTTTTGG	2640
	GGGCTTATTT	TGTGCTTTTT	TACCTTATGT	AGAGATCTTA	TTACAAAGTG	ATTTTCTACA	2700
	TAAAAAAGAG	ACTGAAATTA	ATTGTATAGT	TACTTAACTA	ATGAAGACAT	TTCAGAACTC	2760
	TGGGATGATT	TTAATCTTGA	AGTAGTAGGT	GGTATAGTCA	TAAACCAATT	CATCCCCCTC	2820
45	TTGATTGTAT	CTTAATTTTC	TGGCTTTAAG	GTGACATCTG	AGAGGTAATG	CATTCTTTTT	2880
	TATATTGAAA	TCATAAACTA	TCACCCGCTG	CTTCTCTGAG	TTACTTTTAA	TTTTGCCCTG	2940
	TGGTTATGGT	TTGGCGTTTC	CTTCTGTTTG	GTTTTCAGAG	CCCCATGTCT	ATATAGTCTC	3000
	GAGTGCAAGT	AATTACTATA	CTTGTAAGT	AAGATCAGTA	TTCTGCGCTA	GATCTGATAA	3060
	AAAAATTTTC	TGTCTTAGT	TATAAAATTT	CAAAGAAATG	TGTTACAAAG	ATACTTAGTA	3120
50	TAGCTCTCTA	GCCATAACCT	GAGACTTGGG	ATGAAATTTA	AACGAGATAC	GATTACTTTT	3180
	GCAGATCATA	AGGCTTTTTA	TACTCTTGTT	ATCAAAATG	CTTATTTTTT	AGGCACTAAG	3240
	GATTGTTAAG	AGAAAGGCTT	TTCAACGAAG	GATTGCTTTT	CTTCTCCAC	ACTGTTCTTG	3300
	ATTTCTCTCT	TCCTTCAGGC	CTCAACAGGC	ACTGTATTCA	TGCGCAATGT	TCCAAATTAT	3360
	CAAAATTCAG	TGAATTTAT	TGTGTGTTCT	TTACTTATAT	AAAAAAGAT	AACCTTAAGG	3420
55	ATGTGCAAGT	ACATTTCCAA	CTGTAGCAC	AACAGTATT	TGTAATTAA	ACAAATCGCT	3480
	GTATGGTATG	GTCTTCTACA	CATTTATGTC	TATAGATATC	TATCGATCAT	CTTCTATTTC	3540
	TGTTTCAATG	CTGAATAATG	TAAACCAAGT	GTTGGCAATT	GGTATCATCA	ATGATACTAC	3600
	TTTTTTAATA	ACCAAGGCA	GGGGAATAAT	ATTTTACTTA	TAAATAATA	TTTTATGATG	3660
60	TGAAAAAATA	AAAAAATAAT	AAAAAATAAT				

A109 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

70	1	11	21	31	41	51	
	MLSGFLMSPS	TQHRAQYTPG	GKELPWEASI	GAHTSRGRGS	DRERESRPEA	AGLLWDRAAA	60
	GEAEKGNRGE	PPAWIRAQOQ	PRPPPAQAP	GTAAGGAQDP	RLRPGRSRGR	VRLFPVKPPEA	120
	SGRQPRGSD	CIPRPPSASA	THKAVPKGTG	PPAEDGDGLG	APGFRARRRR	LLGVAAEGSG	180
75	PRGKRRTGVS	DEARGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAAPRSP	HPGTPLRSCS	240
	CCNLRCWRNG	RGPSGEYCHG	WLDQAQVWRI	GFQCERPFDG	GDATICCGSC	ALRYCCSSAE	300
	ARLDQGGCDN	DRQGGAGEPG	RADKDGPRRL	GRASCLRGTO	GDGEGAPPPV	RAWQRCSPG	360
	SPKGRQLLRA	FPGLLPRARR	RGFPSSPRGG	PSPLQRPALP	IYVPLIVGS	VFVAFILGS	420
80	LVAACCCCL	RPKQDPQQR	APGNNRLMET	IPMIPSASTS	RGSSSRQSSST	AASSSSSANS	480
	GARAPFTRSQ	TNCLPEGTH	NNVYVNMPTN	FSVLNQQQAT	QIVPHQGGYL	HPPYVGYTVQ	540
	HDSVPMATVP	PPMDGLQPGY	RQIQSPFPHT	NSBQKMPAV	TV		

A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 (H.sapiens)

Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

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1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGTCACAG TTTCTTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTTATG AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGTTTATTC ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
   CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
15 GAAACCCTG ATAAGAATTT ATCACCTGAT GGCCAATATG TGCCCTAGAAT CATGTTTGTA 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAGAGATG GATAGAAAAA AGCCTTCACT TCAAAGAAAT CAAATTTTAT 600
   GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
20 TTAATAATTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
   TCTGAAAAAA AAAAAAATAA AAAAAAATAA

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25 A111 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 (H.sapiens)
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

30

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35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSALGLC LLLVTVSSNL AIAIKKPKRP PQTLRSGWGD DITWVQTYEE GLFYAQKSKK 60
   PLMVIIHLED CQYSQALKKV FAQNEBIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120
   FVDPPLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKGLRL LIQSEL

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A112 DNA SEQUENCE
 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

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50 1      11      21      31      41      51
   |      |      |      |      |      |
   ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
   AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTGG OGAGTATCAT CATTTGGTGT GTCCCTATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCTT CGGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
   GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
   GGGAACTGCT TCTCTGCCTG TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACGTGC TTGCCTGTGG GAAGAGCCTG 600
60 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACCTGGGT 720
   CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCGA CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCAATTGAA 840
   TTCAACCCCA TGTAACCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
65 ACTTTCTCAG GCACAGTCAG GCGCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCAC TCTGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGCAGGGGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAG TGCAGACGAT 1080
   GCGTACCAGG GGGAGTCAC CGAGAAGATG ATGTGTGCGA GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
   AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

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75 A113 Protein sequence:
 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

80

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1      11      21      31      41      51
|      |      |      |      |      |
5  MLQDPDSQPF LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIVV VLIKVILDKY 60
YFLCGQPLHF IPRKQLCDGE LDCPLGEDEB HCVKSPFEPG AVAVRLSKDR STLQVLDSAT 120
GNWFSACFDN FTEALAEATAC RQMGYSKPT PRABEIGPDQ DLDVVEITEN SQBLRMRNSS 180
GPCLSGSLVS LHCLACGKSL KTRPVVGGEB ASVDSWPMQV SIQYDKQHVC GGSILDPHWV 240
LTAACHFRKH TDVFNWVKRA GSKLGSFSPS LAVAKIIIEB FNPMPKDND IALMKLQFPL 300
TPSGTVRPIC LPPFDEELTP ATPLWIIIGW FTEQNGGKMS DILLQASVQV IDSTRCNADD 360
10 AYQGBVTEKM MCAGIEPGEV DTCQGDSSGP LMYQSDQMHV VGVISWGYGC GGPSTPGVYT 420
KVSAYLNWY NVWKRAEL

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A114 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
25  GGAATTCCTT TTTTCTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG 60
CAATGGCACA ATCTCAGCTT ACTGCAACCT CCGCTCCCG GGTTCAGCG ATTCTCCTGC 120
CTCAGCTCTT CAAGTAGCTG GGAATTACAG CATGTGCCAC CACCCCTGGC TAACATAATT 180
CTTTCTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
ACCTCAGGTG ATCCACTTGC CTGGGCTTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300
TGCTGGGCTG ATTTCTTTT TGTGTGTGGA TTTTGAAGAC AGGCTCTCCC TTGGTCGCCC 360
AGGCTGGAGT GCAAGTGGTG GATCTTGGCT CACTATAACC TCCACTCTCT GGTTCAGT 420
GATCTCTCCA CTTAGCTCTC CTGAGTAGCT GTGATTACAG GCGTGACCA CCACACCCGG 480
CTAATTTTGT TATTTTATT AGAGACAGGG TTTACCATG TTGGCCAGCG TGTTCTCAAA 540
CTCTGAGACT CAAGGGATCC GCCTGGCTCC ACTTCCCAA GTCCCGAGAT TACAGGTGTG 600
AGTCACCATG CTGACCTTAA TAATTCCTTA GTCACTTTT CTGGTCCATT TCTTCTTAG 660
GGTCTCTACA ACAATCTGC ATTAGGCGGT ACAATAATCC TTAACCTCAT GATTCAAAA 720
AGGAAGATGA AGTGATTCAT GATTTAGAAA GGGGAAGTAG TAAGCCCACT GCACACTCTT 780
GGATGATGAT CCTAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAA 840
TTTGGTTTAA ATTAATTATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTA 900
ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960
TGCAGTTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT 1020
40  CCATATGAA CAAGTGAGA GACATTAATA ATAAGTTTAA AAATGAAGAC CTACTGATG 1080
AACTAAGCTT GAATAAATT TCTGCTGATA CTACAGATAA CTCGGGAAC GTTAACCAA 1140
TTATGATGAT GGCAACAAC CCAGAGGACT GGTGAGTTT GTTGCTCAA CTAGAGAAA 1200
ACAGTGTTCG GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTGGTTAC AGTCAAGCAA 1260
TTGAAGCGCT TCCCCAGAT AAATATGCC AAAATGAGAG TTTGTCTAGA ATTCAGTGA 1320
45  GATTGTCTGA ATTAAGACT ATTCAAGAGC CAGATGATGC ACGTACTAC TTTCAATGG 1380
CCAGAGCAA CTGCAAGAAA TTTGCTTTTG TTCTATATAT TTTGCACAA TTTGAACGT 1440
CACAAGGTAA TGTCAAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGAGCAG 1500
TACCCTAGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560
TTTCAGAGGA GGAAGAGAG AATTATCAG CATCTACGGT ATTAAGTACC CAAGAATCAT 1620
50  TTTCCGGTTC ACTTGGGCAT TTACAGATA GGAACAACAG TTGTGATTCC AGAGACAGA 1680
CTACTAAGC CAGTTTITA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740
ACCGGAATTC ATTGAGACAA ACTAACAAAA CTAAACAGTC ATGCCCAATT GGAAGAGTCC 1800
CAGTTAACTT TCTAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTCG GTTGTACCTT 1860
GTTTATAGAA AAGACAAGCC TCTAGATCAG AATGCCGAGA TTTGGTTGTG CCTGGATCTA 1920
55  AACCAAGTGG AAATGATTC TGTGAATTAA GAAATTTAAA GTCTGTCAA AATAGTCATT 1980
TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATA 2040
CCCTGAAGAA TAAACGGAA TCAAGTCTT TAGCTAAATT AGAAGAAACT AAAGAGTATC 2100
AAGAACAGGA GGTTCAGAG AGTAACAGGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160
GTATTAACCA GAATCTCTCT GCATCTTCAA ATCACTGGCA GATTCGGAG TTAGCCGAA 2220
60  AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGCTTTTCA GTTTCAAAC 2280
AGTCACCACC AATATCAACA TCTAATAGT TTGACCCAAA ATCTATTGTG AAGACACCAA 2340
GCAGCAATAC CTGGATGAT TACATGAGCT GTTTAGAAC TCCAGTTGTA AAGAATGACT 2400
TTCCACTCTG TTGTCACTG TCAACACCTT ATGGCCAAAC TGCTGTGTT CAGCAGCAAC 2460
AGCATCAAAAT ACTTGCCACT CCACTTCAA ATTTACAGGT TTAGCATCT TCTTCAGCAA 2520
65  ATGAATGCAAT TTGGTTAAA GGAAGAAATT ATCCATATT AAAGCAGATA GGAAGTGGAG 2580
GTTCAAGCAA GTTATTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
TGAATTAATC ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCAGG 2700
ACCAATACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAA 2760
70  AGAAAAATC CATGTATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCG 2820
TTCAACAAT CCATCAACAT GGCATTGTT ACAGTATCTT TAAACAGCT AACTTTCTGA 2880
TAGTTGATGG AATGCTAAG CTAAATTGAT TTGGGATTGC AAACCAAATG CAACAGATA 2940
CAACAAGTGT TGTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3000
TCAAGATAT GTCTTCTCC AGAGAGAATG GGAATCTAA GTCAAGATA AGCCCCAAA 3060
75  GTGATGTTG GTCTTAGGA TGTATTTGT ACTATATGAC TTACGGGAAA ACACCAATTC 3120
AGCAGATAAT TAATCAGATT TCTAATATC ATGCCATAAT TGATCCTAAT CATGAAATG 3180
AATTTCCGGA TATTCCAGAG AAGATCTTC AAGATGTGTT AAGTGTGTT TAAAAAGGG 3240
ACCCAAACGA GAGGATATCC ATTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3300
CTCATCCAGT TAACCAAATG GCCAAGGAA CCACTGAAGA AATGAATAT GTTCTGGGCC 3360
80  AACTGTTGG TCTGAATCT CTAATCTCCA TTTGAAAGC TGCTAAACT TTATATGAA 3420
ACTATAGTGG TGTGAAAGT CATAATTCTT CATCTCCCAA GACTTTTGAA AAAAAAGGG 3480
AAAAAAATG ATTTGAGATT ATTGTAATG TCAGATAGGA GGTATAAAT ATATTGACT 3540
GTTATACTCT TGAATCCCTG TGGAAATCTA CATTTGAAGA CAACATCACT CTGAAGTGT 3600
ATCAGCAAAA AAAATTCAGT GAGATTATCT TAAAAGAAA ACTGTAAAA TAGCAACCAC 3720

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TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAAGCTTG 3840
TAAATAAAGT TTTGTGGCTA AAATGA

5

A115 Protein sequence:

Gene name: TTK protein kinase
Unigene number: Hs.169840
Probeset Accession #: M86699
Protein Accession #: NP_003309
Signal sequence: none found
Transmembrane domains: none found
Protein Kinase Domain: 510-775
Cellular Localization: cytoplasmic and nuclear

10

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1	11	21	31	41	51	
MNKVRDIKMK	PKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MMANNPEDWL	SLLLKLEKNS	60
VPLSDALLNK	LIGRYSQAIE	ALPFDKYQGN	ESFARIQVRF	ASLKAIQEPD	DARDYPQMAR	120
ANCKKPAFVH	ISPAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLBIALRN	LNQKKQLLS	180
BEKKNLKLSA	TVLTAQESFS	GSLGHLQNRN	NSCDSRGQTT	KARFLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDSDVVPCE	MKRQTSRSEC	RDLVVPGSKP	300
SGNDSCELRN	LKSVQNSHFK	EPLVSDKSS	BLIITDSITL	KNKTESLLA	KLEETKRYQE	360
PEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	MTEQKHTTPE	QFVFSVSKQS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCF	RTPVVKNDFP	PACQLSTPYG	QPACFQQQKH	480
QILATPLQNL	QVLASSSANE	CISVKGRIYS	ILKQIGSGGS	SKVPQVLNEK	KQIYAIKYVN	540
LEADNQTLD	SYRNEIAYLN	KLQQHSKII	RLYDYBITDQ	YIYVMVECGN	KDLNSWLKCK	600
KSIDPWERKS	YWNMLEAVH	TIHQHGIHVS	DLKPAFLIV	DGMLKLIDFG	IANKMQPDTT	660
SVVKDSQVGT	VNYMPPEAIK	DMSSSRENGK	SKSKISPKSD	VMSLGCILYY	MTYKTPFPQ	720
IINQISKLHA	IIDPNHEIEF	PDIPKDLQD	VLKCKLRDP	KQRISIPELL	AHPYVQIQTH	780
PVNQMAKGT	BEKMYVLGQL	VGLNSPNSIL	KAAKTLVHY	SGGESHNSSS	SKTPEKRGK	840
K						

OVARIAN

40

A116 DNA SEQUENCE

Gene name: G protein-coupled receptor 39
Unigene number: Hs.85339
Probeset Accession #: AA349893
Nucleic Acid Accession #: NM_001508
Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51	
ATGGCTTCAC	CCAGCCTCCC	GGGCAGTGAC	TGCTCCCAAA	TCATTGATCA	CAGTCATGTC	60
CCCGAGTTTG	AGGTGGCCAC	CTGGATCAAA	ATCAACCTTA	TTCTGGTGTG	CCTGATCATC	120
TTGTGTATGG	GCCTTCTGGG	GAACAGCGCC	ACCATTCGGG	TCACCCAGGT	GCTGCAGAAG	180
AAAGGATACT	TGCAGGAAGG	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
TTGTGTCTCC	TCATCGGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCTGAGCC	300
ACGTCCAGCT	ACACCTGTCT	CTGCAAGCTG	CACACTTTCC	TCTTGGAGGC	CTGCAGCTAC	360
GCTACGCTGC	TGCAGGTGCT	GACACTCAGC	TTTGAGCGCT	ACATGGCCAT	CTGTACCCCC	420
TTCAAGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCTCTCTG	480
GTCACCTCCG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTCG	540
GTGAACGTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCCG	CCACCAAGAG	600
CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
CAGTCCAGCA	TCTTGGGCGC	CTTCTGTGTC	TACCTGTGGG	TCTGTCTCTC	CGTAGCCCTC	720
ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGCTCGCTG	GGCCGGGGGC	780
ACGCGGCTCT	CGCAGCTGAG	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
ACCATCATCT	TCCTGAGGCT	GATTGTGTGT	ACATTGGCCG	TATGCTGGAT	GCCCAACCGA	900
ATTTCGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCACGACT	GGACGAGGTC	CTACTTCCGG	960
GGGTACATGA	TCTCTCTCCC	CTTCTCGGAG	ACGTTTITCT	ACCTCAGCTC	GGTCATCAAC	1020
CCGCTCTGTT	ACACGGTGTC	CTCGCAGCAG	TTTCCGCGGG	TGTTCGTGCA	GGTGTCTGTC	1080
TGCGGCTGTT	CGCTGCAGCA	CGCCAAACAC	GAGAAGCGCC	TGCGGTGACA	TGCGCACTCC	1140
ACCACCGACA	GCGCCGCTTT	TGTGCAGCGC	CCGTTGCTCT	TGCGTCCCG	GCGCCAGTCC	1200
TCTGCAAGGA	GAATCTAGAA	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCCAG	1260
TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACCGACC	1320
AATTCTGCTG	CAGAGAATGG	TTTTCAGGAG	CATGAAGTTT	<u>GA</u>		

A117 Protein sequence:

Gene name: G protein-coupled receptor 39
Unigene number: Hs.85339
Probeset Accession #: AA349893
Protein Accession #: NM_001508, NP_001409
Signal sequence: none found
Pfam domains: 7tm_1 [72-172, 224-344]
Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
Cellular Localization: plasma membrane

1	11	21	31	41	51	
MASPSLEPSD	CSQIIDHSHV	PEPEVATWIK	ITLILVYLII	FVMGLLGNSA	TIRVTQVLQK	60

5	KGYLQKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTPLFEACSY 120 ATLLEVLTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVM VTSALVALPL LFMAGTEYPL 180 VNVPSHRGLT CNRSSTRHBE QPETSNSMIS TNLSSRWTFV QSSIIFGAPVV YLVVLLSVAF 240 MCWNMQVLM KSQKGSLLAG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCMMPNQ 300 IRRIIMAAKP KRDWTRSYFR AYMILLPFSE TFFYLSVIN PLLYTVSSQQ FRRVFPVQLC 360 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRETKIFL STPQSEARPO 420 SKSQSLSLSE LEPNSGAKPA NSAAENGPOE HEV
10	<u>A118 DNA sequence</u> Gene name: bone morphogenetic protein receptor IB (ALK-6) Unigene number: Hs.87223 Probeset Accession #: AA250737 Nucleic Acid Accession #: NM_001203 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)
15	1 11 21 31 41 51 CGCGGGGCGC GGAGTCGGGG GGGCCTCGCG GGACGCGGGC AGTGGCGAGA CCGCGGCGCT 60 GAGGACGCGG GAGCGGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTTCTTAGAT 120 GTGAAGAGAA AGGAAGATCA TTTTCATGCT TGTGTGATAA GGTTCAGACT TCTGCTGATT 180 CATAACCAAT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TGGGAAGTGC AGGAAATTA 300 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360 TTGGCTGTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420 GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTGT GTTCACTTCT 480 GGTTCCTAG GACTAGAAGG CTCAGATTTT CAGTGTGGGG ACCTCTCCAT TCCTCATCAA 540 AGGAATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTTACA 600 CTGCTCCAT TGAAAACAG AGATTTTGTG GATGGACCTA TACACCAGAG GGCTTTACTT 660 ATATCTGTGA CTGTCTGTG TTTGCTCTTG GTCTTATCA TATTATTGTT TTACTTCGG 720 TATAAAGAC AAGAAACAG ACCTCGATAC ASCATTGGGT TAGAACAGGA TGAACCTTAC 780 ATTCTCTCTG GAGATCCCT GAGAGACTTA ATTGAGCAGT CTGAGAGCTC AGGAAGTGGA 840 TCAGCCTCC CTCTGCTGCT CCAAAGGACT ATAGCTAAGC AGATTCAAGT GGTGAACAG 900 ATTGAAAAGG GTCTGTATGG GGAAGTTTGG ATGGGAAAGT GGCGTGGCGA AAAGGTAGCT 960 GTGAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020 ACAGTGTGA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080 GGTCTCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140 TATCTGAAGT CACCCACCTC AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTTCTGTC 1200 AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260 CATCGAGATC TGAAAGTAA AAACATTCTG GTGAAGAAAA ATGGAATCTG CTGTATTGCT 1320 GACCTGGGCC TGGCTGTTAA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380 ACTCGAGTTG GCACCAAAAG CTATATGCCT CCAGAGGTGT TGGACGAGAG CTTGAACAGA 1440 AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCTCAT CCTTTGGGAG 1500 GTGCTAGGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560 CTAGTGCCTA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620 CGCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAAACCT 1680 ATGACAGAAAT GCTGGGCTCA CAATCTGCA TCAGGCTGTA CAGCCCTGCG GGTTAAGAAA 1740 ACACTTGCCA AAATGTGAGA GTCCCAAGAC ATTAACCTCT GATAGGAGAG GAAAAGTAAG 1800 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860 TAAGCATCCA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTT 1920 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTT 1980 TCTGTTTGA GCGGAGAAA CCGTTGGGTA ACTTGTCAA GATATGATGC AT
55	<u>A119 Protein sequence</u> Gene name: bone morphogenetic protein receptor IB (ALK-6) Unigene number: Hs.72472 / Hs.87223 Probeset Accession #: AA250737 / U89326 Protein Accession #: NP_001194 Signal sequence: 1-13 Transmembrane domains: 128-144 PFAM domains: activin_receptor [30-111], protein kinase [204-491] Cellular Localization: plasma membrane
60	1 11 21 31 41 51 MLLSRAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCPTMIEED 60 DSGLPVVTSQ CLGLEGSDFQ CRDTPIPHQR RSIECCTERN EQNKDLHPTL PPLKQRDFVD 120 GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180 EQSQSGSGGS GLPLLVRTI AKQIQMVQKI GKGRYGEVVM GWRGEKVAV KVPPTTEBAS 240 WFRTEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300 MLKLAYSSVS GLCHLHTEIF STQGKPALAH RDLKSKNILV KNGTCCCIAD LGLAVKPID 360 TNEVDIPPT RVGTRKYMPP EVLDESINRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420 EEYQLPYHDL VPSDPYSYDM REIVCIKCLR PSPPNRWSSD ECLRQMGKLM TECWAHPAS 480 RLTALRVKKT LAKMSESQDI KL
75	<u>A120 DNA SEQUENCE</u> Gene name: LIV-1 protein, estrogen regulated Unigene number: Hs.79136 Probeset Accession #: U41060 Nucleic Acid Accession #: NM_012319.2 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)
80	1 11 21 31 41 51

5
10
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35
40
45
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60

CTCGTGCCGA ATTOGGCACG AGACCGCGTG TTCGCGCCTG GTAGAGATT CTGGAAGACA 60
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GCGGAGACGA AGCGGCAATG GCGAGGAAGT TATCTGTAA CTGTATCTGT ACCTTTGCCC 180
TCTCTGTGAC AAATCCCTTT CATGAACTAA AAGCAGCTGC TTTCCCCAG ACCACTGAGA 240
AAATTTAGTCC GAATTTGGGAA TCTGGCATTG ATGTTGACTT GGCATTTCC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAAATAA TTCTTTGTCA GTTGAAGGGT 360
TCAGAAAATT ACTTCAAAT ATAGGCTATG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCAAGACCA TCATTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTAC TCAGACCATG 480
AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCATCTCAC CATAATCATG 540
CTGCTTCTCG TAAAAATAAG CGAAAAGCTC TTTGCCGAGA CCATGACTCA GATAGTTTCAG 600
GTAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCACTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAATCTTCC 780
CCAAAGATGT AAGCAGCTCC ACTCCACCA GTGTACATC AAAGAGCCGT GTGAGCCGTC 840
TGGCTGGTAG TAAAAATAAG GAATCTGTGA GTGAGCCCG AAAAGGCTTT ATGTATTCCA 900
GAAACACAAA TGAAAATCCT CAGGAGTGTG TCAATGCATC AAAGCTACTG ACATCTCATG 960
GCATGGGCAT CCAGGTTCCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCATG 1020
TCAACCAAT TGATGCTAGA TCTTGTCTGA TTCATACAA TGAAAAGAAG GCTGAAATCC 1080
CTCCAAAGAC CTATTCATTG CAAATAGCCT GGGTTGGTGT TTTTATAGCC ATTTCCATCA 1140
TCAGTTTCTT GTCTCTGCTG GGGTTATCT TAGTGCTCT CATGAATCGG GTGTTTTTCA 1200
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GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
TTCAACACCA TCATGACTAC CATCATATTC TCCATCATCA CCAACACCAA AACCAACATC 1860
CTCAGATCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTGCCACTT 1920
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GTGCTGCTTT TACTGAAAGC TTATCAAGTG GTTTAAGTAC TTCTGTGTCT GTGTTCTGTC 2040
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GCTTATTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGCAC AATGATGCTA 2280
GTGACCATGG ATGTAGCCGC TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
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TATTTCTACT TGGAGATAAA ATCTGTATGT GCAATTCACC GSTATTACCA GTTTATTATG 2640
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TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
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AAAAATCACA AATTTTGTG TAAATTAGAG GGGAGAAATT TAGAATTAA TATAAAAAGG 2940
CAGAATTAGT ATAGAGTACA TTCAATTAAC ATTTTGTGCA GGATATTTTC CGTAAAAAC 3000
GTAGTGAGCA CTCTCATATA CTAATTAGTG TACATTTAAC TTTGTATAAT ACAGAAATCT 3060
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TATTTGCCAG TTATATATCA CCAAAAGCTG TATGACTGGA TTGTTCTGTT ACCTGGTTTA 3240
CAAAATATC AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAACT ACACTAAGTA 3300
TCATTTGATT CGATTACAAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCAITGT 3360
GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCGTCTGTG GCATCTCTCA 3420
GATGTTTCTT TTTTACAAA TAAATTCCTT ATATCAGCTT G

A121 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Protein Accession #: NP_036451
Signal sequence: 1-21
Pfam domain: Zip[591-743]
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization: plasma membrane

70

75

80

1 11 21 31 41 51
MARKLSVILI LTFALSVINP LHELKAAAFP QTTEKISPNW ESGINVDLAI STRQYHLQOL 60
FYRYGENNSL SVEGFRLILQ NIGIDKIKRI HIHHDHSHS DHEHSDHER HSDHEHSDH 120
EHSDDHSHS HNNHAAAGKN KKKALCPDHD SDSSGKDPFN SQKGAAHPE HASGRNVDK 180
SVSASEVTST VINTVSEGT FLETIETPRP GKLPFKDVSS STPPSVTSKS RVSRLAGRKT 240
NESVSEPRKG FMSRNINEN PQECFNASKL LSHGMGIQV FLNATEFNYL CPAIINQIDA 300
RSCILHTSEK KASIPPKTYS LQIANVGGFI AIBIISFLSL LGVILVPLMN RVFPKLLSF 360
LVALAVGTLG GDAPLHLPLH SHASHHSHS HEEPAMEMKR GPLFSLSSQ NIEBAYFDS 420
TTLGLTALGG LYPMLVEHV LTLIKQFKDK KKKQKKPEN DDDVEIKQL SKYESQLSTN 480
EEKVDTDRT EGYLRADSQE PSHFDSQQA VLEEEVIMIA HAHPQEVYNE YVPRGCKNKC 540
HSHPHDLRG SDLLIHHDH YHHILHHHH QNHHPHSHSQ RYSREELKDA GVATLAWVI 600
MDGLHNFSD GLAIGAAPE GLSSGLSTSV AVFCHELPHR LGDFAVLLKA GMTVKQAVLY 660
NALSAMLAYL GMATGIFIGH YAENVSMWIP ALTAGLFMYV ALVDMVPEML HMDASDHGCS 720

RMGYFFLQNA GMLLGFGLML LISIFEHRIV PRINF

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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CGCCCTTGCC GGGGTGCTCG GCCTCCCTCT CCAGACTGCA GGGACAGCAC CCGGTAACTG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGGCC GCGGCGCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGGGAGA 240
ATGCTCTGCG CCGGAGGCTG TGCGCTCCCG CTGCTGCTCT CCGGGTGGCG AGGTGGTTTC 300
GGGAACGCGG CCAAGTGAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
TGTCACCTATG GAACATAAAT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAAT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGAAAAACC TGCACTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGCG CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAAGCTTG AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
TCAGAGCTCC GCCTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGGTCTCTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCCT AGAGCACCTG GTACCATCAA AGACAGAATC 1080
AAGAAGTTGC TTGCTCACA AAACAGCATG AAAAGAAGG CAAAATTA AAATGTTACC 1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
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CTGGTCCAAA GGAAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAA TATCTCGGTT 1440
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TGAATCTCTG CTGATCGAGA TAATGCTATT GGCCTCTATA TGGCAGTTCC GGCCTTGGCA 1560
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AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
TTTGAAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
TGAAGACAG GAAAAATTCA GTTGTATCAA GGAAGTGAAG CTACCAAAG CATCATTITT 1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGCG GAAATGCGAG TGGATGGCGT CTTCCTTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTGAGTTC CCGGTTTTT TTGATATTGC ATCATAGGAC CTCCTGGCATT 1980
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TATGACATCA AAGATAGACT TTTGCCIAAG TGGCTTAGCT GGGTCTTTCA TAGCCAAACT 2340
TGTATATTTA AATTCCTTGT AATAATAATA TCCAAATCAT CAAAAAAA AAAAAAAA

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55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

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1      11      21      31      41      51
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MPLPWSLALP LLLSWVAGGP GNAASARHGG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
CEATCEPGCK FGECVGNPKC RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKFC 120
LSGHMLMPDA TCNVSRTCAM INCQYSCEDT EGGPQCLCPG SGLRLAPNGR DCLDIDECAS 180
GKVICPYNRR CVNTFGSYTC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTQ 240
GSEKCKCKQG YKGNGLRCSA IPENSVEVL RAPGTIKDRI KLLAHQNSM KKKAKIKNVT 300
PEPTRTPPK VNLQPFNYEE IVSRGNSHG GKKGNEKKK EGLEDEKREE KALKNDIEER 360
SLRGDVPPPK VNEAGEFGLI LVQRKALTSK LEHKOLNIEV DCSFNHGICD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKQDIGRLK LLLFDLPQPS NFCLLDYRL AGDKVGKLRV 480
FVKNSNNALA WKTTSSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKKGKT EIAVDGVLLV 540
SGLCPDLSLLS VDD

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80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

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5      1      11      21      31      41      51
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      CTGCCACCTG GGGCGGTGCG GGGCCCGGAGC CGGGAGCCCG GGTAGCGCGT AGAGCCGCGG 120
      CGATGCAOGT GGGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
      CCTGTTCCT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
      GCTTCATCCA CGGCGCGCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
      CCATTTTGGG CTTCGCCAC CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
      CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCGG 420
      GCCAGGGGCT CTCTACCCCG TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
      GCCTGCAAGA TAGCCATTTC CTCACCGAAG CGACATGGT CATGAGCTTC GTCAACCTCG 540
      TGGAAATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
      TTTCCAAAGT CCCAGAAGGG GAAGCTGTCA CGCAGCCGSA ATTCGGATC TACAAGGACT 660
      ACATCCGGGA GCGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
      AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGGTACCCCT TGGGCTCGG 780
      AGGAGGGCTG CTGGTGTGTT GACATCACAG CCACCAAGCA CCACTGGGTG GTCAATCCCG 840
      GGCACAACTT GGGCCTGCAG CTCTCGGTGG AGACGCTGGA TGGGCGAGGC ATCAACCCCA 900
      AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACA GCAGCCCTTC ATGTTGGCTT 960
      TCTTCAAGGC CACGAGGCTG CACTTCCGCA GCATCCGCTC CACGGGGAGC AAACAGCGCA 1020
      GCCAAGACCG CTCCAAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
      AGAACAACAT GGTGGTCCGG AGGCAGGCTT GTAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
      GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCCGCC TACTACTGTG 1200
      AGGGGGAGTG TGCCTTCCCT CTGAACCTCT ACATGAACGC CACCAACCA GGCATCGTGC 1260
      AGACGCTGGT CCACCTTATC AACCCGAAA CGGTGCCAA GCCCTGCTGT GCGCCACGCG 1320
      AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTGATC CTGAAGAAAT 1380
      ACAGAAACAT GGTATTGGCT GGCCTGTGGT GCCACTAGCT CCTCCGAGTA TTCAGACCTC 1440
      TTGGGGCCAA GTTTTCTGG ATCCTCCATT GCTCGCTTGG GCCAGGAACC AGCAGACCAA 1500
      CTGCCCTTTG TGAGACCTTC CCTTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
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      TCCTACAAAG TGTGCAGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
      GCCGGGCGAG GTGATTGGCT GGGAAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
      TTATGAGCGC CTACCAGCCA GGCACCCAG CGGTGGGAGG AAGGGGGCGT GGCAGGGGT 1800
      GGGCACATTG GTGCTCTGTC GAAAGGAAAA TTGACCCGGA AGTTCTCTGA ATAAATGTCA 1860
      CAATAAACG AATGAATG

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40 A125 Protein sequence:
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 Pfam domains: TGFb_propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

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50      1      11      21      31      41      51
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      ILGLPHRPRP HLQGGKHSAP MFMLDLINAM AVEGGGGPGG QGFSYPYKAV FSTQGPPLAS 120
      LQDSHFLTDA DMVMSFVNLV EHDKEFPFHR YHEREPRPDL SKIPEGEAVT AAEFRIYKDY 180
      IRERPDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGMVLVEDITA TSNHVVNPR 240
      HNLGLQLSVE TLDGQSINFK LAGLIGRHGP QNKQPPMVAF FKATEVHFRS IRSTGSKQRS 300
      QNRSTPKNQ EALRMANVAE NSSSDQRQAC KXHELYVSPR DLGWQDWIIA PEGYAAYYCE 360
      GECAFFLNSY MNAITHAIVQ TLVHFIPNET VPKPCCAPTQ LNAISLVLYD DSSNVILKXY 420
      RMNVVRACGC H

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A126 DNA SEQUENCE
 Gene name: integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

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      CTGCCGACTT GTCTTTGGCC GCTGCTCCGC AGAGCGGGCT GCAAGAGTGC AACTAATGGT 120
      GTTGGCTCCG CTGCCCACTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180
      TCCCTTCGAC CTGCGCGGCG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
      TAGGGTGGTT TCCCCCCAG CTTCGGGCTT TGTITGGGTT TGATTGTGTT TGGCTCTTCG 300
      CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCTTTTCTT 360
      TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTGGCC GCGGGGCCCT 420
      TGGCGGTGCA AGGAGGTGCT TCTCGCGGAG ACCGCGGGAC CCGCCGTGCC GAGCCGGGAG 480
      GGCCTGAGGG GCCTGAGAT GCCGAGCGGT GCGCGGGCCC GCTTACCTGC ACCGCTTGCT 540
      CGGAGCGCGG GGGTCCGCT GCTAGCGCTG CGGAAAACGT CTTAGCGACA CTGCGCGCGG 600
      GGCCTCGAGG TCGCCCGGGA GGCAGAGCCC GCGTCCGGAA GGCAGCCAGG CGGCGGGGCG 660
      GGGGCGGGCT GTTTTGCAAT ATGTGCGGCT CGGCGCTGGC TTTTITTTACC GCTGCATTGT 720
      TCTGCTGCA AACGACCGG CGAGGTCCCG CTCTGTTCTT CTGGGCGAGC TGGGTGTTTT 780

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	CACTTGTTCT	TGGACTGGGC	CAAGGTGAAG	ACAATAGATG	TGCATCTTCA	AATGCAGCAT	840
	CCTGTGCCAG	GTGCTTGGC	CTGGGTCCAG	AATGTGGATG	GTGTGTTCAA	GAGGATTTC	900
	TTTCAGGTGG	ATCAAGAAAGT	GAACGTTGTG	ATATTGTTTC	CAATTTAATA	AGCAAAGGCT	960
5	GCTCAGTTGA	TTCAATAGAA	TACCCATCTG	TGCATGTTAT	AATACCCACT	GAAAAAGAAA	1020
	TTAATACCCA	GGTGACACCA	GGAGAAGTGT	CTATCCAGCT	GGGTCCAGGA	GCCGAAGCTA	1080
	ATTTTATGCT	GAAAGTTCAT	CCTCTGAAGA	AATATCCTGT	GGATCTTTAT	TATCTTGTG	1140
	ATGTCTCAGC	ATCAATGCAC	AATAATATAG	AAAAATTAAA	TTCCGTTGGA	AACGATTTAT	1200
	CTAGAAAAAT	GGCATTTTTC	TCCCGTGAAT	TTGCTCTTGG	ATTGGGCTCA	TACGTTGATA	1260
10	AAACAGTTTC	ACCATACATT	AGCATCCACC	CCGAAAGGAT	TCATAATCAA	TGCAGTGACT	1320
	ACAATTAGA	CTGCATGCCT	CCCATGGAT	ACATCCATGT	GCTGTCTTGT	ACAGAGAACA	1380
	TCACGTAGTT	TGAGAAAGCA	GTTCATAGAC	AGAAGATCTC	TGGAACATA	GATACACGAG	1440
	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
15	GCAAAATTGGC	AGGCATAGTG	GTGCCCAATG	ACGAAACCTG	TCATCTGAAA	AACAACGCTCT	1620
	AGTCAAAATC	GACAACCATG	GAACACCCCT	CACATAGGCA	ACTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAATGTCATC	TTTGCACTTC	AAGGAAACAA	ATTTCACTGG	TATAAGGATC	1740
	TTCTACCCCT	TTGCGCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAGGCTG	GCAACCTCA	1800
	ATAATTTGGT	AGTGAAGGCC	TATCAGAAGC	TCATTTTCAG	AGTGAAGTT	CAGGTGGAAA	1860
20	ACCAGGTAA	AGGCATCTAT	TTTAACTTA	CGCCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAACAG	1980
	TTACAATGAA	AAATGTGAT	GTCAAGGAG	GAAAAAACTA	TGCAATAATC	AAACCTATTC	2040
	GTTTTAAATGA	AACCGCTAAA	ATTCAATATC	ACAGAAACCTG	CAGCTGTGAC	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AACTTTTCTC	AGATTCCAAAG	TGTTTCCAGT	2160
25	GTGATGAGAA	AAATGTGAT	TTTGATGAAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAC	2220
	ACAAGGATCA	GCCTGTTTGC	AGTGGTGGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTTATGTC	2280
	ACAAAATTAA	GCTTGGAATA	GTGTATGGAA	AATACGTGTA	AAAGGATGAC	TTTTCTTGTG	2340
	CATATCACCA	TGGAATCTG	TGTGCTGGGC	ATGAGAGGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCTTTC	AGCAGCAGCC	CAGCACTGTG	2460
30	TCAATTCAAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAA	CTGGAATGTG	ATGCAATGCC	TTCCACCTCA	CAATTTGTCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
	CAGAAATGTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTT	CATCATTTTC	ATAGTTACAT	2760
35	TCTTGATGG	GTGCTTAAA	GTCCCTGATCA	TTAGACAGST	GATACTACAA	TGGAATAGTA	2820
	ATAAAATTAA	GTCTCATCA	GATTACAGAG	TGTCAGCCTC	AAAAAAGGAT	AAGTTGATTC	2880
	TGCAAGTGT	TTGCACAAGA	GCAGTCACCT	ACGAGCGTGA	GAAGCCTGAA	GAAATAAAAA	2940
	TGGATATCAG	CAAAATTAAAT	GCTCATGAAA	CTTTCAGGTG	CACTTCTTAA	AAAAAGATT	3000
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40	AAGTCACAGG	AGGAGACAAA	TTGCTCAOAG	TCATGCCAGT	TGCTGGTGTG	ACACTCGAAC	3120
	GAAGACTGAC	AGTATCCTC	ATCATGATGT	GACTCAGATA	GCTGCTGACT	TTTTTACAGA	3180
	AAAAATGCTC	TTACTACTGT	TTGAGACTAG	TGTCGTTGTA	GCATTTTACT	GTAATATATA	3240
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45	CACCTACAAG	GTACAGTAAT	CCCTGCACTG	GACATGTGAG	GAAAAAATA	ATCTGGCAAG	3420
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	AAAGATTATT	GCTTTTAAA	GTGTGTAGTT	TTATGATGTT	GTGTTTATGG	TTTGCTTATT	3600
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50	TTTTTACAG	ATAAGTTTAT	GTATGTCACA	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
	TACTGCCATA	AAAACTAAT	AATACAATGT	CACCTTATCA	GAATACTAGT	TTTAAAGCT	3780
	GAATGTTAA						

55	<u>A127 Protein sequence:</u>	
	Gene name:	Integrin, beta 8
	Unigene number:	Hs.52620
	Probeset Accession #:	AA479726
	Protein Accession #:	NP_002205.1
	Signal sequence:	1-39
60	Transmembrane domains:	682-704
	EGF domain:	552-584
	INB domain:	54-469
	Cellular Localization:	plasma membrane

65						
	1	11	21	31	41	51
70	MCQSALAFFT	AAFVCLQNDR	RGPASFLWAA	WVPSLVGLG	QGEDNRCASS	NAASCARCLA
	LGPECGWCVC	EDFISGGRS	ERCDIVSNLI	SKGCEVDSIE	YPSVEVLIPT	ENEINTQVTP
	GEVSIQLRPF	AEANFMLKVH	PLKKYPVDLY	YLVDSVSMH	NNIEKLSVSG	NDLSRRMAFP
	SRDFRLGFGS	YVDKTVSPYI	SIHPERIHNG	CSVDNLDGMP	PHGYIHVLSL	TENITEPEKA
	VHRQKISGNI	DTPEGGFDM	LQAAVCESHI	GWRKEAKRL	LVMTDQTSHL	ALDSKLAGIV
75	VPMNDGNCHL	MNVVVKSTTM	EHPSLGQLSE	KLIDNNINVI	PAVQKQFHW	YKDLLPLLP
	TIAGEIESKA	ANLNLVVEA	YQKLISSEVK	QVENQVQGIY	FNITAICPDG	SRKPGMBCGR
	NVTSNDEVLF	NVTVMKCCD	VTGGKNYAI	KPIGFNETAK	IHIHRNCSCQ	CEDNRGPKGK
	CVDETFLDSK	CFQCDENKCH	FDEDDQFSSES	CKSHKQPV	SGRGVVCVGR	CSCHKIKLKG
	VYQKYCEKDD	FSCPYHNGNL	CAGHGECEBAG	RQCPSGWEG	DRQCQPSAAA	QHCNVSKGQV
80	CSGRGTCVCG	RCECTDPRSI	GRPCEHCPTC	YTACKENMNC	MQCLHPHMLS	QAILDQCKTS
	CALMEQQHVV	DQTECEPSSP	SYLRIFFIIP	IVTFLIGLLK	VLIIHQVILQ	MNSNRIKSSS
	DYRVSAKSKD	KLILQSVCTR	AVTYRREKPE	EIKMDISKLN	ABETFRCNF	

A128 DNA SEQUENCE

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942
 Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5

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    CTGCGGTCGA GGATGGTTTT CTCTGTGTCAG CAGTGTGGCC ATGTGGCAG AACTGAAGAA 120
    GTTTTACTGA CGTTCAAGAT ATTCTTGTCT ATCATTGTCT TTCATGTCTG TCTGGTAACA 180
    TCCTGGGAAG AAGATACTGA TAATTCCAGT TTGTACCCAC CACCTGCTAA ATTATCTGTT 240
    GTCAGTTTTG CCCCTCTCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
    AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
15  GCTTCAGCGC TCAAAACCCA GAGAAATATC TGCAATTGT CATCTATTG CAATGACTCA 420
    GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCAGAAAT 480
    CAACATATAA CGAATGGCAC CTTAACTGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA 540
    GAGCTCAACA AAACCTTGCA AACCTTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
    GAGGCCCAAA GCACATTAAA TTGTACATT ACAATAAAAC TGAATAATAC AATGAATGCA 660
20  TGTGTGTCRA TAGCCGCTTT GGAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
    TCTGTGAGGA TACCTTGCCC TTCTTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
    CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCAAGTGGCC CACCATTTTC TTCCAGCCAA 840
    TCCATCCAGC TGTGTGCTCG GGCCACTGTG CTTTCCCAAG TCCCAGCAAG TACCTCTTTT 900
    GCTGAGCCTC CAGATTATTC ACCTGTGACC CACAAATGTT CCTCTCAAT AGGGGAGATT 960
25  CAACCCCTTT CACCCAGGCC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020
    CCACAGTCTG AAGCATCTCT TTCCCTTATG CCCCAGACCC ATGTCTCCGG CACCCACCTT 1080
    CCTGTGAAGC CCTCATTTTC CTCTCCCAAC GTGTCTGCCC CTGCGAATGT CAACTACTAC 1140
    AGGCACCTC CTGTCCAGAC AGACATGTCT AACACAGCA GTATTCTGA TCTTGAGAAC 1200
    CAAGTGTTC AGATGAGAAA GGCTCTGTCC TTGGGACAGC TGGAGCTTAA CCTGCGAGGA 1260
30  GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTTCCCGC CTGACATGCT GGCCCTCTG 1320
    GCTCAAGATG TGCTGAAAGT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAAACAGC 1380
    ACTATAGTCT TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
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    CAAGCTCTTG AGAACAGTAT TGGCACAATT ACTCTTCTCT CATCGCTGAT GAATAATTTA 1560
35  CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTCTTGA AACACCTGCT 1620
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    GTTGCAAAAC TGACCGTGAC GAACTTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
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    GGCAGAGGAG GCTGGTCAGA CAATGGCTGC TCTGTCAAAG ACAGAGATT GAATGAACCC 1860
40  ATCTGTACCT GTAGCCATCT AACAGCTTC GGCGTCTGTC TGGACCTATC TAGGACATCT 1920
    GTGCTGCTCG CTCAAATGAT GGCTCTGACG TTCATTACAT ATATTGGTTG TGGGCTTTCA 1980
    TCAATTTTTT TGTCAATGAC TCTTGTAAAC TACATAGCTT TTGAAAAGAT CCGGAGGGAT 2040
    TACCTTCCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCTGCTCTTC 2100
    TTCTGAGACT CGTGGATTGC TCTGTATAAG ATGCAAGGCC TCTGCATCTC AGTGGCTGTA 2160
45  TTCTCTCAT ATTCTTCTCT GGTCTCATT ACATGGATGG GCCTAGAAGC ATTCCATATG 2220
    TACCTGCCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATTTCTG 2280
    ATTGTCTGTT GGGGGGTACC AGCTGTGGTT GTGACCATCA TCCTGACTAT ATCCCCAGAT 2340
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    TCCACCACAC TGTAGTGAA TAATGATTGC TCAGTACACG CAAGCGGGAA TGGAAATGCT 2940
    TCTACAGAGA GGAATGGGGT CTCTTTTAGT GTTCAGATG GAGATGTGTG CCTTCACGAT 3000
    TTCACTGGAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCCGT 3060
    ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
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    GGGAACTGTG CTACACTGCT ATGTTGTGTA CATGTATGGA GCCTTGATTG CTCCTAGTTA 4380
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    TTATTAGGAA CATTTCAAAC CCCTTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGATATC 4500
    ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560

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CTGACTGTGC TTGCAATAT TTCTTTCTG ATTTATTAA TTTCTTGTA TTTATATGT 4620
 AAAATCAAAA ATGTTAAAA CAATGAAATA AATTGCACT TAAGA

A129 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MVFSVRQCGH VGRTEEVLLT FKIPVLVLC HVVLVTSLEE DTDNSSLSP PAKLSVVSFA 60
 PSSNEVETTS LNDVTLSELL SNTEKTKIT IVKTFNAGV KPQRNICNLS SICNDSAPFR 120
 GEIMFYDIB STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYP IMCATAEAQS 180
 TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCCCSVRI PCPSSPBEEL KLQCDLQDPI 240
 VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSFAPPP DYSFVTHNPV SPIGBIQPLS 300
 PQPSAPIASS PAIDMPPQSE TISSFMPQTH VSGTPPPVKA SPSSPTVSAP ANVNTTSAPP 360
 VQTDIVNTSS ISDLNQVLQ MEKALSLGSL EPNLAGEMIN QVSRLHSP DMLAPLAQRL 420
 LKVVDDIGL LNFSTTISL TSPSLALAVI RVNASSPNTT TFVAQDPANL QVSLETQAPE 480
 NSIGTITLPS SLMMNLPAHD MELASRVQFN PFETPALFQD PSLENLSLIS YVSSSVANL 540
 TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNGGRRG WSDNGCSVKD RRLNETICTC 600
 SHLTSPGVLL DLSRTSVLPA QMMALTFITY IGCGLSSIFL SVTLVITYIAF BKIRRDYPSK 660
 ILIQLCAALL LNLVFLDLS WIALYKMQGL CISVAVFLHY FLLVSPVWNG LBAPHYMLAL 720
 LKVFNTYIRK YILKPCIVGW GVPVAVVTII LTISPQNYGL GSYGKFPNGS PDDPCWINNN 780
 AVFYITVVG FCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840
 ITWGFAPFPA GPNVNTFMYL FAIPNTLQGF FIFIPYCVAK ENVRKQWRRY LCCGKLRLAE 900
 NSDWSKATIN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNNGMASTER 960
 NGVSFVSQNG DVCLHDFTGK QHMFNEKEDS CNGKGRMALR RTSKRGLSLF IBQM

A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 ProbeSet Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GTGGCGGCAA CCGGCACCTC AGTCCCGGCC GCGCTTCTCC TCGCCGCCCA CGCCGTGGGG 60
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 CGCCCGCGCC GCCACGCCCC GTAGCAGTCC GGTGCTGCTC TCCGCCCCCG TCCGGCTCGT 180
 GCGCCCGCTAC TTGGGGCACC ATGGACACCT CCGGCTCGG TGTGCTCTGT TCCTTGCTGT 240
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GAGACCTGGA GAATATTGG GACTGCTCTA TGGTAAAAACA CATTGCCCTG TTGCTCTTCA 2520
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 AGAGCTGCCA TCTTCTCTCT GTGGCAATTG TCCATGTCT CTAATTAATA TGTGAAGGAA 2940
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 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

A131 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80

MDTSRLGLVLL SLFVLLQLAT GSSSPRSGLV LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LSLSMNNISQ LLFNPPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
 LQNNQLREVP TEALQNLRLSL QSLRLDANHI SYVPPSCFSG LHSRLRLMLD DNALTEIPVQ 180
 AFRSLSLAQ MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLETLD 240
 LNYNNLDEFP TAIRTLNLK ELGFHNNIR SIPEKAFVGN PSLITIHFDY NPIQFVGRSA 300
 FQHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDSL 360
 YNLLLEDLPF SVCCQLQKID LRHNEIYBIK VDTFQQLLSL RSLNLAWNKI AIHPNAPST 420
 LPSLIKLDLS SNLLSFPFIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480
 AFGVCENAYK ISNQNKNGDN SSMDDLHKKD AGMFQAQDER DLEDFLDPE EDLKLHLSVQ 540
 CSPSPGPFKP CEHLLDGWL I RIGVWTIAVL ALTGNALVTS TVFRSPLYIS PIKLLIGVIA 600
 AVNMLTVGSS AVLAGVDAPT FGSFARHGAW WENGVGCHVI GFSLIFASES SVFLTLAAL 660
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEF 720
 STMGMVALI LLNSLCPLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLPTNCILNC 780
 VFAFLSPSSL INLTPISPEV IKFILLVVP LPACLNPLLY ILFNPFPKED LVSLRKQTYV 840
 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
 VAFVPCFL

A132 DNA SEQUENCE

Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Probeset Accession #: U25128
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

50
55
60
65
70
75
80

1 11 21 31 41 51
 GGCGGTGGC CCAGGCCCGA CCACCCAGC TCGCGGTGTT TACTGGCCAC AAGTTTGCTC 60
 TGGGCCAGCC AAGTTGGCAA CTGTGAAGCT TCTCCCGGC TCTGGAGGAG GGTCCCTGCT 120
 TCTTCTTACA GCGTTCCGG GCATGGCCGG GCTGGGGGCG TCGCTCCAGC TCTGGGGTTG 180
 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCAGAGCT GATTCTGATG GCACCATTAC 240
 TATAGAGGAG CAGATTGTCC TTGTGCTGAA AGCGAAAGTA CAATGTGAAC TCAACATCAC 300
 AGCTCAACTC CAGGAGGGAG AAGGTAATTG TTTCCCTGAA TGGGATGGAC TCATTGTGTT 360
 GCCCAGAGGA ACAGTGGGGA AAATATCGGC TGTTCCATGC CCTCCTTATA TTTATGACTT 420
 CAACCATAAA GGAATTGCTT TCCGACACTG TAAACCCAAAT GGAACATGGG ATTTTATGCA 480
 CAGCTTAAT AAACATGGG CCAATTATTC AGACTGCCTT CGCTTTCTGC AGCCAGATAT 540
 CAGCATAGGA AAGCAAGAAT TCTTTGAACG CCTCTATGTA ATGTATACCG TTGGCTACTC 600
 CATCTCTTTT GGTCTCTTGG CTGTGGCTAT TCTCATCATT GGTACTTCA GACGATTGCA 660
 TTGCACTAGG AACTATATCC ACATGCACTT ATTTGTGTCT TTCATGCTGA GAGCTACAAG 720
 CATCTTTGTC AAAGACAGAG TAGTCCATGC TCACATAGGA GTAAAGGAGC TGGAGTCCCT 780
 AATAATGACG GATGACCCAC AAAATTCCAT TGAGGCAACT TCTGTGGACA AATCAATA 840
 TATCGGGTGC AAGATTGCTG TTGTGATGTT TATTTACTTC CTGGCTACAA ATTATTATTG 900
 GATCCTGGTG GAAGGTCTCT ACCTGCATAA TCTCATCTTT GTGGCTTTCT TTTCGACAC 960
 CAAATACCTG TGGGGCTTCA TCTGTATAGG CTGGGGGTTT CCAGCAGCAT TTGTGTCAGC 1020
 ATGGGCTGTG GCACGAGCAA CTCTGGCTGA TGCAGAGTGC TGGGAACCTA GTGCTGGAGA 1080
 CATCAAGTGG ATTTATCAAG CACCGATCTT AGCAGCTATT GGGCTGAATT TTATCTGTGT 1140
 TCTGAATACG GTTAGAGTTC TAGCTACCAA AATCTGGGAG ACCAATGCAG TTGGGCTATG 1200
 CACAAGGAG CAATACAGGA AACTGGCCAA ATCGACACTG GTCCCTGGTCC TAGTCTTTGG 1260
 AGTGCAATTAC ATCGTGTTCG TATGCCTGCC TCACCTCTTC ACTGGGCTCG GGTGGGAGAT 1320
 CGCCTGACG TGTGAGCTCT TCTTCAACTC CTTTCAAGGT TTCTTTGTGT CTATCATCTA 1380
 CTGCTACTGC AATGGAGAGG TTCAGGCAGA GGTGAAGAAG ATGTGGAGTC GGTGGAATCT 1440
 CTCCTTGGAC TGGAAAAGGA CACCGCCATG TGGCAGCCCG AGATGCGGCT CAGTGCTCAC 1500
 CACCGTAGCG CACAGCACCA GCAGCCAGTC ACAGGTGGCG GCCAGCACAC GCATGGTGTG 1560
 TATCTCTGCG AAGCTGCCA AGATCGCCAG CAGACAGCCT GACAGCCACA TCACCTTACC 1620
 TGGCTATGTC TGTGAGTAACT CAGAGCAGGA CTGCCTGCCA CACTCTTTCC ACGAGGAGAC 1680
 CAAGGAAGAT AGTGGGAGGC AGGAGATGA TATTCTAATG GAGAAGCCTT CCAGGCCTAT 1740
 GGAATCTAAC CCAGACACTG AAGGATGCCA AGGAGAACT GAGGATGTTT TCTGAATGGA 1800
 CATTGTGTC TACTTTTCAT GGGCTGGTCC AATGGCTGGT TGTGTGAGAG GGCTTGGCTG 1860
 ATACTCCTAT GCTTGAGTTC AAAGGCTGAA AATTCAGTTA AGGTGTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCTGTAAA TACTAACGAC ATGAAAATGC AAGTGTCAAT 1980

5 GGAGTAGTTT ATTACCTTCT ATTGGCATCA AGTTTTCCTC TAAATTAATG TATGGTATTT 2040
 GCTCTGTGAT TGTTCAATTT TTTCTGTACT TTTTGGGTAG AAAAAGATT CAATTGCTTG 2100
 GCTGTAGCTT TCTCTCATAT ATATCACCCT AAATATAATG AAGATCTTTT AGTGTGTATC 2160
 ATTTTCTTTT TAGAACTAG TATTCTCTTA TTTCTTACTT TAATGTACTT CTATCACTGC 2220
 ATTTATTTTG CCTGTGCATA GGAGCAATTA GGATCTAAAA AAATATATGG GAAGATAAAA 2280
 GATCTAAGAA CAAGTACTTG CTGGAAAATT AGTTGGCTGG ACATTGATAA AATAATGCAT 2340
 TTATAACAAT TACATGTGTT TTTGGGAACA AGGAAAATTT CTCAAAAAG AATATTTTAC 2400
 ACATCCCTTC TTTTGAATGG CCTCTTTTGG ACCAGCCAGA CCTCAGGTCT TCACTCTTTC 2460
 TCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCTCTAGTT AGTGAGCTTG TGTCTGCAAA 2520
 TTGATTTTGT TTGTAATGTA TTTTGATAGC AAATCATGCT GCATCTATAT CTTTTCCTTG 2580
 TTTGAGCTGT TACTACATTG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640
 T

15 A133 PROTEIN SEQUENCE

Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Protein Accession #: NP_005039.1
 Signal sequence: 1-25
 Pfam domain: 7tm_2 [141-420]
 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 MAGLGASLHV WGWMLGSLCL LARAQLDSDG TITIEQIVL VLKAKVQCEL NITAOQLQEGE 60
 GNCPEPMDGL ICMFPGTGVK ISAVPCPPYI YDFMHKGVAF RHCNPNGTWD FMHSLNKTWA 120
 NYSDCLRFQ PDISIGKQEF FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180
 30 MHLFVSFMLR ATSIFVKDRV VHAHIGVKEL ESLIMQDDPQ NSIEATSDVK SQYIGCKIAV 240
 VMFIYFLATN YWILVEGLY LHNLIPIVAF SDTKYLWGFPI LIGWGFPAAP VAAWAVARAT 300
 LADARCWELS AGDIKIYQA PILAAIGLNF ILFLNTVRVL ATKIWETNAV GHDTRKQYRK 360
 LAKSTLVLVL VFGVHYIVFV CLPHSPTGLG WEIRMHCELF FNSPQGFVVS ILYCYCNGEV 420
 QAÉVKHWSR WNLSDVKRRT PPGSRRRCGS VLTIVTHSTS SQSQVAASR MVLISGKAAK 480
 35 IASRQPDSEI TLEGVVWSNS EQDCLPHSPH RETKEDSGRQ GDDILMERPS RPNESNPDE 540
 GCGGETEDVL

A134 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251.
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 ATGCTGTCTG CTTCTTGTAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCAGC 120
 GACCCGAGAGA GGGAGAGCCG GCCGAGGGCT CCGCGGCTCC TGTGGGACCG CGCTGCAGCC 180
 50 GGGAGAGCGG AGAAGGGGAA CCGGGGCGAG CCGCCGCGCT GGATCCGCGC CCAGCAGCAG 240
 CGCGCGCGCG CGCCAGCTGC GCAGGCTCCC GGGAGTCCGG CTGGGGGCGC GCAGGACCTC 300
 CGCTCGGTCT CTGGAGCTTC CCGGGGAGG GTCCGGTTGC CAGTGAACCC TCCAGAGCCT 360
 TCCGAGACGAC AGCCCGCGGG GCCTTCTGAC TGATATCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 55 GCTCTGAGAC CTAGGGCCCG GGTCTGTGCG CTCTGCGGCA TCGCGGAGTA GGGGAGTGGC 540
 CGCGCGGAAA AGCGCGCGCG GACAGTCAGT GAOCAGGCCG GGGGGTCCGC GGGGCCACGA 600
 CTTCTCGGAG ACCGTCTGCG GCTCTCTGGA GAOCGCTGT CCGGCCACG GGTGGTGCCA 660
 TGTGGGGCGC TCGCCGCTCG TCCGTCTCCT CATCTGGA GCGCGCTTG CTCTGTCAGC 720
 TGCTGTGCGC TCGCTGCTG GCGCGCGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGCG 780
 TGGCTGAGCG CTGAGGGCGT CTGGCGCATC GGTTCAGT GTCCGAGCG CTTGACGCGC 840
 60 GGGGAGGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTGAG ACCAGGGCGG CTGCGACAAT GAOCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGCC CCGACGCTC GGCAGGGCT CATGTCTTAG GGGTACCCAA 1020
 GGAGAAGCGG AGGGTGCGCC CCCACCGTGG AGGGCCTGGC AGCGGTGCTC CCCTGAAGGC 1080
 65 TCCCGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGGC TGCTGCCCGG TGCCAGACGC 1140
 CGCGGATTCC CATCTCTCC ACGCGCGGCG CCCTCTCCCG TGCAGCGGCC CGCCTTGCCC 1200
 ATCTACGTGC CGTTCTCTCAT TGTGGCTCC GTGTTGTGCG CTTTATCAT CTTGGGGTCC 1260
 CTGGTGGCAG CCTGTGCTG CAGATGTCTC GGGCCTAAGC AGGATCCCCA GCAGAGCGA 1320
 GCGCCAGGGG GTAAACGCTT GATGGAGACC ATCCCATGA TCCCGAGTGC CAGCACTCC 1380
 70 CGGGGCTGCT CCTCACGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440
 GGGGCCCGGG CGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCGGGA AGGGACCATG 1500
 AACAAAGTGT ATGTCAACAT GCCACGAAAT TTCTCTGTGC TGAACCTGCA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCCAT ACGTGGGTA CACGGTGCAG 1620
 CAGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATG ACGGCTGCA GCCTGGCTAC 1680
 75 AGGCAGATG AGTCCCTCT CCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGTG 1740
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTCT GTGGTATTTA TGGCACGATT CCTTTGGATG 1860
 GCTTCATTGG CCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTC GATATGTTT 1920
 CATCCAGGTT ATCATTTGAT TATGATGGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 80 TTGCTAGAGT GTGTATAACA AATGCTTGAG TCCGAAAGTC CCTTGAGATA TGGTTGACGA 2040
 AAGAAATTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTATTAT TATTTCTTTT 2100
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC CTTTACTGCG GACTTTTTTT 2160
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGGATG TCGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCTGCTCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTATTTT 2340

5 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCTCTGA CCTCAAGCAA 2400
 TCTGCTCTTC TCAGCCTCCC AAGTGTCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTCTAAAAG GAACCTCTGT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 GGCACACCTT AATTTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
 GGGCCTAITT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TTA AAAAGAG ACTGAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCATT CATCCCTTC 2820
 10 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880
 TATATTGAAA TCATAAACTA TCACCCGCTG CTCTCTGAG TTAATTTTAA TTTTGCCTTG 2940
 TGGTTATGTT TGGCGTTTC CTCTGTGTTG GTTTTCAGAG CCCATGTCT ATATAGTCTC 3000
 GAGTGCAAGT AATTACTATA CTGTGTAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
 AAAAAATTTT TGTCTTAGT TATAAAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTT 3180
 15 GCAGATCTA AGGCTTTTAT TACTCTTGT ATCAAAATGG CTTATTTTC AGGCACTAAG 3240
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCTTT CTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
 CAAATTCAG TGAATTTAT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAG 3420
 20 ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAAATCGT 3480
 GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATTC 3540
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTAAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
 TGA AAAAAA AAAAAA AAAAAA

25 A135 Protein sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 30 Transmembrane domains: 402-424
 Cellular Localization: not determined

35 1 11 21 31 41 51
 MLSGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEKGNRGE PPAWIRAQQQ PRPPFAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA 120
 SGRQPRGSPD CIPRFPASASA THKAVPKGTG PPAEDGGDLG APGPARRRRR LLGVAAEGSG 180
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAAPRVVP CGALAAPRSP HPGTPIRSCS 240
 40 COWLRWRRRG RGPSSGEVCHG WLDAGGVKRI GPQCPERFDG GDATCCGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQQAGGEPG RADKDGPRRL GRASCLRGTD GDGEGAPPPV RAWQRCSPFG 360
 SPKGRLQRA PPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420
 LVAACCCRL RPKQDPQQR APGGNRLMET IPMIPSASTS RGSRRSQST AASSSSSANS 480
 45 GARAPPTRSQ TNCLPEGTM NNVYVNMPTN FSVLNCQQA QIVPHQGYL HPPYVGYTVQ 540
 HDSVPMTAVP PFMGLQPGY RQIQSPFPH T NSEQNMPAV TV

A136 DNA SEQUENCE
 Gene name: selectin E (endothelial adhesion molecule 1)
 50 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGG 60
 GCTGGTCTT ACACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAAGT ACACACACCT GGTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
 TCCATATTGA GCTATTAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
 60 TGGTCTGGG TAGGAACCA GAAACCTCTG ACAGAAGAG CCAAGAACTG GGCTCCAGGT 300
 GAACCCAAAC ATAGGCAAAA AGATGAGGAC TGGTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 TACACTTGA AGTGTGACCC TGGCTTCAGT GGAATCAAGT GTGAGCAAA TGTGAATCTG 540
 65 ACAGCCCTGG AATCCCTGGA GCATGGAAGC CTGCTTGAAG GTCAACCACT GGGAAACTTC 600
 AGCTACAAAT CTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGGA 780
 70 AGCTTCCCAT GGAACACAAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840
 GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CCTGCTGGAG AGTTCACTT CAAATCATCC TGCAACTTCA CTTGTGAGGA AGGCTTCATG 1020
 TTGACGGGAC CAGCCCAAGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAAAATCCCA 1080
 75 GTTGTGAGG GATTTCAGT CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCCTAGTG CTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200
 GGTTTTGTGT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
 GAGAAAGCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTCAATCCCC TATTGGAGAA TTCACTTACA AGTCTCTTG TGCCTTCAGC 1380
 80 TGTGAGGAGG GATTGTGAAT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGA 1500
 AAGATCAACA TAGCTGACAT TGGGGAGCCC GTGTTTGGA CTGTGTGCAA GTTCGCTGT 1560
 CCTGAAGATG GGAACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 CTTCCTGCTG CTGACTCTC CTCTCTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740

TGCTTAACGA AAGCAAAGAA ATTGTTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5 **A137 Protein sequence:**
Gene name: Selectin B (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
10 Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | | |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRTHLVAI QNKEBIEYLN 60
SILSYSPSY WIGIRKVN NVWVGTQKPL TBEAKNMAPG EPNNRQKDED CVEIYIKREK 120
20 DVGMNDERC SKKKLALCYT AACTNTSCSG HGECVETINN YTKCDPQFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
ECDAVINPAN GFVECFQNPQ SPPWNTICTF DCEBGFELMG AQSLLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSSHS PAGEFTFKSS CNFTCEEFGM LQGPAAVECT TQGWTTQIIP 360
VCEAPQCTAL SNPERGYMNC LPSASGSPRY GSSCBPSCFQ GFVLKGSKRL QCGPTGENDN 420
25 EKPTCEAVRC DAVHQPFGGL VRCASHPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
WTEVPSQCV VKCSSLAVPG KINMSCSGEP VEGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
SGLLPCEAP TESNIPLVAG LSAAGLSLLT LAPFLNLWRK CLRKAKKVPV ASSCQSLESD 600
GSYQKPSYIL

30 **A138 DNA SEQUENCE:**
Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 (H.sapiens)
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
35 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
| | | | | |
GGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTCGTACAG TTTCTTCCAA CCTTGCCATT 120
GCATATAAAA AGGAAAAGAG GCCTCTCTAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
45 ATGGTTATTG ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATTT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAAT CAAATTTTAT 600
GAAGAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
TCTGAAAAA AAAAAA AAAA

55 **A139 Protein sequence:**
Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 (H.sapiens)
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
60 Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

65 1 11 21 31 41 51
| | | | | |
MMLHSALGLC LLLVTSSNL AIAIKKEKRP PQTLRSGWGD DITWVQTYEE GLFYAKSKK 60
PIMVIHLED CQYSQALKKV FAQNEEIQEM AQNKPFIMNL MHETTDNLS PDGQYVPRIM 120
70 FVDPSELTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A140 DNA SEQUENCE
Gene name: TMPRSS3a
Unigene number: Hs.298241
Probeset Accession #: AIS38613
75 Nucleic Acid Accession #: AB038157
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
| | | | | |
ACCGGGCACC GGACGGCTCG GGTACTTTG TTTCTAATTA GGTCAATGCC GTGTGAGCCA 60
GGAAAGGCT GTGTTTATGG GAAGCCAGTA ACACGTGGC CTACTATCTC TTCCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGATGTC 180
AGAGGTCTGT AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240

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TCATTCGGAT CGCTTTTGG CCTTGATGAT TTGAAATAA GTCCCTGTTC ACCAGATGCA 300
GATGCTGTTC CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCQACTGC 420
TCAGGGAAGT ACAGATGTG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
AATGCGGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
AAGGGTCACT ACGCAAATGT TGCCCTGTGC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
CACTCTTTCG CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
TGTGCTCTCG GCCACGTGGT TACCTTGCG TGACACAGCT GTGGTATAG AAGGGGCTAC 840
AGCTCAGCA TGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCAAGCCCTC GTGGATCATC 960
ACTGCTGCAC ACTGTGTTTA TGACTTTGAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
CTAGTTTCCG TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
CTACAGTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTCCCC 1200
GATGGAAGA TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
TCCCTGTGCC TGAACACGC GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCAACAGG 1320
GACGTGTAGC GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGCTACCT GACGGGTGGC 1380
GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCGCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACCA CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620
TCCTCCCTCC GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTGG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CGGAAGAGG CACCCCTCCA TCTGATTOCA GCACAACCTT 1740
CAAGCTGCTT TTGTTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
TTGCTCTCAG TTCCCAAGTA GCTGGGACCA CAGGTGCCCG CCAACACACC CAACTAATTT 1920
TTGTAATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
CCTCAATATG TGTGCTGCTG TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
ACGCTAGTCC TACGCTCCTT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAAGCC AGAAGTGACG AACTGCAGTC ACTGCAAGTT TTCATCTCTA GGGACCAAG 2280
CCAAACCCAC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTCGTT TAAGGCTTAT TTTCATGATT TCCTTGTAGC ATTTGGTGCT TGACGTATTA 2400
TTGCTCTTGG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
AAAAAAA

A141 Protein sequence:

Gene name: TMPRSS3a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Protein Accession #: BAB20077
Signal sequence: none found
Transmembrane domains: 43-65, 239-261
Tryp_SPC domain: 216-444
Cellular Localization: plasma membrane

1 11 21 31 41 51
MGENDPPAVE APFSFRSLFG LDDLKISPIA PDADAVAAQI LSLPLKFPF IIVIGIILI 60
LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDDCK GEDEYRCVRV GGQNAVLPV 120
TAASWKTMS DWDKHYANV ACAQLGFPSY VSSDNLKRVSS LEGQFREEFV SIDHLLPDDK 180
VTALHHSVYV REGCASGHV TLOCTACGHR RGYSSRIVGG NMSLLSQWFW QASLPQGYH 240
LCGGSVITPL WIITAHCYV DLYLPKSWTI QVGLVSLDNL PAPSHLVEKI VYHSKYKPKR 300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGVKVCWT SGNGATEDGA GDASPVNLHA 360
AVPLISNLIK NHRDVYGGII SPMLCAGYL TGGVDSQCGD SGGPLVCQER RLWLKLVGATS 420
FGIGCAVSNK PGVYTRVTSF LDWIEQMER DLKT

A142 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
Unigene number: Hs.105484
Probeset Accession #: AA314779
Nucleic Acid Accession #: none found
Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

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75
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1 11 21 31 41 51
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
CTGAGATCCT TGCACATGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
CGGCTGCTCC TATTGCTGAG CTGCTGGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
AGACCCAGCT GTGCTCCTGG ATGGTTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
AAGCTGAGGA ACTGGTCTGA TGCAGAGCTC GAGTGTCACT CTTACGGAAA CGGAGCCAC 300
CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
CAGAGGAAGC AGCGGATATG GATTGGCCTG CACGACCCAC AGAAGAGGCA GCAGTGGCAG 420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGCTCTG GCAAGTCCAT GGGTGGGAAC 480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540
AACAGCGCC AACACTTCCT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
AACTCTGCA CCAGCCCGCT CCTCTTCTT TCTGCTAGCC TGGCTAAACT TGCTCATTTAT 660
TTAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720

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GGCTTAGAGA CAGAACTTT AGCATTGGGC CCAGTAGTGG CTCTAGCTC TAAATGTTTG 780
 CCCC GCCATC CCTTTCCACA GTATCCTTCT TCCCTCCTCC CCTGTCTCTG GCTGTCTCGA 840
 GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
 AAAGATTGA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
 ACACCCCTCT GCCTCTCTC CATTCGCTGC ACCCAACCCC AGCCACTCAA CTCCTGCTTG 1020
 TTTTCTCTTT GGCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCCA 1080
 TACATTCTTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

A143 Protein sequence:
 Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

1 11 21 31 41 51
 MASRSMLLL LLCLAKTGV LGDIIMRPSC APGWFYHKSX CYGYFRKLKN WSDABLECQS 60
 YNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQWQWIDG AMYLRSWSG 120
 KSMGGKHKCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP

A144 DNA SEQUENCE
 Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

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1 11 21 31 41 51
 GCGGAACACC GCGCCGCCGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCGATGGGGC 60
 TCCCTCGTGG ACCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
 CCTCCGAGCC GTGCGCGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
 CGGAGCAGGA GCGCGGCCAG GCGCTGGGGA AAGTATTGAT GGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAT GGCAAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCGGCGG GCAGACAGCC CCCCTGAGGG TGCTTTCGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTC AAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
 TCATCGTGAG CGACCAAGAT GACCAACAAG CCAAGTTTAC CCAGGACACC TTCCGAGGGC 720
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGACAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGCCT GGACCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGCTCCACCC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 ACAATGTCTC CATGTTTGAC CCCCAGAAAT ACGAGGCCCA TGTGCTGAG AATGCACTGG 1080
 GCCATGAGGT CGCAGGGCTG ACGTCACTG ATCTGGAGCG CCCCACCTCA CCGAGTGGCG 1140
 GTGCCACCTA CCTTATCATG GCGGGTGAAG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGAATTTGAG GCCAAAAACC 1260
 AGCACACCTC GTAAGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCGCAACCT 1320
 CCACAGCCAC CATAGTGCTC CAGCTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAGA CCTGACAAG GAGAATCAAA AGATCAGCTA CGCATCTCTG AGAGACCCAG 1500
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGAAC 1620
 ATGGAAGCCC TCCCACTACT GGCACGGGAA CCCCTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
 ACGTGTGAA CATCACGGAC AAGACCTGT CTCCCCACAC CTCCCTTTC CAGGCCACGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTTT TCTGTCTCTG 1920
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGGCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGAAAC CTGCTCTGGA CCTGGGAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTCTCTC CTGCTGGTGC TGCTTTTGTT GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCTACTC CCAGAAAGAT ACACCCGTGA CAACGTCTTC TACTATGGGG 2160
 AAGAGGGGGG TGGCGAAGAG ATGACATCAC CCAGGCTCCAC CGAGGCTCTG 2220
 AGGCAGGCCC GAGAGTGTTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AATCGGCCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCGGC CCTACGACAC CCTCTTGGTG TTAGACTATG 2400
 AGGGCAGGCG CTCGACGCCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGGCG GAGGAGCAGC TAGGCGGCTT GCCTGACAGG CTGGGAGACA AACGTGAGGC 2580
 CACAGAGATC CTCCAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGCCC GTAGCAACTT GCGGAGACA GGCATATGAG CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
 CACCTGGGCG AGGTTTGCTG CAGAGGCCAA GTTTCAGAAA GCCTCTTACC TGCGTAATAA 2820
 TGCTCAACCC TGTGTCCTGG GCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCTCTCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940

TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGCG CCACTGGCCG 3000
 TCCTGCATT CTGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGTG TGCTAGGTT GCCCCTTATT TTTTATTTTC CTTGTTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAAATCGTG TATATGTACT AGAATCTTTT TATTAAAGAA A

A145 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51
 MGLPRGPLAS LLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DDPVVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDMV VAPISVPENG 120
 KGPPFQRLNQ LKSNKDRDRTK IFYSITGPGA DSPPEGVPAV EKETGWLLLN KPLDREEIAK 180
 YELFGHAFSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSGTT TAVAVVEILD ANDNAPMFDQ QKYEAHVPEN AVGHEVQRLT VTDLDAPNPS 360
 AMRATYLIWG GDDGDHFTIT THPESNQIL TTRKGLDPEA KNQHTLVVEV TNEAPFVLKL 420
 FTSTATIVH VEDVNEAPV VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLAMP DSGQVTAAGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLLID 540
 VNDHGVPPEP RQITICNQSP VRHVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGPFILPVL 660
 GAVLALLFL LVLLLVVRKK RKIKEPLLLP EDDTRDNVVF YGHEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTII PFMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN ENGSRFKKLA DMYGGGEDD

A146 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGAATTCCTT TTTTCTTTT TTTGAGATGG AGTTTCACTC TTGTTGCCA GGCTGGAGTG 60
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CGCCTCCCGG GGTTCAGCGG ATCTCCTGTC 120
 CTCAGCCTCT CAAGTACGCTG GGATTACAGG CATGTGCCAC CACCCTCGGC TAACTAATT 180
 CTTTCTTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
 ACCTCAGGTG ATCCACTTGC CTGGCCTCC CAAAGTGCTA GGATTACAGC CGTGAACCTG 300
 TGCCCTGGCTG ATTCTTTT TGTGTTTGA TTTTGAAC AGGGTCTCCC TTGGTCGCC 360
 AGGCTGGAGT GCACTGGTGC GATCTTGGCT CACTATAACC TCCACCTCCT GGTTCAGAGT 420
 GATCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GCGTGACCA CCACACCGCG 480
 CTAATTTTGG TATTTTATT AGAGACAGGG TTTACCATG TTGGCCAGCG TGTCTCTCAA 540
 CTCTCGACT CAAGGGATCC GCCTGCCCTC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG 600
 AGTCACCATG CCGGACCTTA TAATCTTAA GTCAATTTT TCGTCCATT TCTCTCTTAG 660
 GGTCTCTACA ACAATCTGC ATTAGCGGT ACAATAATCC TTAACCTCAT GATTACACAA 720
 AGGAAGATGA AGTGATTAT GATTTAGAAA GGGGAAGTAG TAAGCCCAT GCACACTCCT 780
 GGATGATGAT CCTAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAA 840
 TTGTTTAA ATTAATTATC TAAATATCTA AAAACATTT TGGATACATT GTTGATGTGA 900
 ATGTAAGAT GTACAGACTT CCTAGAAAAC AGTTTGGGT CCATCTTTTC ATTTCCCGAG 960
 TGCACTTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATGTATT 1020
 CCATAATGAA CAAAGTGAGA GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080
 AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAAC GTTAACCAA 1140
 TTATGATGAT GGCAACAAC CCAGAGGACT GGTGTAGTTT GTTGCTCAA CTAGAGAAAA 1200
 ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCGTAC AGTCAAGCAA 1260
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA 1320
 GATTTGCTGA ATTAAGAGCT ATTCAAGAGC CAGATGATGC ACGTACTAC TTTCAAATGG 1380
 CCAGAGCAA CTGCAAGAAA TTTGCTTTT TTTATATATC TTTTGACAA TTTGAACCTG 1440
 CACAAGGTAA TGTCAAAAAA AGTAACAAAC TTCTTCAAAA AGCTGTAGAA CGTGGAGCAG 1500
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 TTTCAAGAGA GGAAGAAGAG AATTTATCAG CATCTACGGT ATTAACCTGC CAAGAATCAT 1620
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 AAACCAAGTG AAATGATTCC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980
 TCAAGGAACC TCTGGTGTCA GATGAAAAGA GTTCTGAAC TATTATTACT GATTCAATAA 2040
 CCTGAAGAA TAAACGGAA TCAAGTCTTC TAGCTAAATT AGAAGAACT AAGAGATGAT 2100
 AAGAACCAGA GGTTCACAG AGTAACAGA AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160
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 AAGTTAATAC AAGACAGAAA CATACCATT TTGAGCAACC TGTCTTTTCA GTTTCAAAAC 2280
 AGTCACCACC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGTT AAGACACCAA 2340

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GCAGCAATAC CTGGATGAT TACATGAGCT GTTTAGAAC TCCAGTTGTA AAGAATGACT 2400
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AGCATCAAACT ACTTGCCACT CCACITCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520
ATGAATGCAT TCGGTTAAAG GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG 2580
GTTCAAGCAA GGTATTTTCAG GTGTTAAATG AAAAGAAACA GATATATGCT ATAAAATATG 2640
TGAACCTTAGA AGAAGCAGAT AACCAAACCT TTGATAGTTA COGGAACGAA ATAGCTTATT 2700
TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG 2760
ACCAATACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2820
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TTCACACAAT CCATCAACAT GGCATTGTCT ACAGTGATCT TAAACCAAGT AACTTTCTGA 2940
TAGTTGATGG AATGCTAAAG CTAATTGATT TTGGGATTGC AAACCAAATG CAACCCAGATA 3000
CAACAAGTGT TGTAAAGAT TCTCAGGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060
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GTGATGTTTG TCTGATTGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCAATTC 3180
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AATTTCCCGA AATTCCAGAG AAAGATCTTC AAGATGTGTT AAAGTGTGTT TTAAGAAAGG 3300
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CTCATCCAGT TAACCAAATG GCCAAGGGAA CCACTGAAGA AATGAAATAT GTTCTGGGCC 3420
ACCTTGTTGG TCTGATTCTC CCTAATCTCA TTTTGAAAGC TGCTAAACTT TTATATGAAC 3480
ACTATAGTGG TGGTGAAGT CATAATCTT CATCTCCAA GACTTTTGAA AAAAAAGGG 3540
GAAAAAATG ATTTCAGTT ATTCTGTAAT TCAGATAGGA GGTATAAAAT ATATTGGACT 3600
GTTATACTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660
ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAAA TAGCAACCAC 3720
TTATGGCACT GTATATATTG TAGACTTGTG TTCTCTGTTT TATGCTCTTG TGTAACTAC 3780
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTTG 3840
TAAATAAAGT TTTGTGGCTA AAATGA

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30 A147 Protein sequence:
 Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86599
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

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1 11 21 31 41 51
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MNKVRDIKKN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS 60
VPLSDALLANK LIGRYSQAIK ALPPDKYQGN ESPARIQVRP AELKAIQEPD DARDYFQMAR 120
ANCKKFAFVH ISFAQFELSQ GNVKRSKQLL QKAVERGAVP LEMLEIALRN LNLQKQQLLS 180
REBKKNLSAS TVLTAQESFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR 240
NSLRQTNKTK QSCPFGRVPV NLLNSPDCDV KTDSDVVPFC MKRQTSRSEC RDLVVPGSKP 300
SGNDSCELRN LKSVQNSHPK RPLVSDKSS ELIITDSITL KNTKSSLLA KLEETKEYQE 360
PEVPESNQKQ WQAKRKSECI NQNPAAASNH WQIPELARKV NTEQKHITFE QVPFVSQKQS 420
PPISTSKWFD PKSIKCTPSS NTLDDYMSCF RTPVVKNDFF PACQLSTPYG QPACFQQQOH 480
QILATPLQNL QVLASSANE CISVKGRYS ILKQIGSGGS SKVFQVLNEK KQIYALKYVN 540
LEBADNQTLN SYRNEIAYLN KLQHSKDKII RLYDYEITDQ YIYMVMECGN IDLNSWLKKK 600
KSIDPWERKS YKWNLEAVH TIHQHGIHVS DLKPANFLIV DGMKLIDFG IANQMOPDTT 660
SVVKDSQVGT VNYMPPEAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYKTPFPQ 720
IINQISKLHA IIDPNHEIEF PDIPEKDLQD VLKCKLRKDP KQRISIPELL AHPYVQIQTH 780
PVNQMAKGT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTPEKKRGK 840
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60 A148 DNA SEQUENCE
 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
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CTTCITTAAG TTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
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TCTAATCTCT TGGTCATCGC GGCAGTGATC AAAAAACAGAA AATTTCAATT CCCCTTCTAC 240
TACCTGTTGG CTAATTTAGC TGCTGCGAT TTCTTCGCTG GAATTGCCTA TGTATTCTCT 300
ATGTTTAAAC CAGGCCCACT TTCAAAACT TTGAGTGTCA ACCGCTGCTT TCTCCGTCAG 360
GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
AGGCACATGT CAATCATGAG GATGCGGCTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
CTGCTCATTT TGCTGTCTCG GGCCATCGCC ATTTTATATG GGGCGTCCC CACACTGGGC 540
TGAATTTGCC TCTGCAACAT CTCTGCTGCT TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600
TACCTTGTTT TCTGGACAGT GTCCAACCTC ATGGCCTTCC TCATCATGGT TGTGGTGTAC 660
CTCGGATCTC ACCTGTACAT CAAGAGGAAA ACCAACGTC TGTCTCGCA TACAAGTGGG 720
TCCATCAGCC GCCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
GCGTTTGTGG TATGCTGGAC CCCGGGCTCG GTGGTTCTGC TCCTCGACGG CCTGAACTGC 840
AGGCAGTGGG GCGTGCAGCA TGTGAAAAGG TGGTTCTGTC TGCTGGGCTC GCTCAACTCC 900
GTGCTGAACC CCATCATCTA CTCCTACAAG GACGAGGACA TGTATGCGAC CATGAAGAAG 960
ATGATCTGCT GCTTCTCTCA GAGAAACCCA GAGAGGCGTC CCTCTCGCAT CCCCTCCACA 1020
GTCTCTAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

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GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGGCCACCCA GGTGATGACT 1140
GTCTTAGG

5 A149 Protein sequence:
Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number: Hs.258583
Probeset Accession #: NM_012152
Protein Accession #: NP_036284
10 Signal sequence: none found
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
Cellular Localization: plasma membrane

15 1 11 21 31 41 51
MNECHYDKIM DFPYNRSNTD TVDDWTGTXL VIVLCVGTFF CLFIPFNSL VIAAVIKNRK 60
PHFFPYLLA NLAAADFPAG IAYVFLMNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
20 LVIAVERHMS IMRMVRHSNL TKRVRTLLIL LVWALAIIMG AVPTLGWNL CNISACSSLA 180
PIYSRSYLVF WTVSNLMAFL IMVVVLYRIY VYVKRKTIVL SPHTSGSISR RRTPMKLMKT 240
VMTVLGAFVV CWTPLVLL LDGLNCRQCG VQHVKNWFLL LALLNSVNP IISYKDEDM 300
YGTMKRMICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

25 Prostate

A150 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.293616
30 Probeset Accession #: AW043782
Nucleic Acid Accession #: none found
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
AGCAACGACG CCGGGCAGCG GGAGCGCGCG CGCGCCATG TGGCTGCTGG GGCCGCTGTG 60
CCTGCTGCTG AGCAGCGCGG CGAGAGCCCA GCTGCTCCCG GGGAAACAAT TCACCAATGA 120
40 GTGCAACATA CCAGGCAACT TCATGTGCG CAATGGAGCG TGCAATCCCG GCGCCTGGCA 180
GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
GTGCAAAATG GGGCCAACT TCTTCCCTCG TGCCAGCGCG ATCCATTGCA TCATTGGTCG 300
CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
AAACCCCTCG CTTGTCTCCA CCGCCCGCTA CCATGCAAG AACCGCCTCT GTATTGACAA 420
GAGCTTCATC TGCGATGGAG AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
45 AAGTTCTCAA GAACCCCGCA GTGGGCGAGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
TTACCCGAGC ATCACTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
CCTGCTGCA CTGGTCTTGC ACCACGAGCG GAAGCGGAAC AACCTCATGA CGCTGCCGCT 660
GCACCGGCTG CAGCACCCCTG TGCTGCTGTC CGCCTGCTGT GTCTTGAGCC ACCCCACCA 720
CTGCAACGTC ACCTACAAAG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
50 GAATAGGCTG GAAGTAGGCT CCCCACCTCT CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840
TGCGTGTGAT GACCTTCTCT CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900
CGACCTGCGC CCTACCGCT CCGGTCGCG GAGTGCCAAC AGTGCCAGCT CCCAGGCAAG 960
CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCGCCAGGA 1020
GGGCAGTCTG GAGCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAGG TATAAGTCCC 1080
55 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140
TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
AACTATCTCT GCATTCCCT CTTCCCCAG ACTTCAGAGA TGTTTTCTG CGCTCTCAGT 1260
TGACATGATC TGTGTGCGT CTTTCTGTC AGGTCACTCT TCCCTTGGGA CCGAGATCA 1320
CACCTCATI TTTACATTA TTCTGTTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380
60 AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATAITGG ATGCTCAGAA GTGCAGGAGA 1440
CGCTGGAACC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTAG 1500
ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCACCCGCC CAAAAAATT CCATTGAGC 1560
ATCAAAACCT GCTTTGCACA ATCTTATTG ATGCCCCCG TTCAGCAGAG TCAGTGGCCA 1620
AAGAAACTT TGGACGTGAG TAACACCCCT CAGCAGTCGC AACGTTATT TGTTTTGTG 1680
65 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTG CCAAGAAATG 1740
CTCATCTGAG GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
GAGCCCTCTC CATGAGTTTA TCCAAGTTCT CAGCTCTTAA AATGCAGGCT GCCAAGACCC 1860
TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTACCC CTCOCAGCTG 1920
ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGAACCTGGC 1980
70 GTATGTCCCT GTGGCCCAACA CCGAGCCTGT CTTGCTCATT CATGCAGCCT CAACACTGGC 2040
CTCCAAAGTT CCTTAAACAC TTGCAAAGTC CTTTAACT GTGCATTGG ACTTGAGGAC 2100
ACTGGTTCT ATCAAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
CTGCACTGTG CAGCTCCTC TCCCAAGGT CCAATACCA GCACCTCTAG TTAGAGTTAG 2220
GGTCAGGGT AGGCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
75 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTAATTT AAATCTTTTA GAAATGCATT 2340
TGAAACAGTG TGTGTGTTT TTCCCTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400
AGCTGTCTCT TTTTGTGTT TTCTTTAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460
ACACCTTTCG CCGCTGAGC CCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
80 ACATTGTGTC ATTTGTGTC TTTGAGGTTA TTAATTTATCA AGTTCTTGAA GGAAGCAGAA 2580
AGAGGACTC CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
TTCTCTGTGT CCACTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAACTGT 2700
AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGGAA CCAGGTAGAG 2760
CCACTCCGGG CAGCTGTAC CCATTAGAA CTCTTTTCCG CAGCTGAAGA AATGTTCACT 2820

AACCTGTTTG AGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTGAG 2880
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAAAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAAAT GTGTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CCTGTAGTTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCCTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTGTAGT 3300
 AGATAAGGGA TGCCCTACTAA TGCTTTTAA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTAT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAAACCAG 3540
 AAAATAGTCT CATCTCTTTT TTCTCAAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGGTGT GTGTGCTGC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 TTATACITTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC AMYWTGGGG GGGCTTGGGC CTGGGAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGCGCGG GGGCCACGT AGGTACGGCG ACCACGCGGG CCAAAACGGG ACCCCAGAG 3960
 GAAACCTCG CCAAGAAAAA GTTGGGAGA ATTCTCCACA CCAAGAAAAA ACCGCGCGG 4020
 GAAACCGCA GAGTGTGCG TAAACCACAC CCAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGAATCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A151 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MNLLGPLCLL LSSAAESQLL PGNNPTNECN IPGNFMCNNG RCIPGANQCD GLPDCFDKSD 60
 EKECFKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGNNQCD NSDEESSCSS QEPGSGQVFP TSENQLVYYP SITYAIISS 180
 VIFVLVALL ALVLHHQRKR NNLMTLFVHR LQHPVLLSRL VVLDHPHNC VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPAW YDLPPPPYSS DTESLNQADL PPRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQSGT AEPRDSEPSQ GTEBV

A152 DNA SEQUENCE
 Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGTATAAC AGCAAGATGG 60
 CTTTGAACCT AGGGTCAACA CCAGCTATTG GACCTTACTA TGA AAAACCAT GGATACCAAC 120
 CGGAAAACCC CTATCCCGCA CAGCCCACTG TGCTCCCAAC TGTCTACGAG GTGATCCCGG 180
 CTCAGTACTA CCGTCCCGCC GTGCCCAAGT ACGCCCGAGG GTCTCTGAGC CAGGCTTCCA 240
 ACCCGTCTGT CTGCAACGAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAGACTA 300
 AGAAAGCACT GTGCATCAC TTGACCTCGG GGACCTTCTT CGTGGGAGCT GCGCTGGCGG 360
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGCTCCAA CTCTGGGATA GAGTGGGACT 420
 CCTCAGGTAC CTGCATCAAC CCTCTAACT GTGTGTATGG GTGTGCACAC TGCCCGGGGG 480
 GGGAGGACGA GAATCGGTGT GTTCGCTCTT ACGGACCAAA CTTCATCCTT CAGATGTACT 540
 CATCTCAGAG GAAGTCTGTG CACCTGTGTG GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGCGGCTGT GAGGACATG GGCTATAAGA ATAATTTTTA CTCTAGCCAA GGAATAGTGG 660
 ATGACAGCGG ATCCACCAGC TTTATGAAAC TGAACACAAG TGCCCGCAAT GTCGATATCT 720
 ATAAAAAAT GTACCACAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGGC GGTGAGAGCG 840
 CGCTCCCGGG GGCTGGGCC TGGCAGGTCA GCTTGACCGT CCAGAACGTC CACGTGTGCG 900
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCGCG CCACTGCGTG GAAAAACCTC 960
 TTAACAATCC ATGSCATTGG ACGGCATTGG CGGGGATTTT GAGACAATCT TTCAATGTTCT 1020
 ATGGAGCGGG ATACCAAGTA CAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080
 AGAACAAATG CATTCGCTGT ATGAAGCTGC AGAAGCTCT GACTTTCAAC GACTTGTGA 1140
 AACCAAGTGT TCTGCCCAAC CCAGGCATGA TGCTGCAGCC AGAACGCTC TGCTGGATT 1200
 CGGGTGGGG GGCACCGAG GAGAAAGGGA AGACCTCAGA AGTGTGAAC GCTGCCAAG 1260
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320
 CAGCCATGAT CTGTGCGGCG TTCTTCAGG GGAACGTCGA TTCTTGCCAG GGTGACAGTG 1380
 GAGGCGCTCT GGTCACTTGC AACAAACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TGCCAAAGCT TACAGACAGG GAGTGTACCG GAATGTGATG GTATTCAACG 1500
 ACTGGATTTA TCGACAAATG AAGGCAACCG GCTAATCCAC ATGGTCTTCT TCCTTGAAGT 1560
 CGTTTACAA GAAACCAATG GGGCTGGTTT TGCTTCCCGG TGCAATGATT ACTCTTAGAG 1620
 ATGATTACGA GGTCACTTCA TTTTATTATA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680
 TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTGT 1740

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COGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800
GTTGGAGGCT GCCCCATTG AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGGG 1860
TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
GGAAGGGGAG ACAGCCAGGT GGCACTGCA GCGGCTGCCC TCTGGGGCCA CTGGGTAGTG 1980
TCCCCAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
GATGGTGGCC AGAAATAAAG GGACCGCCCT TTCATGGGTG GTGACGTGGT AGTCACITGT 2100
AAGGGGAACA GAAACATTTT TGTTCTTATG GGGTGAGAAT ATAGACAGTG CCCTTGGTGC 2160
GAGGGAAGCA ATTGAAAAAG AACTTGCCTT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
CATGGGTGGG GGCTCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCCCTGC 2280
TCCTAGCACC CTGAGAGTGT AATGCCCTT GGTCCCTGGC AGGGGCGCAA GTTTGGCACC 2340
ATGTGGGCTT CTTCAGGCTT GATAGTCATT GGAATTTGAG GTCCATGGGG GAAATCAAGG 2400
ATGCTCAGTT TAAGGTACAC TGTTCCTATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
CTGAGTTCAA AGCCATCTT

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A153 Protein sequence:

Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Protein Accession #: NP_005647.1
 Signal sequence: none found
 Transmembrane domains: 85-107
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60
 SNFVVCTQPK SPSTGTCTSK TKKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
 DSSGTCTNPS NWCDGVSHCP GGEDENRCVR LYGPFPILQM YSSQRKSNWP VCQDDWNENY 180
 GRAACRDMGY KNNFYSSQGI VDDSGSTSFM KLNTSAGNVD IYKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAMPWQ VSLHVQNVHV CGGSIITPEW IVTAHCVKEK 300
 PLNNFWHMTA PAGILRQSPM FYGAGYQVQK VISHPNYDSK TKNDIALMK LQKPLTFNDL 360
 VKPVCLFNPQ MHLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLETORC NSRYVYDNL 420
 TPAMICAGFL QGNVDSQGD SGGPLVTENN NIWNLIGDTS WSGCCAKAYR PGVYGNVMVF 480
 TDWIYRQMK NA

A154 DNA SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
 Unigene number: Hs.129179
 Probeset Accession #: AI694767
 Nucleic Acid Accession #: AI694767
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CAGAGAGGCT GTATTTCACT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
GGGGTCACAC ATTCTCTCCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCCACAGTTC 120
AGCTTCTTCA TGATGGTGA TCCCAATGGC AATGAATCCA GTGCTACATA CTTCATCCTA 180
ATAGCCCTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCATT GTGCTCCCTC 240
TACCTTATG CTGTGCTAGG TAACITGACA ATCATCTACA TTGTGGCGAC TGAGCACAGC 300
CTGCATGAGC CCATGTATAT ATTCTTTGC ATGCTTTGAG GCATTGACAT CCTCATCTCC 360
AOCCTATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTC 420
GATGCTTGTC TGCTACAGAT GTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
CTGCTGGCCA TGGCTTTTGA CCGCTATGTG GCCATCTGTG ACCCACTGCG CCATGCCACA 540
GTACTTACGT TGCTCTGTGT CACCAAAATT GGTGTGGCTG CTGTGGTGCG GGGGGCTGCA 600
CTGATGGCAC CCCTTCCTGT CTTCATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660
TCCCATCTCT ACTGCTTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720
AATGTGHTCT ACCATGCTTAT GTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780
TCCTTCTCAT ATCTGCTTAT TCTTAAGACT GTGTTGGGCT TGACACGTGA AGCCACGGCC 840
AAGGCATTTC GCACTTGGCT CTCTCATGTG TGTGCTGTGT TCATATTTCTA TGTACCTTTC 900
ATTGGATTGT CCATGGTGCA TCGCTTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCATC 960
TTGGCCAATA TCTATCTGCT GGTTCCTCCT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
ACAAAGGAGA TCGACAGCG CATCCTTCGA CTTTTCCATG TGGCCACACA CGCTTCAGAG 1080
CCCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTCAGAGT CCTCTGATTC AGATTTTAAT 1140
GTTAATCATTT TGAAGAGCAG TATTCAGAAA AAAAAATTTCC TTAATAAAAA TACAACCTAG 1200
ATCCTTCAAA TATGAAACTG GTTGGGGAAT CTCCATTTT TCAATATTAT TTTCTTCTTT 1260
GTTTCTTTC TACATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320
TTTTCATTTT ACCATGCTAGT CCAATCTTAA ACTGCTTCTA CTGATGGTTT ACAGCATTCT 1380
GAGATAAGAA TGGTACATCT AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAAGGAAAA 1440
TAAACACAGA ATATAATAAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500
ACTGCCAAC ACCATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAAG 1560
AAATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
AGAGTACATT TAAGTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGCAT 1680
ATGGACCCCTG TTTTCTCTAT TTAATTTTCT TATCAACCCCT TTAATTAGGC AAAGATATTA 1740
TTAGTACCCCT CATTTGATGC ATGGGAAAAAT TGATGTTTCA TGGGGATCAG TGAATTAAT 1800
GGGGTCAATA AAGTATAAAA ATTAAAAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860
GGAAGAGACTG TTAAGAGAC CAACAGGGTA GTGGGTTAGA GATTTCAGAG GTCTTACATT 1920
TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGATTTTGA GAATTTCTG 1980
GCAACAGAAC TCATGGCTTT AATCCACTA GCTATTGCTT ATTGTCTGCG TCCATTTGCC 2040
AATTACCTGT GTCTTGGAAAT AAGTATTTT TAGGTTTACC ATTATGGAAG ATTCTTATTC 2100
AGAAAGTCTG CATAGGGCTT ATAGCAAGTT ATTTATTTT AAAAGTTCCA TAGGTGTTTC 2160
TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220
TGAAGATAAC ATTGGCCTTT TGAATGTGAC TGTAGTCTGG AAAGTGAGGG AATCTTCAGG 2280

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ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGGAAACAGG ACTTTGAGAC CGGAAAGCA 2340
ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAAACTC AAATTACATA 2460
TACTAAAACA TGTGATCATA TATGTGTAA GTTTCATTTT CTTTTCATAT CCTCAGGTTT 2520
CCTGATATGG ATTCTCTATNA CATGCTTTCA TCCCTTTTGT TAATGGATAT CATATTGGGA 2580
AATGCTATT TAATACTTGT ATTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT 2640
TATTGAATGT CATCTCTGTT CATCATTGAC TGCTCTTTGC TCATCATTTGA ATCCCCCAGC 2700
AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTTC TCAAACTCTGA 2760
TTCTTCTGT GCTGAACACA TAGCCAGGCA ATTTCCAGC CTCTTTGAG TTGGGTATTA 2820
TTAAATTTTA GCCATTACTT CCAATGTGAG TGGAAAGTAC ATGTGCAATT TTTATACCTG 2880
GCTCATAAAA CCTCCCATG TGCAGCCTTT CATGTTGACA TTAAATGTGA CTGGGAAGC 2940
TATGTGTTAC ACAGAGTTAA TTAACCGAA AGGCCTGGA ATTTTGTGN AANNAAACTG 3000
TGGCCNNGAG GCCNCAACC CTTTTNNNA ATTTGGCAAN NTCCCACCTT GTANTTTGGT 3060
AAGGAGGCCA GTTGATAAG TGAAAAATAA AGTACTATTG TGTC
  
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A155 PROTEIN SEQUENCE

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Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
Unigene number: Hs.129179
Protein Accession #: not available
Signal sequence: none found
Pfam domain: 7tm_1 [43-293]
Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295
Cellular Localization: not determined
  
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1 11 21 31 41 51
MVDPNNGNESS ATYFILIGLP GLEBAQFWLA PPLCSLYLIA VLGNLTIIYI VRTEHSLHEP 60
MYIFLCMLSG IDILISTSM PMLAIFWPN STTIQFDACL LQMFALHSLS GMESTVLLAM 120
AFDRYVAICH PLRHATVLT PRVTKIGVAA VVRGAALMAP LPVFQIKLPF CRSNILSHSY 180
CLBQDVMLKA CDDIRNVVY GLIVIIISAIG LDSLLISFSY LLILKTVLGL TREBAQAKAFG 240
TCVSHVCAVF IFYVPPFGLS MVHRFSKRRD SPLPVILANI YLLVPPVLNP IVYGVKTKEI 300
RQRLRLRFHV ATHASEP
  
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A156 DNA SEQUENCE

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Gene name: vasoactive intestinal peptide receptor 1
Unigene number: Hs.198726
Probeset Accession #: X77777
Nucleic Acid Accession #: NM_004624.1
Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)
  
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TCGGAGCCTG CGGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTGCGCCGCC TCACTCATGC 60
CTCTCTCTCC TCTGCTCTCG CTCAGSGGCC TGGTGGCGGG TTGGTGGGGG GTTAGCGGGC 120
TGGTGGTGGC GCGCGCCGGG GCTCGCTCTC GGGAGGGCCG GGGCGGATCT CGCGGCGCAG 180
GCGGCGCGCG CGAGAGTGGG GTGCGCGCGG GAGGCGGGCT CGAGCTTCGT GCTGGCGGCT 240
CGCTCTTGGG CTCTCGCTCG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300
ACAAAGCAGT CCGGAGGAGG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360
GGGACAACCT CACCTGCTGG CCAGCCACCC CTGCGGGCCA GGTAGTTGTC TTGGCCTGTC 420
CCCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCGGCAA TGTAAGCCGC AGCTGCACCG 480
ACGAAGGCTG GAGCGACCTG GAGCCTGGCC CGTACCCCAT TGCTGTGGT TTGGATGACA 540
AGGCAGCGAG TTTGGATGAG CAGCAGACCA TGTTCTACGG TTCTGTGAAG ACGGCTACA 600
CCATTGGCTA CGGCTGTCTC CTGCGCACCC TTCTGCTGCG CACAGCTATC CTGAGCCTGT 660
TCAGGAAGCT CCACTGCACG CGGAACCTACA TCCACATGCA CCTCTTCATA TCCTTCATCC 720
TGAGGGCTGC CGCTGTCTTC ATCAAAGACT TGGCCCTCTT CGACAGCGGG GAGTGGGACC 780
AGTGTCTCCA GGGCTCGGTG GGTGTGAAGG CAGCCATGGT CTTTTCCTAA TATTGTGTCA 840
TGGCTAACTT CTTCTGCTG CTGGTGGAGG GCCTCTACCT GTACACCCCTG CTTGCCGTCT 900
CCTTCTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960
GCACATTCAC CATGGTGGG ACCATCGCCA GGATCCATTT TGAGGATTAT GGTCTGTCTCA 1020
GGTGTCTGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCCTCACCT 1080
CCATCTTGGT AAACCTTCATC CTGTTTATTT GCATCATCCG AATCTGTGTT CAGAAACTGC 1140
GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATCTC AAGGCTAGCC AGGTCCACAC 1200
TCCTGTCTGAT CCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CCGGACAATT 1260
TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTCTGGGG GTCTTCCAG GGTTTTGTGG 1320
TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380
GGCGCTGGCA CCGTCAGGGC GTCTGCGGCT GGAACCCCAA ATACCGGCAC CCGTCGGGAG 1440
GCAGCAACCG CGCCACGCTG AGCAACGAGG TTTCATGCT GACCCGCGTC AGCCCAAGTG 1500
CCGCGCGCTC CTCAGCTTTC CAAGCCGAGG TCTCCCTGGT CTGACCAACA GGATCCACAG 1560
CCAAAGCGGCC CCTCCGCCCC CTTCCTCACTC GCAGCAGAGC CCGGGGACAG AGGCCTGCC 1620
GGGCGCGCCA GCCCCGCCCC TGGGCTCGGA GGTCTGCCCC GGGCCCTGG TCTCTGGTCC 1680
GGACACTTCT AGAGAAGGCA GCCCTAGAGC CTGCTTGAGG CGTTCTTAGC AAGTGAGAGA 1740
GATGGGAGCT CCTCTCTGG AGGATGCAGG TGGAACTCAG TCATTAGACT CCTCTCCCAA 1800
AGGCCCCCTA CGCCATCAAA GGGCAAAAG TCTACATACT TTATCTCTGA CTCTGCCCCC 1860
TGCTGGCTCT TCTGCCAAT TGGAGGAAAG CAACGGGTGG ATCTCAAAAC AACACTGGTG 1920
TGACCTGAGG GCAGAAAGGT TCTGCCCGGG AAGGTACCA GCACCAACAC CACGGTAGTG 1980
CCTGAAATTT CACCAATTGT GTCAAGTTCC TTTGGGTTAA GCATTACAC TCAGGCATTT 2040
GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTTACGC TTAGTTATCA GCTTTTAAAA 2100
GTGGGTATT CTGGAGTTT TGTTTGAGA GCACACCTAT CTTAGTGGTT CCCCACCGAA 2160
GTGACTGGC CCTGGGTCA GTCTGGTGGG AGGAAGGTGC AACCAAGGA CTGAGGAGCT 2220
CTGAAGCCTC TGGGAAATGA GAAGGCAGCC ACCAGCGAAT GCTAGGCTCT GSACTAAGCC 2280
TACCTGTCTC CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GGACTCTGTC ACACAGCCA 2340
TTCTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTGTCCACC 2400
CACCTATGTG CCAACTGTTG TAACTAGGCT CAGAGATGTG CACCATGGG CTCTGACAGA 2460
  
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5
AAGCAGATCC TCACCTGCT ACACATACAG GATTGAACT CAGATCTGTC TGATAGGAAT 2520
GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACAGCCAG ATCCTCTTGG 2580
TTATTTGTTT ACCACTTGTA TTATTAATGC CATTATCCCT GAATTCCTCT TGCCACCCCA 2640
CCCTCCCTGG AGTGTGGCTG AGGAGGCCCTC CATCTCATGT ATCATCTGGA TAGGAGCCTG 2700
CTGGTCACAG CCTCTCTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760
CCTCTGCCAG AAGATCCCTC CAGGACTGCA ACAGGCTTGT GCAACATAA ATGTTGGCTT 2820
GGAAAAAAA AAAA

10 A157 Protein sequence:

Gene name: vasoactive intestinal peptide receptor 1
Unigene number: Hs.198726
Probeset Accession #: X77777
Protein Accession #: JC2195
Signal sequence: none found
15 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430
Cellular Localization: plasma membrane

20
1 11 21 31 41 51
| | | | | |
MPPFPLLSLR RLGGGWSAVT RLVVAAAGAR SRGGRGGRG AGGGGRGVA RRRRLRLRAA 60
RSLGSSSLQE ECDYVQMIEV QHKQCLEEAQ LENETIGCSK MWDNLTCWPA TPRGQVVVLA 120
CPLIFKLFS IQGRNVSRSC TDEGWTHLEP GFYPIACGLD DKAAASLDEQQ TMFYGSVKTG 180
25 YTIYGLSLA TLLVATAILS LPRKLHCTRN YIHMHLFISP ILRAAAVFIK DLALFDSGES 240
DQCEGSGVGC KAAWVFFOYC VMANFFWLLV EGLYLYTLA VSFFSERKYP WGYILIGMGV 300
PSTTFMWIIT ARIHFEDYGL LRCWDTINSS LMWIKGPIL TSILVNFIPL ICIIIRILLQK 360
LRPPDIRKSD SSFYSRLARS TLLLIPLFGV HYIMFAFFPD NFKPEVKMVF ELVVGSFQGF 420
VVAILYCFNL GEVQALRRK WRRWHLQGV L GWNPKYRHP S GGSNGATCST QVSMILTRVSP 480
GARRSSSPQA EVSLV

30 A158 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.29383
Probeset Accession #: AW207206
35 Nucleic Acid Accession #: AL133619
Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

40
1 11 21 31 41 51
| | | | | |
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCGAC CC GG GGTCT 60
CGGGCGCGGC GCCAGCGGCC CTCTGTGGGC GTCCAGTCTT TGAGGCGCGA GAGCCCGCAG 120
CTCAGGCAGA GCGACCGGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180
CAGCAGCAGC ACTCGGAGAT GCTGGCCAA GCTCATGAGG AGATCGAGCA TCTGAAGCGG 240
45 GAAACAGAG GTGAGCGGCG GGGGGGCCCT AGGCCCGCCC TGCCCTCCCA GGCACACTCA 300
ACACTGCGCG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCTGGGCTCA 360
GGGGGAACAC AGGACGCGGA GCCCTCCAG ACTGTCTCTG CCCACCTGCG TGCACTGGCC 420
CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480
AGCGGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAGC TGCTGTCTCT GGGAGGCCCA 540
GGGCGCTGAG TCATTCGAGG GCGGCGAGTG GCCACAGGCT GCTCCCGAGA CCTCCCTCCT 600
50 CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CCGTCCCTGC TAGATCTTTG 660
CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCCCTAC 720
ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
GCAGCAACCA TGGGACAAAG GGGAGGAAGC AGAGTCTGTT TTCCCTGCCA CTGTGCTCAAG 840
GCACTTCCCC ATCTGACAGC CGGCCCCAC CCAGCCCGAG ATCCTGGGCT GTGGTCTCAA 900
55 GCTCACTTCC CATTATCTTT GGGGCTGGG CTGACATCAG GAGGACATCT GACTGGTGGG 960
TGGAGCCAGC CTGGGAACAT GCGAGCTGG GCACTGCCCTA GGGCTCTCCC TTCCAGGGA 1020
GACATGGAGA AGGGGTTTGA GGGAGGGGCC TTCCCTAGCC GCTGTGGCAA CTCCAGTGG 1080
CTGTTCTGGG CAAGTGTGG CCAAGTGGG CAGCCCCAGC CCGCAGTGC TGGGAGCGCT 1140
GACAGGACAC GGAAGAGGCG CATGCTTTCC CTGGGACCT GCTGTTCCAT GTGTCCCAAG 1200
60 CCTCCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG 1260
GGGCTCGCT GGTCTGCTAT CAACGAGTG TGGGTAGAGC CGGAGGACC CAGCCCTGCC 1320
AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGGTTGG GCGTCTTGG 1380
GGGCTAGCG CCGCACTGT GCGCTCTCT GCGAGACAGC TCTCCATGTC AAGCTTCCAG 1440
TCTGTCAAGT CCATCTCTAA TTCAGCCAA TCTCAAGGCA AGGCCAGGC CCAGCCCGGC 1500
65 TCCTTCAACA AGCAAGATT AAAAGCTGAC GTCTCCAGA AGGCGGACCT GGAAGAGGAG 1560
CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGCA GGCAGAAAG 1620
GAGAAAGCAG AGGCCTCTAA TGCAGGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680
AGGCAGATGG GGGCGGGGCG ACACCCCOCA ATGATCCTGC CCTTCCCTC GCGAAAGCCC 1740
ACCACTCTTA GGCAGTGGGA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCCTGAG 1800
70 ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCGAGAGGCC CCAGGCGAGC 1860
CCGAGGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920
AAGAGCTCT CCAGGAATG CCTGAGCCCA CCGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980
CTGAAGCAGA CCCGAGGAA CAACCTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCG 2040
AAACGCGGCC TGCATCGCTC AGTGCTTTGA

75 A159 Protein sequence:

Gene name: ESTs
Unigene number: Hs.29383
Probeset Accession #: AW207206
80 Protein Accession #: T43457
Signal sequence: none found
Transmembrane domains: 303-322
Cellular Localization: not determined


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1      11      21      31      41      51
5      |      |      |      |      |
MSGAGVAAAGT RPPSSPTPGS RRRRQRPSVG VQSLRPOSPO LRQSDPQKRN LDLEKSLQPL 60
QQQHSSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAHs TLPLPQHRNT AINSSTRLGS 120
GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAAITS SRGWTMLCSQ AQHVLLSGSP 180
GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSPCPARSL PQIAAVARPR ISSPMALSPH 240
MLGAQGIWTH SIQGSPLPAIW AATMGTKGGS RVLFPCHLSK ALFHPDSEGPH PAQDPGLWSQ 300
10      AHFPLSLGLG LITSGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVVEGPH FPSRCGNSSSE 360
LFWAKCGPSR QPQPCSAQDA DRTREEMLS LGTCCSMCPK PSCFPDGPSP NHLSRASAPL 420
GARWVCINGV WVEPGGSPSA RLKGGSSRTH RPKGKRGRLA GGSADTVRSP ADSLSMSSFO 480
SVKSISNSAN SQGKARPPQG SPNKQDSKAD VSQKADLEEE PLLHNSKLDK VPGVQQGARK 540
EKARASNAGA ACMGNsqHqG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
15      TQELRHLKSL LBGSRQPQAA PEEASFPRDQ BATHFPKVST KSLSKKCLSP PVAERAILPA 660
LKQTFKNNFA ERQKRLQAMQ KRRLHRSVL

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A160 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Probeset Accession #: U41060
 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
30     |      |      |      |      |
CTCGTGGCCGA ATTGGGCACG AGACCCGCGTG TTGCGCGCTG GTAGAGATTG CTCGAAGACA 60
CCAGTGGGCCG CGTGTGGAAAC CAAACCTGCG CGCGTGGCCG GGCCTGGGGA CAACGAGGCC 120
GCGGAGACGA AGCGCGCAATG GCGAGGAAGT TATCTGTAAT CTGTATCCTG ACCTTTGCCG 180
TCTCTGTTCAC AAATCCCTTT CATGAATAA AAGCAGCTGC TTTCCTCCAG ACCACTGAGA 240
AAATTAGTCC GAATTGGGAA TCTGGCATTG ATGTTGACTT GGCATTTCC ACACGGCAAT 300
ATCATCTACA ACAGCTTTTC TACCGCTATG GAGAAATAAA TTCTTTGTCA GTTGAAGGGT 360
35     TCAGAAATTT ACTTCAAAT ATAGGCATAG ATAAGATTAA AAGAATCCAT ATACACCATG 420
ACCACGACCA TCACTCAGAC CACGAGCATC ACTCAGACCA TGAGCGTCAC TCAGACCATG 480
AGCATCACTC AGACCAAGAG CATCACTCTG ACCATGATCA TCACTCTCAC CATAATCATG 540
CTGCTTCTGG TAAAAATAG CGAAAAGCTC TTTGCCCAGA CCAATGACTCA GATAGTTTCA 600
GTAAAGATCC TAGAAACAGC CAGGGGAAAG GAGCTCACCG ACCAGAACAT GCCAGTGGTA 660
40     GAAGGAATGT CAAGGACAGT GTTAGTGCTA GTGAAGTGAC CTCACCTGTG TACAACACTG 720
TCTCTGAAGG AACTCACTTT CTAGAGACAA TAGAGACTCC AAGACCTGGA AAACCTCTCC 780
CCAAAGATGT AAGCAGCTCC ACTCCACCCA GTGTCAATC AAAGAGCCGG GTGAGCCGGC 840
TGCGTGGTAG GAAACCAAT GAATCTGTGA GTGAGCCCGG AAAAGGCTTT ATGTATTCCA 900
45     GAAACACAAA TGAAATCCCT CAGGAGTGTG TCAATGCATC AAAGCTACTG ACATCTCATG 960
GCATGGGCAT CCAAGTTTCG CTGAATGCAA CAGAGTTCAA CTATCTCTGT CCAGCCCATG 1020
TCAACCAATG TGATGCTAGA TCTTGTCTGA TTCATACAA TGAAAGAAAG GCTGAAATCC 1080
CTCCAAAGAC CTATTCATTA CAATAGCCTT GGGTTGGTGG TTTTATAGCC ATTTCCATCA 1140
TCAGTTTCTC GTCTCTGTCT GGGGTTATCT TAGTGCTCTC CATGAATCGG GTGTTTTTCA 1200
50     AATTTCTCTC GAGTTTCTCT GTGGCACTGG CCGTTGGGAC TTTGAGTGGT GATGCTTTTT 1260
TACACCTTCT TCACATTTCT CATGCAAGTC ACCACCATAG TCATAGCCAT GAAGAACCCG 1320
CAATGGAATG GAAAGAGAGA CCACCTTTTCA GTCATCTGTC TTCTCAAAC ATAGAAGAAA 1380
GTGCTTATTT TGATTCCACG TGGAAAGGTC TAACAGCTCT AGGAGGCCCTG TATTTTCATG 1440
TTCTTGTTGA ACATGTCTCT ACATTGATCA AACAAATTA AGATAAGAAG AAAAAGAAATC 1500
55     AGAAGAAACC TGAAATGATG GATGATGTGG AGATTAAAGG CAGATTGTCT AAGTATGAAT 1560
CTCACTTTTC AACAAATGAG GAGAAAGTAG ATACAGATGA TCGAACTGAA GGCTATTTAC 1620
GAGCAGACTC ACAAGGCCCT TCCCACTTTG ATTCTCAGCA GCCTGCAGTC TTGGAAGAA 1680
AAGAGGTCAT GATAGCTCAT GCTCATCCAC AGGAAGCTTA CAATGAATAT GTACCCAGAG 1740
GGTGCAAGAA TAAATGCCAT TCACATTTCC ACGATACACT CGGCCAGTCA GACGATCTCA 1800
60     TTCACACCA TCATGACTAC CATCATATTC TCCATCATCA CCACCAACAA AACCAACATC 1860
CTCACAGTCA CAGCCAGCGC TACTCTCGGG AGGAGCTGAA AGATGCCGGC GTGCCCACTT 1920
TGGCCTGGAT GGTGATAATG GGTGATGGCC TGCACAATT CAGCATGGC CTAGCAATG 1980
GTGCTGCTTT TACTGAAGGC TTATCAAGTG GTTTAAGTAC TTCTGTGCT GTGTTCTGTC 2040
ATGAGTTGCC TCATGAATTA GGTGACTTTG CTGTCTACT AAAGGCTGGC ATGACCGTTA 2100
65     AGCAGGCTGT CCTTTAATG GCATTGTGAG CCATGCTGGC GTATCTTGGG ATGGCAACAG 2160
GAATTTTCAT TGGTCATTAT GCTGAAATG TTTCTATGTG GATATTGCA CTACTGCTG 2220
GCTTATTTCAT GTATGTTGCT CTGGTTGATA TGGTACCTGA AATGCTGAC AATGATGCTA 2280
GTGACCATGG ATGTAGCCCG TGGGGGTATT TCTTTTACA GAATGCTGGG ATGCTTTTGG 2340
GTTTGTGAAT TATGTTACTT ATTTCCATAT TTGAACATAA AATCGTGTG CGTATAAATT 2400
70     TCTAGTTAAG GTTTAAATGC TAGAGTAGCT TAAAGAGTTG TCATAGTTTC AGTAGGTCAT 2460
AGGGAGATGA GTTTGTATGC TGTACTATGC AGCGTTTAAA GTTAGTGGGT TTTGTGATT 2520
TTGTATTGAA TATTGCTGTC TGTTACAAAG TCAGTTAAAG GTACGTTTTA ATATTAAAGT 2580
TATTCTATCT TGGAGATAAA ATCTGTATGT GCAATTCAAC GGTATTACCA GTTTATTATG 2640
TAAACAGAGG ATTTGGCATG ACATGTTCTG TATGTTTCAG GGAAGAAATG CTTTAAATGT 2700
75     TTTTCAAGAA CTAACACAGT TATTCCTATA CTGGATTITA GTCTCTGAA GAACTGCTGG 2760
TGTTTAGGAA TAAGAATGTG CATGAAGCCT AAAATACCAA GAAAGCTTAT ACTGAATTTA 2820
AGCAAGAGAA TAAAGAGAA AAGAGAGAA TCTGAGAATT GGGAGGCAT AGATTCTTAT 2880
AAAAATCACA AAAATTGTTG TAAATTAGAG GGGAGAAATT TAGAATTAAG TATAAAAGG 2940
CAGAAATAGT ATCAGATACA TTCAATTAAC ATTTTGTGCA GGATTATTTC CGTAAAAAAC 3000
80     GTAGTGAGCA CTGATATATA CTAATTAGTG TACATTAAAC TTTGTATAAT ACAGAAATCT 3060
AAATATATTT AATGAATCCA AGCAATATAC ACTTGACCAA GAAATTGGAA TTTCAAAATG 3120
TTCGTGCGGG TTATATATCA GATGAGTACA GTGAGTAGTT TATGTATCAC CAGACTGGGT 3180
TATTGCCAAG TTATATATCA CCAAAAGCTG TATGACTGGA TGTTCGTGTT ACCTGGTTTA 3240
CAAAATATAT AGAGTAGTAA AACTTTGATA TATATGAGGA TATTAAGACT ACATAAGTA 3300
TCATTTGATT CGATTACAGAA AGTACTTTGA TATCTCTCAG TGCTTCAGTG CTATCATTGT 3360

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GAGCAATTOT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

5

A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Protein Accession #: NP_036451
Signal sequence: 1-21
Pfam domain: Zip[591-743]
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization: plasma membrane

10

15

1	11	21	31	41	51	
MARKLSVILI	LTFALSVTNP	LHELKAAAFP	QTTEKISPNW	ESGINVDLAI	STRQYHLQQL	60
FYRYGENNSL	SVYGFRLKLLQ	NIGIDKIKRI	HIHHDHHDHS	DHEHSDHER	HSDHEHSDH	120
EHSDDHHDHS	HNNHAASGKV	KRKALCPDHD	SDSSGKDPFN	SQKGAHRPE	HASGRNRVKD	180
SVSASEVTST	VYNTVSEGTH	FLETIETPRP	GKLFPPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
NESVSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMGIQV	PLNATEPNYL	CPAINQIDA	300
RSCLIHSTSEK	KAEIPPKTYS	LQIANVGGFI	AISIISPLSL	LGIVILVPLMN	RVFFKPLLSF	360
LVALAVGTLG	GDAFLHLPLH	SHASHHSHS	HEEPAMEMKR	GPLFSHLSSQ	NIEESAYFDS	420
TKGGLTALGG	LYFMFLVHV	LTLIKQPKDK	KQGNQKPKEN	DDVZEIKQL	SKYESQLSTN	480
EKVDTDDRT	EGYLRADSQE	PSHFDSQQFA	VLEEEVMI	HAHPQEVYNE	YVPRGCKNKC	540
HSHFEDTLQG	SDDLHHDH	YRHILHHDH	QNHHPHSHSQ	RYSEELKDA	GVATLAWMVI	600
MCDGLHNFSD	GLAIGAAPE	GLSSGLSTSV	AVPCHLPHE	LGDFAVLLKA	GMTVKQAVLY	660
NALSAMLAYL	GMATGIPIGH	YAENVSMWIF	ALTAGLFMYV	ALVDMVPEML	HNDASDHGCS	720
RMGYFFLQNA	GMLLGGFIML	LISIFEHKIV	PRINF			

30

A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

35

40

1	11	21	31	41	51	
CGCGGGGCGC	GGAGTCGGCG	GGGCGCTCGG	GGACGCGGGC	AGTGCAGAGA	CCGCGGCGCT	60
GAGGACGCGG	GAGCCGGGAG	CGCACGCGCG	GGGTGAGATT	CAGCCTACTC	TTTCTTAGAT	120
GTGAAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180
CATAACCAAT	TGGCTCTGAG	CTATGACAA	AGAGGAAACA	AAAAGTTAAA	CTTCAAGCC	240
TGCCATAAGT	GAGAAAGCAA	CTTCCTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAATTA	300
AATGTGGGCA	CCAAGAAAGA	GGATGGTGAG	AGTACAGCCC	CCACCCCGG	TCCAAGGTC	360
TTGCGTTGTA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TTGCAGCACA	420
GACGATATT	GTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCTGT	GGTCATTCT	480
GGTTGCTGAG	GACTAGAAAG	CTCAGATTTT	CAGTGTGGGG	ACACTCCCAT	TCCTCATCAA	540
AGAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAAGACCT	ACACCTACA	600
CTGCTCCAT	TGAAAAACAG	AGATTTTGTT	GATGGACCTA	TACACCACAG	GGCTTTACTT	660
ATATCTGTGA	CTGCTCTGAG	TTTGCTCTTG	GTCTTTATCA	TATTATTTTG	TTACTTCCGG	720
TATATAAAGC	AAGAAACACG	ACCTCGATAC	AGCAATTGGT	TAGAACAGGA	TGAAACTTAC	780
ATTCTCTCTG	GAGAAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGA	840
TCAGGCTTCC	CTCTGCTGGT	CCAAAGGACT	ATAGCTAAGC	AGATTAGAT	GGTGAAACAG	900
ATTGAAAGAG	GTGCTATGAG	GGAAAGTTGG	ATGGGAAAGT	GGCGTGCGGA	AAAGGTAGCT	960
GTGAAAGTGT	TCTTCACCAC	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
ACAGTGTGTA	TGAGGCATGA	AAACATTTTG	GGTTTCATTG	CTGCAGATAT	CAAAGGGACA	1080
GGGTCTCTGA	CCCAAGTTGA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
TATCTGAAGT	CCACCACCT	AGACGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
AGTGGCTTAT	GTCAATTACA	CACAGAAATC	TTTAGTACTC	AAGGCAAAAC	AGCAATTGCC	1260
CATCGAGATC	TGAAAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACCTG	CTGTATTGCT	1320
GACCTGGGCC	TGGCTGTTAA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
ACTOGAGTGT	GCACAAAACG	CTATTGCCT	CCAGAAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCTCAT	CCTTTGGGAG	1500
GTGCTAGAGA	GATGTGTATC	AGGAGGTATA	GTGGAAGAA	ACCACTTCC	TTATCATGAC	1560
CTAGTGCCCA	GTGACCCCTC	TTATGAGGAC	ATGAGGGAGA	TTGTGTGAT	CAAGAAAGTTA	1620
CGCCCTCAT	TCCCAAAACG	GTGGAGCAGT	GATGAGTGT	TAAGGCAGAT	GGGAAAACCTC	1680
ATGACAGAA	GCTGGGCTCA	CAATCCTGCA	TCAAGGCTGA	CAGCCCTGCG	GGTTAAGAAA	1740
ACACTTGCCA	AAATGTCAGA	GTCCAGGAC	ATTAACTCT	GATAGGAGAG	GAAAAGTAAG	1800
CATCTCTGCA	GAAAGCCAAC	AGGTACTCTT	CTGTTGTGG	GCAGAGCAAA	AGACATCAAA	1860
TAAGCATCCA	CAGTACAAGC	CTTGAACATC	GTCTGCTTC	CCAGTGGGTT	CAGACCTCAC	1920
CTTTAGGGA	CGGACCTGGG	CAAAGACAGA	GAAGCTCCCA	GAAGGAGAGA	TTGATCCGTG	1980
TCTGTTGTA	GGCGGAGAAA	COGTGGGTA	ACTTGTTCAA	GATATGATGC	AT	

75

A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane

80

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1      11      21      31      41      51
5      |      |      |      |      |
MLRSAGKLN VGTKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCPTMIEED 60
DSGLPVVTSQ CIGLEGGSDFO CRDTPIPHQR RSIECCTERN ECKNDLHPTL PPLKNRDFVD 120
GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
EQSQSSSGSGS GLPLLVQRTI AKQIQMVVKI GKGRYGEVWM GKWRGEKVAV KVPFTTEAS 240
WFRTEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
MLKLAYSVS GLCHLHTEIF STQKPAIAH RDLKSKNIV KKNGTCCIA LGLAVKFISD 360
10     TNEVDIPFNT RVGTRKYMPP EVLDESINRN HFQSYIMADM YSFGLILMEV ARRCVSGGIV 420
EYQLPYHDL VPSDPSEYDM REIVCIKKLR PSPFNWSSD ECLRQMGKLM TECAHNPAS 480
RLTALRVKKT LAKMSSEQDI KL

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A164 DNA sequence

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15     Gene name:          ESTs
Unigene number:         Hs.157601
Probeset Accession #:   W07459
Nucleic Acid Accession #: AC005383
20     Coding Sequence:    328-2751 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
25     |      |      |      |      |
GACAGTGTTT GGGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
TTTTATTTCG AGACCTGGGC CGATGCCGCT TTAACAAACG CGAGGGGCTC TATGCACCTC 120
CCTGGGGGTA GTTCTCTCGA CCTCAGCCGG GTCCGGTCTG GCGGCCCTCT CCCAGGAGAG 180
ACAAACAGGT GTCCCACTGG GCAGCCGCGC CCCGGGCGCC CCTCCTGTGA TCCCGTAGCG 240
CCCCCTGGCC CGAGCCGCGC CCGGCTCTGT GAGTAGAGCC GCGCGGCAC CGAGCGCTGG 300
TGCGCGCTCT CCTTCGTTA TATCAACATG CCCCCTTTC TGTGTCTGGA GSCCGTCTGT 360
30     GTTTTCTCTG TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420
GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
ATCATGTTCG TGTAGATGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAAG 540
CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CGAGAGGGGT CAGAGTGGGA 600
GCATTCCAGT TCAGTTCAC TCCTCATCTG GAATTCCTCT TGGATTCAAT TTCACCCAA 660
35     CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAG GAGGCGGCAC GGAGACGGAA 720
CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCTGAGAG GCAGAAATGC TTCTGTGCCC 780
CAGATCCTCA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840
CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGG TCAGGTTCCT CAGTGGGAG 900
GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCAGC TGCTGTGGC TGAGCAGGTG 960
40     GAGGATGCCA CCAACGGCTT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
AOCOCAGACT GCAGGGTCTG GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080
GAGTTCGTTG GCAATGCCCC ATGCTGGAGA GGATCGCGGC GGACCTTTCG GGTGCTGGCT 1140
GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCCACCTTGC CACTGTCTAC 1200
45     AGGACCACCT GCCCAGGCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
CCAGAAGGAC TGGAGCGTGA CCAAGTGCCT TCCTGCTGAG CTTTGGAGG GGAGGCTAAC 1320
TGTGCCCTGA AGCTGAGCCT GGAATGCAAG GTGCACTTCC TCTTCTGCT GACAGCTCT 1380
GCGGGCAGCA CTCGTGACGG CTTCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
GCCGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
50     CTGGTGGCGG TGCGCTGTGG GGAGTACCAG GATGTGCTGT ACCTGGTCTG GAGGCTCGAT 1560
GGCATTCCTT TCCGTGGTGG CCCCACCTTG ACGGGCAGCT CTTTGGGCA GCGGCGAGAG 1620
CGTGGCTTCG GGAGGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTGT 1680
CTCACTGAGT CCACTCGCA GGATGAGGTT GCGGGCCAG CGGCTCACGC AAGGGCGCGA 1740
GAGCTGCTCC TGCTGGGTGT AGGCAAGTGA GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
55     GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAG ATCTGTTCAC CCAATCCCT 1860
GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGT GCGGACACA AGCCTTGAC 1920
CTCGTCTTCA TGTGAGACAC CTCTGCCCTA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTGCGC 2040
CTGGTGGTGT ATGCGAGCCA GGTGCAGACT GCCTTCGGGC TGACACCAA ACCCACCCG 2100
60     GCTGGGATGC TGCGGGCCAT TAGCCAGGCC CCCTACCTAG GTGGGGTGGG CTCAGCGGC 2160
ACCGCCCTGC TGACATCTTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220
GTCCCAAAAG CTGTGGTGTG GCTCAGAGGC GGGAGAGGCG CAGAGGATGC AGCGGTTCT 2280
GCCAGAGAGC TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGCTGGG GCTGTCTCTA 2340
AGTGAGGGTC TGCGGAGGCT TGCAAGTCCC CGGATTCCC TGATCCAGT GGCAGCTTAC 2400
65     GCGACCTGCG GGTACCAACA GGACGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460
CCAGTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520
GGGAGCTACC GCTGCAAGTG TCGGATGGC TGGGAGGGCC CCACTGCGA GAAACGCTAG 2580
TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATT TTAGAGCGCC CCTGAGGCAC 2640
ATGGCTCCCG TGCAAGGAGG CAGCAGCCGT ACCCTCCCA GCACTACAG AGAAGGCTTG 2700
70     GGCAGTGAAG TGGTGCTTAC CTCTGGAAT GTCTGTGCC CAGGTCTCTA GAATGTCTGC 2760
TTCCGCGCGT GGCAGGAGC ACTATTCTCA CTGAGGAGG AGGATGTCCC AACTGCAGCC 2820
ATGCTGCTTA GAGCAAGAA AGCAGCTGAT GTCAACACA AACGATGTT TGAAGAGTT 2880
TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CCTGTGAG GCTATGTCAT 2940
CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTGAAAG ACTTAAATTT AGCGGCTTGA 3000
75     CGTTCCTTTG CACACATCA ATGCTGCCA GAATGTTGTT GACACAGTAA TGCCACGCA 3060
AGGCTTTTAC TGAGAGCATCC TTTGAGCGGC GAAGGCCACG GCCTTTCAAG ATGGAAGCA 3120
GCAGCTTTTC CACTTCCCCA GAGACATCTT GGATGCAATT GCATTGATC TGAAGGGGG 3180
CTTGAGGGAC GTTGTGACT TCTTGGCGAC TGCTTTTGT GTGTGGAAGA GACTTGAAGA 3240
GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGTGTTA TGATGGGGA GGGGCTGAGT 3300
80     TGTGATGGG CCCAGGTCTG GAGGGCCACG TAAATCGTT CTGAGTCTG AGCAGTGTCC 3360
ACCTTGAAGG TCTTC

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A165 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLEAV CVFLPSRVPP SLPLQEVHVS KETIGKISAA SROMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFPAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRRET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFPFRW BELHALASEP RGQHVLLAEQ VEDATNGLPS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMW REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVPLTHPATC YRTTCFPGPCD 300
SQPCQGGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEB RVDLLFLLDS SAGTTLDDGFL 360
RAKVVFVRXRV RAVLSEDSRA RVGVATYSRE LLVAVFVGEY QDVPLDVLNSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVS 480
BAVRAELEEI TGSPKRVVMY SDPQDLFNQI PELQGLCSR QRPGCRTQAL DLVFMLD TSA 540
SVGPENFAQM QSPVRSALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRNNGI 660
SVLVVVGVPV LSEGLRLLAG PRDSLHVA AADLRVHQDV LIEWLCEAK QPVNLCCKPSP 720
CHNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
RTFPSNYREG LGTEMVPTFW NVCAPGP

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A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Probeset Accession #: AA011176
 Nucleic Acid Accession #: AF272890
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCCGC GCCCGGGCTT CTGGGGTGT CCCCACCCAC GGCACAGCCC TGCCACACCC 60
CCCGCCCCCG GCCTCCGCAG CTCGGCATGG GCGCGGGGT GCTCGTCTG GCGCGCTCG 120
AGCCCGGTAA CTTGTCTGTG GCGCGACGCG TCCCGACGCG GCGCGCCACC GCGCGCGGC 180
TGCTGGTGCC CGCGTCGCGC CCGCGCTCGT TGCTGCTCTC CGCGAGGAAA AGCCCGGAGC 240
CGCTGTCTCA GCACTGGACA GCGGGCATGG GTCTGCTGAT GCGCTCATC GTGCTGCTCA 300
TGCTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACCGCGCGG CTGCAGACGC 360
TCACCAACCT CTTCATCATG TCCCTGGCCA GCGCCGACCT GGTATGGGG CTGCTGGTGG 420
TGCGGTGCGG GCGCCACCAT GTGGTGTGGG GCGCGTGGGA GTACGGCTCC TTCTTCTGGC 480
AGCTGTGGAC CTCAGTGGAC GTGCTGTGGC TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
TTGCCCTGGA CGCTACCTC GCCATCACTC CGCCCTTCCG CTACCGAGAG CTGCTGACGC 600
GGCGCGGGGC GCGGGGCTCT GTGTGCACCG TGTGGGCCAT CTGCGCCCTG GTGTCTCTCC 660
TGCCCATCTC CATGCACTGG TGGCGGGCGG AGAGCGACGA GCGCGGCCGC TGCTACACCG 720
ACCCCAAGTG CTGCGACTTC GTCAACCAAC GCGCTACGCG CATCGCTCG TCCGTAGTCT 780
CCTTCTAGT GCCTCTGTGC ATCATGGCTT TCGTGTACCT GCGGTGTTT GCGAGGCCCC 840
AGAAGCAGGT GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCGCGCGGCG CCAGCGCGGC 900
CGCGCTCGCG CTGCGCTCGC CCGCTCCCGC GCGCGCGGCG GCGCGCGGGA CCGCGCGGCC 960
CGCGCGCGCG CGCGGCCACC GCGCGCTGCG CCAACGGGCG TCGCGGTAA GCGCGGCCCT 1020
CGCGCTGTCT GCGCGGCGCG GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
TCTTCAAGCT CTGCTGGCTG CCGTCTCTCC TGGCCAAAGT GGTGAAGGCC TTCCACCGCG 1140
AGCTGTGTCC CGACCGCTCT TCGTCTCTCT TCAACTGGCT GGGCTAGCGC AACTCGGCT 1200
TCAACCCCAT CATCTACTGC CGCAGCCCGC ACTTCGSCAA GGCCTTCCAG GACTGTCTCT 1260
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CGGGCTGTCT GCGCGGCGCG GAGCCCGCGC CATCGCGCGG GCGCGCTCG GACGACGAGC 1380
ACGACGATGT CGTCGGGGCC ACGCGCGCGC CGCGCTGCT GAGCGCCTGG GCGCGCTGCA 1440
ACGCGCGGCG GCGCGCGGAC AGCGACTCGA GCCTGGACGA GCGGTGCCCG CCGCGCTTCC 1500
CCTCGGAATC CAAGGTGTAG GCGCGCGCGC GCGCGCGCGA CTCGCGGCAC GCGCTTCCAG 1560
GGGAACGAGG AGATCTGTGT TTACTTAAGA CGATAGCAG GTGAAGTCTG AGCCCAACAT 1620
CCTGTCTTGA ATCATCCGAG GCAAAGAGAA AAGCCACGGA CCGTTCACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGGAGAG TGGCTTGTCT ATGTTCTCTG TTG

```

A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Protein Accession #: AA011176
 Signal sequence: none found
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248
 Pfam domain: 7tm_1 [75-377]
 Cellular Localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVLGA SEPNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQQNTAG 60
MGLLMALIVL LIVAGNVLVV VAIKTPRLQ TLTNLFIMSL ASADLVMLGL VVPPGATIVV 120

```

5 WGRNEYGSFF CELWTSVDVL CVTASIELTL VIALDRYLAI TSPFRYQSLT TRARARGLVC 180
 TVWAISALVS FLPLIMHWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSPYVPLCIM 240
 AFVYLVRVRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPP RFAAAAAATAP 300
 LANGRAGKRR PSRLVALREQ KALKTLGIIM GVFTLWLFP FLANVVIKPH RELVPRDLFV 360
 FFWNLGYANS AFNPIIYCRS PDFRKAPQGL LCCARRAARR RHATHGDRPR ASGCLARPGP 420
 PPSFGAASDD DDDVDVVGATP PARLLEPNAG CNGGAAADSD SSLDEPCRP GFASESKV

10 Al68 DNA sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 | | | | |
 GGCGTCCGCG CACACCTCCC CGCGCCGCGC CGGCCACGCG CGCACTCCG CGGCTCTGCG 60
 CCGCAACGCG TGAGCCATCC ATGGGGGTCG CGGGCCGCAA CGTCCCGGG CGGGCTGCG 120
 20 CGGTGCTGCT GCTGCTGCTG CTGTGCGCGC CACTGCTGCT GCTGCGGGGG GCGTCCCGCG 180
 CGGTGCGGGG CGGTGCGCGG GGGCCGCGAG AGGATGTAGA TGAATGTGCC CAAGGGCTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTGAGA ACACACCCAC CTCTACCAAG TGCTCCTGCA 300
 AGCCTGGCTA CCAAGGGGAA GGCAGGCAAT GTGAGGACAT CGATGAATGT GGAAATGAGC 360
 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420
 25 TTGATGGCTT CATGTTGGCT CATGAAGGTC ATAATTGTCT TGATGTGGAC GAGTGCTGCG 480
 AGAACAAATG CGGCTGCCAG CATACCTGTG TCAACGTCTAT GGGGAGCTAT GAGTGCTGCT 540
 GCAAGGAGGG GTTTTTCTTG AGTGACAATC AGCACACCTG CATTCAACGC TCGGAAGAGG 600
 GCGTGAAGCT CATGAATAAG GATCACGGCT GTAGTCACAT CTGCAAGGAG GCGCAAGG 660
 GCAGCGTCCG CTGTGAGTGC AGGCTGTGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
 30 TCTTGACCTG TAACCATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 GCCCAGATG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
 AGCGAGAGGA CACTGTCTTG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
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 GTGATCATTT CTGCAAAAAC ATCGTGCGCA GTTTTGACTG CGGCTGCAAG AAAGGATTTA 1140
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 75 TTGGTCAAGC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTACTCTCC TCAAGGAGTC 3420
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 CAGAGGGGGA GGAAGGAGA CCGCTGCAGG CTCCCTCCAC CCACCTTGAG ACCTGGGAGG 3600
 ACTCAGTTTC TCCACAGCCT TCTCCAGCCT GTGTGATACA AGTTTGATCC CAGGAACCTG 3660
 80 AGTTCTAAGC AGTGTCTGTG AAAAAAATAA GCAGAAAGAA TTAGAAATAA ATAAAACTA 3720
 AGCACTCTG GAGACAT

Al69 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399

Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442] CUB_domain [809-918]
 Cellular Localization: may be secreted

10 1 11 21 31 41 51
 MGAVAGNRNPG AANAVLLLLL LLPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
 LQONTPTSYK CSCKPGVQGE GRQCEDIDEC GNELNGGCVH DCLNIPGNVR CTCFDGFMILA 120
 HDGHNCLDLD ECLENNNGCCQ HTCVNVMGSY ECCCCKEGFFL SDNQHTCIHR SEBGLSCMNK 180
 15 DHGCSHICKE APRGSVACEK RPFGLAKNQ RDCILTCNHG NGGQCHSCOD TADGPECSCH 240
 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVRKR LLMETCAVNN GGCDRTCKDT 300
 STGVHSCFPV GFTLQLDGKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360
 SQQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCGQVCVN 420
 TVGSYECQCH PQYKLHWNKK DCEVKGLLP TSVSPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 SSDVTITRTS VTFKLNEGKC SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGKQV 540
 20 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEIKRLRAIR TLRKAVHREQ 600
 PHLQLSCMNL DVAKKPPRPS ERQAESCGVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660
 TFQNESEGQMT CEPFPRPQNS GALKTFEAWN MSECGLCQP GEYSADGFAP CQLCALGTFO 720
 PEAGRTSCFP CGGLATKHQ GATSPQDCET RVQCSFGHFY NTTTHRCIRC FVGTYQPEFG 780
 25 KNCVSCPGN ITTDFDGSIN ITQCKNRRCG GELGDPGTGYI ESPNYPGNYP ANTECTWTIN 840
 PPPKRRLLIV VPEIFLPIED DCGDYLVMRK TSSSNVTTY ETCQTYERPI APTSRSKKLW 900
 IQFKSNBEGNS ARGFOVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILDO KKLIALFDV 960
 LAHPQNYPKY TAQESREMPF RSPFIRLLRSK VSRFLRPYK

30 A170 DNA sequence
 Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Nucleic Acid Accession #: AF007170
 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

35 1 11 21 31 41 51
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 40 AGCTACCTCA AGCCAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
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 45 GAGGTCTGCT ATGCAGAGTG CCTGCTGAGC CAGCAGAGCC TGACCTTCTC GCAGGACGAG 420
 AACATGGTGA GCTTCATCAA AGGCGGCATC AAGTTCGAA ACAGCTACCA GACCTACAG 480
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 70 TGTATCCGTG CAGAAGCCGA GCTGGCATT TCAACAGTGT AGCCAAAGGC CTTTGCCAAG 1920
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 TATCATCTGG AGGTAAATCT CTTTATATGA TGATGCCAAA GGGCAAAATG CTTTTCAAAT 2160
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 CATTGTCTTA CTGACAGCAT TTTTGTATA ACTGTTATTC TTGAAAAA AAAAAA 2640
 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Protein Accession #: AAC39582
 Signal sequence: none
 Transmembrane domains: 210-226
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 10 MTALDLPLTN QFSEALSVLK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMKEA 60
 QMLCQRHRRK SSVTDSFSSL VNRPTLGQFT EEBIHAEVCY AECLLQRAAL TFLQDENMVS 120
 PIKGGIKVRN SYQTYKELDS LVQSSQYCRG ENHPHFEGGV KLGVGAPNLT LSMPLTRILR 180
 15 LLEPVGFSGN KDYGLQLLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLTG NVNIEEAEKL 240
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFECCCE AQQHWKQPHH MCYWEIWMCF 300
 TYKGGWKMYS FYADLLSKEN CWSKATYIYM KAAVLSMFGK EDHKFPGDDE VELFRAVPGL 360
 KLKIAGKSLP TEKFAIRKSR RYFSSNPISL FVPALEMMYI WNGYAVIGKQ PKLTDGILEI 420
 20 ITKAEEMLEK GPENYSYVDD ECLVKLLKGL CLKYLGRVQE ABENFRSISA NEKKIKYDHY 480
 LTPNALLELA LLLMEQDRNE EAIKLLSEAK QNYKNYSMES RTHFRIQAT LQAKSSLENS 540
 SRSMVSSYSL

A172 DNA sequence

Gene name: EST
 Unigene number: Hs.200102
 Probeset Accession #: AL117406
 Nucleic Acid Accession #: none found
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 35 ATGACTAGGA AGAGGACATA CTGGGTGCC AACTCTTCTG GTGGCCTCGT GAATCGTGGC 60
 ATCGACATAG GCGATGACAT GGTTTCAGGA CTTATTATATA AAACCTATAC TCTCCAAGAT 120
 GGCCCTCGGA GTGAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCCCAACG 180
 TGGGGGAAGT ATGATGCTGC CTTGAGAAC ATGATCCCT TCGTCCCAA GCGAGGTTT 240
 CCGTCCCCC AGCCCTTGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC 300
 ACCCGCTCA TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACACCAT CCGTCCACTG 360
 TCAGTCCATG ATGCTCTAGA CAAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA 420
 40 GTCTCAAGGC GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA 480
 ACAAGGTGGA TTTTGGATGC ACTTCTGGGC ATCTGCTTCT GCATTGCCAG TGTACTCGGG 540
 CCAATATTGA TTATACCAA GATCCTGGAA TATTGAGAAG AGCAGTGGG GAATGTTGTC 600
 CATGGAGTGG GACTCTGCTT TGCCCTTTT CTCTCCGAAT GTGTGAAGTC TCTGAGTTTC 660
 TCCTCCAGTT GGAATCATCA CCAACGCACA GCCATCAGT TCCGAGCAGC GTTTCTCTCC 720
 45 TTTGCTTTG AGAAGCTCAT CCAATTAAAG TCTGTAAATC ACATCACCTC AGGAGAGGCC 780
 ATCAGCTTCT TCACCGGTGA TGTAACATAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA 840
 GTACTGATCA CTTGCGCATC GCTGGTCATC TGCAGCAATT CTTCCTACTT CATTATTGGA 900
 TACACTGCAT TTATTGCCAT CTTATGCTAT CTCTCGGTTT TCCCATCGGC GGTATTTCATG 960
 50 ACAAGAATGG CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA CGCATCCGT 1020
 GTGACCAATG AAGTCTCTAC TTGCATTAAG CTGATTAAAA TGTACACATG GGAGAAACCA 1080
 TTTGCAAAAA TCATTGAAGG TATGGAAGT CTGACTTTCT GCTCCAAACC TGGTGATGGC 1140
 ATGGCCTTCA GCATGCTGGC CTCTTGAAT CTCTTGGGC TGTGAGTGT CTTTGTGCCT 1200
 ATTGCAGTCA AAGGTCTCAC GAATTCCAAG TCTGCAGTGA TGAGGTTCAA GAAGTTTTC 1260
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 55 TTTGAGGAGG CCACCTGTGC ATGGCAACAG ACCTGTCCCG GGATCGTCAA TGGGGCACTG 1380
 GAGCTGGAGA GGAACGGGCA TGCTTCTGAG GGGATGACCA GGCTAGAGA TGCCCTCGGG 1440
 CCAGAGGAAG AAGGGAACAG CCTGGGCCCA GAGTTGCACA AGATCAACTT GGTGGTGTCC 1500
 AAGGGAGTGA TGTAGGGGT CTGCGGCAAC ACGGGGAGTG GTAAGAGCAG CCGTGTGTCA 1560
 60 GCCATCCTGG AGGAGATGCA CTTGCTCGAG GCTCTGGTGG GGGTGCAGGG AAGCTTGACC 1620
 TATGTCCCCC AGCAGGCTTG GATCGTCAG GGGAAACAT GGGAGAACAT CCTCATGGGA 1680
 GGCGCATATG ACAAGGCCCG ATACCTCCAG GTGCTCCACT GCTGCTCCCT GAATCGGGAC 1740
 CTGGAACCTC TGCCCTTTTG AGACATGACA GAGATTGGAG AGCGGGGCTT CAACCTCTCT 1800
 GGGGGGCGAG AACAGAGGAT CAGCCTGGCC CGCGCCGTCT ATTCGACCG TCAAGTCTAC 1860
 CTGCTGGACG ACCCCCTGTC TGCTGTGGAC GCGCCAGTGG GGAAGCACAT TTTTGAAGAG 1920
 65 TGCAATTAAGA AGACACTCAG GGGGAAGACG GTGCTCTGG TGACCCACCA GCTGCAGTAC 1980
 TTAGAATTTT TGGGCCAGAT CATTTTGTG GAAAAATGGGA AAATCTGTGA AAATGGAACT 2040
 CACAGTGAAT TAATGCAGAA AAAGGGGAAA TATGCCCAAC TTATCCAGAA GATGCACAAG 2100
 GAAGCCACTT CGGACATGTT GCAGGACACA GCAGAGATAG CAGAGAAGCC AAAGGTAGAA 2160
 70 AGTCAGGCTC TGGCCACCTC CTTGGAAGAG TCTCTCAACG GAAATGCTGT GCGGAGCAT 2220
 CAGCTCACAC AGGAGGAGGA GATGGAAGAA GGCTCCTTGA GTTGGAGGGT CTACCCACAC 2280
 TACATCCAGG CAGCTGAGG TTACATGGTC TCTTGCAATA TTTTCTTCTT CGTGGTCTGT 2340
 ATCGTCTTCT TAACGATCTT CAGCTTCTGG TGGCTGAGCT ACTGTTTGA GCAGGGCTCG 2400
 GGGACCAATA GCAGCGGAGA GAGCAATGGA ACCATGGCAG ACCTGGGCAA CATTCAGAG 2460
 75 AATCCTCAAC TGTCTTCTA CCAGCTGGTG TAAGGGCTCA ACGGCTGCT CCTCATCTGT 2520
 GTGGGGGTCT GCTCTCAGG GATTTTCACC AAAGTCAAGA GGAAGGCATC CAGCGCCCTG 2580
 CACACACAGC TCTTCAACAA GGTTTTCCGC TGCCCCATGA GTTCTTTTGA CACCATCCCA 2640
 ATAGGCCGGC TTTTGAACCT CTTGCGAGGG GACTTGAAC AGCTGGACCA GCTCTTGGCC 2700
 ATCTTTTACG AGCAGTTCCT GGTCTGTCC TTAATGTTGA TCGCGTCCCT GTTGATTGTC 2760
 80 AGTGTGCTGT CTGCAATAT CCGTTAATG GGAGCCATAA TCATGGTTAT TTGCTTCATT 2820
 TATTATATGA TGTTCAGAA GGCCATCGGT GTGTTCAAGA GACTGGAGAA CTATAGCCGG 2880
 TCTCCTTTAT TCTCCACAT CCTCAATTCT CTGCAAGGCC TGAGCTCCAT CCATGTCTAT 2940
 GGAAAACTG AAGACTTCAT CAGCCAGTTT AAGAGGCTGA CTGATGCGCA GAATAACTAC 3000
 CTGCTGTGTT TTCTATCTTC CACACGATGG ATGGCATTGA GGCTGGAGAT CATGACCAAC 3060
 CTTGTGACCT TGCTGTTTGC CCGTTCGTG GCTTTTGGCA TTCTCTCCAC CCCCTACTCC 3120

5 TTTAAAGTCA TGGCTGTCAA CATCGTGCTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180
 CGGATTGGCT TGGAGACAGA GGCACAGTTC ACGGCTGTAG AGAGGATACT GCAGTACATG 3240
 AAGATGTGTG TCTCGGAAGC TCCTTTACAC ATGGAAGGCA CAAGTTGTCC CCAGGGGTGG 3300
 CCACAGCATG GGGAAATCAT ATTTACAGGAT TATCAGATGA AATACAGAGA CAACACACCC 3360
 ACCGTGCTTC ACGGCATCAA CCTGACCATC CGCGGCCAAG AAGTGGTGGG CATCGTGGGA 3420
 AGGACGGGCT CTGGGAAGTC CTCTTGGGCT ATGGCTCTCT TCCGCTTGGT GGAGCCCATG 3480
 CGAGGCCGGA TTCTCATTGA CGGCGTGGAC ATTTGCAGCA TCGGCTTGGG GGAATTGGGG 3540
 TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600
 10 CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCCCTTGA GAGGACATTG 3660
 CTGACCAAGG CCATCTCAAA GTTCCCCAAA AAGCTGCATA CAGATGTGGT GGAAAACGGT 3720
 GGAAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGCTGTG GCTTCGCAAC 3780
 TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCTTG 3840
 ATCCAGGSCA CAATCCGTGA AGCCTTCCAG GGCTGCACCG TGCTCGTCAT TGCCCAACCG 3900
 15 GTCACCACTG TGCTGAACCTG TGACCACATC CTGGTTATGG GCAATGGGAA GGTGGTAGAA 3960
 TTTGATCGGC CGGAGGTACT GCGGAAGAGG CCTGGGTGAT TGTTCGCAGC CCTCATGGCC 4020
 ACAGCCACTT CTTCAGTAGG ATAAGGAGAT GTGAGAGACT CATGGAGGCT GGCAGCTGAG 4080
 CTCAGAGGTT CACACAGGTG CAGCTTCGAG GCCACAGTTC TGCGACCTTC TTGTTTGGAG 4140
 ATGAGAACTT CTCTGGAAGG CAGGGGTAAA TGTAGGGGGG GTGGGGATTO CTGGATGGAA 4200
 20 ACCCTGGAAT AGGCTACTTG ATGGCTCTCA AGACCTTAGA ACCCCAGAAC CATCTAAGAC 4260
 ATGGGATTCA GTGATCATGT GGTCTCTCTT TTAACCTACA TGCTGAATAA TTTTATAATA 4320
 AGGTAAAGC TTATAGTTT CTGATCTGTG TTAGAAGTGY TGCAATGCT GTACTGACTT 4380
 TGTAAATAT AAAACTAAGG AAAACTCAAA AAAAAA AAAAAA

A173 Protein sequence

25 Gene name: EST
 Unigene number: Hs.200102
 Probeset Accession #: AL117406
 Protein Accession #: none found
 30 Signal sequence: none found
 Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034
 PFAM domains: ABC transporter [502-673], ABC membrane region [163-432, 771-1060]
 ATP-binding domains [508-516, 1139-1147]
 Cellular Localization: plasma membrane

35
 1 11 21 31 41 51
 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQRNP EAPGRAAVPP 60
 40 WKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLDENTIPPL 120
 SVHDASDKNV QRLHRLWEEE VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICPCIASVLG 180
 FILIIPKILE YSEBQLGNVH HVGGLCFALF LSECVKLSLF SSSWIINQRT AIRFRAAVSS 240
 FAFEKLIQPK SVIHITSGEA ISFFTGDVNY LPEGVVCYGL VLITCASLVI CSISSYFIIG 300
 YTAFIAILCY LLVFPPLAVFM TRMAVKAQHH TSEVSDQRIR VTSEVLTCIK LIKMYTWEKP 360
 45 FAKIIEGMES LTPCSKPGDG MAFSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRFKKFF 420
 LQESVPYVQ TLQDPKALV FEEATLSWQQ TCGIVNGAL ELERNHASE GMTRPRDALG 480
 PEEBGNLGP ELHKINLVVS KGMMLGVCGN TSGSKSLLS AILEEMHLE GSVGVQGS LA 540
 YVPQAMIVS GNIRENIMLG GAYDKARYLQ VLHCCSLNRD LELLFPDGMT EIGERGLNLS 600
 GGQKQRISLA RAVYSDRQIY LLDDPLSAVD AHVGKHIPEE CIKKTLLRGT VVLVTHQLQY 660
 50 LEFCQIILL ENGKICRNGT HSELMQKKGK YALQIQMHK EATSDMLQDT AKIAEKPKVE 720
 SQALATSEEE SLNGNAVPEH QLTQEEEMEE GSLSWRVYHH YIQAGGYMV SCIIFFVVL 780
 IVFLTIFSEW WLSYWNLEQGS GTNSSRESNG TMADLGNID NPQLSFYQLV YGLNALLLIC 840
 VGVCSGSGFT KVRKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP 900
 IFSEQLVLVS LMVIAVLLIV SVLSPYILIM GAIMVICFI YMMFKKAIG VFKRLNYSR 960
 55 SPLFSHILNS LQGLSSIHVY GKTEFISQF KRLTDAQNNY LLLFLSSTRW MALRLBIMTN 1020
 LVTALAVALFV AFGISSTPYS FKVMAVNIVL QLABSFQATA RIGLETEAQF TAVERILQYM 1080
 KMCVSEAPLH MBGTSCPGWG PQHGBIIPQD YHMKYRENTF TVLHGINTLI RGEVVGIVG 1140
 RTGSGKSLSG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRPN 1200
 60 LDPPDRHTDQ QIWDALERTF LTKAISKFPK KLHTDVVENG GNFSVGERQL LCIAARAVLRN 1260
 SKIILIDEAT ASDIMBTDL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNGKVVE 1320
 FDRPEVLRKK PGSLFAALMA TATSSLR

A174 DNA sequence

65 Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 ATGCTGTCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCGAG 120
 75 GACCCGGAGA GCGAGAGCCG GCGGAGGCT GCGGCGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCGCCGCT GGATCCGCGC CCACAGCAGG 240
 CGCGGCGCGC CGCAGCTCCG GCGACTGCGG CTGGGGGCGC GCAGGACCTT 300
 CGCTTGGCTC CTGACGTTTC CCGGGGAGG GTCCGGTTGC CAGTGAAACC TCCAGAGGCT 360
 TCGGAGCAGC AGCCCGGGGG GCCTTCTGAC TGATCCCGGA GATTTCATC AGCGAGTGCA 420
 80 ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 GCTCTGAGAC CTAGGGCCCG GCGTCTGCGC CTCTGGGCGC TCGGCGCAGA GGGGAGTGGC 540
 CGCGCGGAAA AGGCGCGCGG GACAGTCAGT GACGAGGCCG GGGGGTTCGC GGGGCCACGA 600
 CTCTCTGAGG ACCGTCTGCG GCTCTCTGGA GACGCGCTGT CCGCGCCAGG GGTGGTGCCA 660
 TGTGGGGCGC TCGCGCTGCG TCGCTCTCCT CATCTGTGAA CGCGCTTTCG CTCTCTGAGC 720
 TGCTGCTGCG TGGCTGTGCT GCGGCGGGGG CGAGGGCCCA GCGGCGAGTA CTGCCACGGC 780

5 TGGCTGGACG CGCAGGGCGT CTGGGCGATC GGCTTCCAGT GTCCCGAGCG CTTCGACGGC 840
 GGGGACGGCA CCATCTGCTG CGGCGAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCCTGG ACCAGGGCGG CTGGGACAAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CGGGCGGACA AAGACGGGCC CCGACGGCTC GGCAGGGCTT CATGTCTTAG GGGTACCCAA 1020
 GGAGACGGCG AGGGTGCGCC CCCACCCGTG AGGGCGCTGG AGCGGTGCTC CCCTGAAGGC 1080
 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCGGGGC TGCTGCCCG TGCCAGAGCG 1140
 GCGGATTTC CATCTTCTCC ACGCGCGCGC CCCTCTCCCC TGCAGCGCGC GCGCTTGCCC 1200
 ATCTACGTGC CGTTCTCAT TGTGGCTCC GTGTTTGTG CCTTTATCAT CTGGGGTCC 1260
 CTGGTGGCAG CCGTGTGCTG CAGATGTCTC CGGCTAAGC AGGATCCCCA GCAGAGCCGA 1320
 GCGCCAGGGG GTAAACGCTT GATGGAGACC ATCCCATGA TCCCGAGTGC CAGCAGCTCC 1380
 CGGGGTCGT CTCAAGCCA GTCCAGACA GCTGCCAGT CCAGCTCCAG CGCCAACTCC 1440
 GGGGCGCGG CGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTGCCGA AGGGACCATG 1500
 AACAACTGT ATGTCAACAT GCCCACGAAT TTCTCTGTG TGAACGTCA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGTA CAGGTGCGAG 1620
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCCTGGCTAC 1680
 AGGCAGTCT CCTCAACC AACAGTGAAC AGAAGATGA OCCAGCGTG 1740
 ACTGTATAAC CAGAGTAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTG GTGTTATTTA TGGCAGATT CTTTGGATG 1860
 GCTTCACTG CCCCAGACT GTATGAAAC ATCTCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGT ATCATGATT TATGATGAA AACCGGCTC AGCTGGAGAT GACTGTGATG 1980
 TGTCTGATG CTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA GGTGAGCA 2040
 AAGAATTTTA TAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100
 TTGTTGTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
 25 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGTCTG TTGCCAGGC TGGAGTGCG 2220
 TGGTGGCATC TGGGCTCACT GCAACTTCAG CCTCTGGAT TCAGGCAACA CTCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCAT GGCTAATTTT TTGTTATTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCTGA CCTCAAGCAA 2400
 TCTGCTGTG TCAGCTCCC AAGTGTCTGG GATTACAGGC GTGAGCCACC GCGCCAGCC 2460
 30 TGAGCCTTTT TTGTTTCTA ATGCATCCAA GGTAAAGGG AAGACGAAA TAACAGGACT 2520
 ATTCTAAAG GAAACCTGTT TGAACCTGT GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
 GGCACACTT AATTTCATTG TAAAAAGATA TATATATTT GTCTATTTT TGCTTTTGG 2640
 GGGCCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TAAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
 35 TGGGATGAT TGAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAAT CATCCCCTC 2820
 TTGATTGAT CTAAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAAATG CATTCTTTT 2880
 TATATTGAAA TCAATTAATA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCTTG 2940
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 GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCCA GATCTGATAA 3060
 40 AAAAAATTT TTGCTTAGT TATAAAATTT CAAAGAAATG TGTTACAAAG ATACTTAGTA 3120
 TAGCTCCTCA GCCATAAACC GAGACTTGGG ATGAAATTTA AACAGATAC GATTTACTTT 3180
 GCAGATCATA AGGCTTTTTA TACTCTGTT ATCAAAATGG CTTATTTTC AGGCACTAAG 3240
 GATTGTTAAG AGAAAAGCTT TTCAACGAAG GATTGCTTTT CTCTCCAC ACTGTTCTG 3300
 ATTTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATG TCCAATTTAT 3360
 45 CAAATTCAG TGAATTTATT TGTGTTTCT TACTTATAT AAAAAAGAT AACTTTAAGG 3420
 ATGTGCAAGT ACATTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTAA ACAAATCGCT 3480
 GTATGGTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTTCTATT 3540
 TGTTCATGA CTGAATAATG TAAACACAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTTTAATA ACCAAGGCA GGGGAAAAATC ATTTTACTTA TTAATAATA TTTTATGATG 3660
 TGAATAAAAA AAAAAAATA AAAAAAATA

A175 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

1 11 21 31 41 51
 | | | | |
 MLSGFLMSPS TQHRAQYTPG GKPLPWEASI GAHTSRGRGS DRERESRPEA AGLLMDRAAA 60
 GEAEGNRGE PPWIRAOQQ PRPPAGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPFA 120
 65 SGRQPRGSD CIPRFPASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180
 PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAVRVVP CGALAAARPSF HPGTFLRSCS 240
 CCLWRCWRG RGPSEYCHG WLDAQGVWRI GFQCPERFDG GDATICGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTO GDGEGAPPV RAWQRCSPEG 360
 70 SPKGRQLLRA FPGLLPRARR RGFPSRFRGG PSPLQRPALF IYVFLIVGS VFVAFIILGS 420
 LVAAACCCRL RPKQDPQQR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480
 GARAPPTRSQ TNCCLEPGTM MNVIVNMPTN PSLVNCQQAT QIVPHQGYL HPFYVGYTVQ 540
 HDSVPMATVP FFMGLQPGY RQIQSPFPHT NSEQMYPVAV TV

A176 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60

5 CTGAAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAAGGTTT GGAGATGATG 120
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 CTGGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTGG GAGAGCTGCT GGCTGCAGCC 240
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 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTTCATGC TGAAGGAGCA GAACCGACTC 360
 CTCACCCAGG AGGTGACCGA GAAGAGTGAO GCATCAACGC AGCTGGAGCA GGAGAAGTCG 420
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCCCTGAGCC AGCAGGACGG GGGACCTCTG 480
 10 GATTCCACCT TCATCTAGTC CTGTGGGCC CGGTGGGCC CCAGGCCAG CCTGGCACTC 540
 AGCCCTTCGA GGGTGGGGCC CCATCGCAC CCACCTCTC TGGCTGGAGA CCCCAGGAG 600
 GCGCAGGCAC AGTCCCGGAG TGGGCGCTT CTGCGGCC TTGCCAGATG GGCTCCCGAG 660
 GGCTGCCCCC GGCTGGTCCC CGCACCGAGC GCTTGACTCC GTTGTGGCTC CTGGTTGTYG 720
 ACATGGGCTG GGGCTCTCTC TGAGTCCGCA TAGTCCGAG CTACTACTGG CCGCTGTCAG 780
 15 TGAACAGTGG GGTACCCCTC CATGAGTTAG CGTCCGCCG TTTCAGCGG TGCCGCGCTG 840
 GGTCCCATCT TCAGGAAAGC GCAGTCCCA CGCCAGGCTG CACTTCCAC AACGGGCAGC 900
 AGAGGGCGCG TGGCGGCTCC GAOCGGGTC CAAGGGCAGC TTCCGCTCA ACCAGGGCAC 960
 CAGGACGAGG TGGCTGTAGC TCGGACGAGC GGAAGTAGAT GAGGGGGGTG GGGACGGCCT 1020
 GTAAGCGGGG GGTGCTCTCC TGGCTGGGGA GCCCAGGGA TAGCGGTGCG ACTTCAGGTT 1080
 20 CTGGCCAAAG CTGGCTGAGC CTGGCTGAGC CGGATCGCA CGCCGGGTG GCGAGAGCTT 1140
 GGCTGTCATG TGCCCTCCAC AGACCTCGGG GTGATGGCTT TCCCTCTCTT GCGCGGGAAG 1200
 TTGCCCAAGC TTGAGTCCCA CACAACATCC TGTGAGCCTG GCTCCCGAG AGGGCCCCCA 1260
 GACAGCTCCC AGGCAACGTC TAGGCAAGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1320
 CTGGGGTCTT GCTCACCCCC CTGTGCTCTC ACGCCAGCC TGTCCTCCAGG TTTCACTGAG 1380
 25 GAGAGGGCCG CTGCTCCAGC CAAGGAAAC GAGAACCCCG AGGGTACAGG AGGAGGCTGG 1440
 GGCAGGTCCC CTGGGTGTC ACTCCCTCAG CCGCTGCCCA GCGCCACTCC CGCTGGTGTCT 1500
 GGAGTAGGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GAGGGGTCCC AGTGTCAACA 1560
 GAACAGGGGG CACGCAACA GCATCGATGG GTTCTGCAGC CCAGGGCCCC CAGTGGCGGG 1620
 TCAGTGTGTG TGGGGCGCAG GGCTCCGATG GCGGGGTGAG TGCGTGGGGG GCGCAGGGCC 1680
 30 CCGATGCTGG GGTGCTGGG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACCTTTGGT 1740
 ACACGTGCTCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAATCT 1800
 CCTTCCGAGG CCGCAGTCCA TGCTAACCTG CCAACAGCAA CCCCAGAGC ACACATTTCC 1860
 TGCTGCACCT GGTCTGCAGG GGTGTCCAG GACAGGCCCA AGTCAGCCCA GCATGCAGCT 1920
 GCGCTTCCTAC CTGGAAGATG GAGTGGGCTT TTCCAGGGGA CATAAGGATG TCAGGCCTGG 1980
 35 ACCTCTCTGG CAGGAAAGGG TGCAAGTCTT GAGGGCCTGT GCGCCACAGC CCCAGCACCC 2040
 AGGTGGAAGT CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GAGAGAGCCC CCGCTCAGCA 2100
 GGCTGGGGTC TGCCCAACCA GCGCTCCCA CGTCTGCTT TGAGGGTGGC TGCCATGCC 2160
 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCG 2220
 GGTGACTTCA TCAGGAGACC GCCCAGATAG AGCTGAGACC CGCAGCTGAA GCGGAAATGT 2280
 40 GAGACAGGCT CAGCACTCCG GAAAACTGC CTTTCAGCCT TGGTGTTCG TGCAAGGTGA 2340
 AAAGAAATAG GTCTCCAGC TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2400
 GCAGAGGGGA GAATTTAAAG GCGCCGCTG GCAAGGCTTA GGTGGCTGCG AGAGGCACAT 2460
 GCAGACCCCTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAAGATGT 2520
 GAGCAGCGTC CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACAGCT 2580
 45 CGGTGCACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAAATGT TCCTTGGGGG 2640
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 TTTTGTGTTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCTGG TGGTTACGC 2760
 CTGGAATCCC AGCAGTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2820
 CCCCATTCTT ACARAAAAA AAAAGAAAG AAAAGAAATG AGAGATCCAG GTTTAAAAAT 2880
 50 TCATAAAGCA CACAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 2940
 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3000
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA 3060

A177 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51
 | | | | |
 GCGGAACACC GCGCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCTCTGTGG ACCTCTCGCG TCTCTCTCTC TTCTCCAGGT TTGCTGGCTG CAGTGGCGCG 120
 CCTCGAGACC GTGCGGGGGG GTCTTCAGGG AGGCTGAAAT GACCTTGGAG GCGGGAGGCG 180
 65 CGGAGCAGGA GCGCGGCCAG GCGCTGGGGA AAGTATTCAI GGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCATCTGTGG GAATGGCGAG ACAGTCCAGG 300
 AAAGAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCGATCCAAA GGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCGTGAATAA GGCAGGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 70 ACAGCATCAC GGGCGCGGGG GCAGACAGCC CCGCTGAGGG TGTCTTCTCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGACCGGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGTGTGTGTA GAGAATGGTG CCTCAGTGGG GACCCCATG AACATCTCCA 660
 TCATCGTGAC CGACAGGAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
 GTGTCTTAGA GGGAGTCCCT CAGGTACTCT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 75 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAC 840
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGCCT GAGCCGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 80 ACRATGCTCA CATGTTTGAC CCCCAGAAAT ACAGGGCCCA TGTGCTGAG AATGCACTGG 1080
 GCCATGAGGT CGAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCACCTCA CCAGGTGGC 1140
 GTGCCACCTA CCTTATCATG GCGGTGACG ACCGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CAGGGGCATC CTGACACCA GGAAGGGTTT GGATTTTGGG GCCAAAAACC 1260
 AGCACACCCCT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
 CCACAGCCAC CATATGGTCT CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380

5 CCTCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAAG CCTTGACAAG GAGAATCAAA AGATCAGCTA CGCATCCTGT AGAGACCCAG 1500
 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTGACCC 1560
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCCACCACT GGCAAGGGAA CCTTCTGTCT AACACTGATT GATGTCAAAG 1680
 ACCATGGCCC AGTCCCTGAG CCCCCTCAGA TCACCATCTG CAACCAAGGC CCTGTGCGCC 1740
 AGTGTCTGAA CATCAGCGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCCGAC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 10 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTTT TCTCTGTCTG 1920
 ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGAAAC CTGCCCTGGA CCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTCTCTC CTGCTGGTGC TGCTTTTGTG GTGAGAAAG AAGCGGAAGA 2100
 TCAGGAGGCC CCTCTACTCT CAGAAGATG ACACCCGTGA CAACGCTCTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 15 AGGCCAGGCC GGAGGTGGTT CTCGCCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TCGACTATG 2400
 AGGGCAGCGG CTCGACGCGC GGTCTCCCTGA GCTCCCTCAC CTCTCCGCGC TCCGACCAAG 2460
 20 ACCAAGATTA CGATTATCTG AOCAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GGAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTGAGGC 2580
 CACAGAGCAT CTCGACGGG TCTCAGTTCC CCTTCAGCT GAGGACTTCG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GCGGAGACA GGTATGAGT CTGACGTTAG AGTGGTGTCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTACG TTCAGCACTG AAAACCTCTC 2760
 CACCTGGGCG AGGCTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAATA 2820
 25 TGCTCAACCC TGAGTCTCTG GCCTGGGCGT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCTGGT GCAACTTAAT TTTTTTTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCGAGA GCTGCTGGGC CCACTGGCGG 3000
 TCCTGCATTT CTGCTTCCA GACCCCAATG CCTCCATTG GGATGGATCT CTGCGTTTTT 3060
 30 ATACTAGTG TGCTAGGTT GCCCCTTATT TTTTATTTTC CCGTGTGGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAATTTTT TATTAAAGAA A

A178 Protein sequence:

35 Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675
 40 Cellular localization: plasma membrane

45 1 11 21 31 41 51
 MGLPRGFLAS LLLLVQCWLQ CAASEPCRAV FREAEVTLA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DFTVVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGPPFQRLNQ LKSNKORDTK IPYSITGPQA DSPPEGVFAV EKETGWLLIN KPLDREEIAK 180
 YELFGHAYSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVAT 240
 50 DEDDAIITYN GVVAYSISHS EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TMDGDGSGTT TAVAVVEILD ANDNAPMFDP QKYBAHVPEV AVGHEVQRLT VTDLDAPNSP 360
 ANRATYILMG GDDGDHPTIT THPESNQIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTEGPEVC VYTAEDPKKE NQKISYRILR 480
 DPAGWLAMP DSGQVAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLD 540
 55 VNDHGFPVEP RQITICNQSP VRHVLNITDK DLSPTSPFPQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDHLIS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGFPILPVL 660
 GAVLALLFLL LVLLLVRKK RKIKEPLLLP EDDTRDNVFP YGEGGGGEDD QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNPIIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSITSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD

A179 DNA SEQUENCE

60 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 65 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 CTTCTTTAAA TTCTTTTCTA GGATGTTTCA TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
 GGAACAAAGC TTGTGATTGT TTGTGTGTGT GGGACGTTTT TCTGCCTGTT TAITTTTTTT 180
 TCTAATTTCTC TGTCATATGC GCAGTGATC AAAAAACAGAA AATTTCATTT CCCCCTCTAC 240
 75 TACCTGTTGG CTAATTTAGC TGCTGCGCAT TTCTTGTCTG GAATTCGCTA TGTATTCTTG 300
 ATGTTTAACA CAGGCCCACT TTCAAAAATC TTGACTGTCA ACCGCTGGTT TCTCCGTCTG 360
 GGGCTTCTGG ACAGTAGTCT GACTGCTTCC CTCAOAACT TGCTGGTTAT GCGCGTGGAG 420
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGTTGACA 480
 CTGCTCATTT TGCTGTCTG GGCATCGGCC ATTTTATATG GGGGGTCCCC CACACTGGGC 540
 80 TGAATTTGCC TCTGCAACAT CTCTGCTGTC TCTTCCCTGG CCCCATTATA CAGCAGGAGT 600
 TACCTTGTGT TCTGACAGT GTCCAACTCT ATGGCCTTCC TCATCATGGT TGTGGTGTAC 660
 CTGCGGACTC ACGTGTACT CAAGAGGAAA ACCAAGCTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC GCGGAGGAG ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

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CGCTTTGTGG TATGCTGGAC CCGGGGCTG GTGGTTCTGC TCCTGACGG CTTGAAGTGC 840
 AGGCAGTGTG GCGTGACGCA TGTGAAAGG TGGTTCCTGC TGCTGGGCT GCTCAACTCC 900
 GTCGTGAACC CCATCATCTA CTCTACAGG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTCGCAT CCGCTCCACA 1020
 GTCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080
 GTCTGCAATA AAAGCACTTC CTAAGCTCTG GATGCTCTC GCGCCACCCA GGTGATGACT 1140
 GTCTTAGG

A180 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 Protein Accession #: NP_036284
 Signal sequence: none found
 Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MNECHYDKHM DFFYNRSNTD TVDDWTGTKL VIIVLCVGTFF CLPIPPSNLSL VIAAVIKNRK 60
 FHPPFYLLA NLAAADFFAG IAYVFLMNT GPVSKTLTVN RWFLRQGLLD SSLTASLTNL 120
 LVIIVERHMS IMRMVHSNL TKKRVTLIL LVWAIAPMG AVPTLGNL CNISACSSLA 180
 PIYSRSLVLF WTSNLMAPL IMVVVLYRIY VYVKRKTIVL SPHTSGSISR RRTPMKLMRT 240
 VMTVLGAFV CHTPLGVLL LDGLNCRQCG VQHVKKRWLL LALLNSVVP IYYSKDEDM 300
 YGTMGIMIC PSQENPERR SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

A181 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.162859
 Probeset Accession #: AA569531
 Nucleic Acid Accession #: AA569531
 Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGACCTACA GTTACTCATT TTTCAGGCCT GAGTTGATCG TTAATCATCT TAATTATGTT 60
 CATTCTGAAG CCAACAGGAG AACCAAGACC AAAACTTTAT TGCTCTGCT TTCAATTCTT 120
 GATGAAACCT CTGGACTAAG CACACATCTT CCTTGTTTAT CTCTCTCAA GGAGTGTGGA 180
 GTGCTTCATC TGGACATCCA CGGGAAGAAG GAAGACATGA GAATCACCCA ACAGTCTTCC 240
 CAGCTATACC TGTGGGACAT GGGTGGTTTT ACAATATTTA AGAAGCTGTG GATGAGCCTC 300
 ATACCCAGAG GGAACAAACG CTCCCCAAA AGAGTTACAG AACCATCTCT GAGAGATTTT 360
 AAGCAGAAGC AAAGTTCAA GATCCAAGAG GAGAGACGAA GAGAGTCTGC AGGACCAAAC 420
 CTCTCTTCAT TCTGGTTTGT GGGGAATGCT GGAAGAGGAG ACAGGCCCCA GATTGGGGCA 480
 GGAAGTAAAC AGTTTTCAGG CTGAGGCCAA TCTGAGCAGG AACATTCCAA TATTCTTCA 540
 GCTACGTTGT CCCAGCACTT CACTGGTTAA CCTTTTATGT CCACCATTTG TGGATTTCAC 600
 AGCTACTTGT CAATGGTGAA TATTGATCAT CATCATTTAT TACTGAGCTG CTACCATATC 660
 CCAGCTACTC CTGTGATGTT GTTCATTATT TTCTCAACAC TCAGCATATT TGCAATATGT 720
 TATGTAATAT CACAGACAAG GAACTGAAC GCAGAAATGT TTTATTCTT GCCAACATC 780
 ACATAGGAT GAACATGAAC ACGATTGGA AACCAAGATT GTCGATTCC AACATCTCTG 840
 GGTCTTTTTT CACTCTGATA TGCTGCAATT AAAAAGCCAT TTCTAAGACT GT

A182 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.162859
 Probeset Accession #: AA569531
 Protein Accession #: none found
 Signal sequence: 1-46
 Transmembrane domains: none found
 Cellular Localization: not determined

1 11 21 31 41 51
 MTYSYSPFRP ELIVNHLNMYV HSEANRRTKT KTLSSLSSPL DETSGLSTHL PCLSLSKECG 60
 VLHLDINGKK EDMRITQSS QLYLWDMGGF TIFKNLWMSL IPRGNKRSPK RVTETILRDF 120
 KQKQSSKIQE ERRRESAGPN LSSFWFVGNA GRGDRPQIWA GSKQFSG

A183 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.179809
 Probeset Accession #: N95796
 Nucleic Acid Accession #: XM_050197
 Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 TCACACGTGC CAAGGGGCTG GCTCAGCGGA ACCAGCCTGC ACGCGCTGGC TCGGGGTGAC 60
 AGCCGCGCGC CTGGCCAGG ATCTGAGTGA TGAGACGTGT CCCCCTAGAG GTGCCCCACA 120
 GCAGCAGGTG TTGAGCATGG TGGACCGGCA CCAAAGGGCT GGCAGAAATG 180
 GGGCCTTGGC TGATTCTTAG GCAGTTGGCG GCAGCAAGGA GGAGAGGCCG CAGCTTCTGG 240
 AGCAGAGCCG AGACGAAGCA GTTCTGGAGT GCCTGAACGG CCCCCTGAGC CCTACCCGCC 300

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TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCCGCTGC TGGGACACCG GAAAGCCCAG 360
CTCTTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCCG AGGCATCACC 420
TATGTGCCCG CTCTGTGCTT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGTCTG 480
GGCATTTGGT CAGTGTCTGGG CCTGGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACACAC 540
TGGCGTGGAC GCTATGGCCG CCGCCGCGCC TTCACTCTGG CACTGTCTCT GGGCATCTCTG 600
CTGAGCCCTCT TTCTCATCCC AAGGGCCGCG TGGCTAGCAG GGCTGCTGTG CCGGATCCCC 660
AGGCCCTCTG AGCTGGCACT GCTCATCTGT GGCGTGGGGC TGCTGGACTT CTGTGGCCAG 720
GTGTGCTTCA CTCACTGGA GGCCTGTCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780
CGCCAGGCCT ACTCTGTCTA TGCCCTTCATG ATCAGTCTTG GGGCTGCTCT GGGCTACCTC 840
CTGCTGCTCA TTGACTGGGA CACCACTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900
TGCCCTCTTT GCCTGCTCAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGCTGGTG 960
GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAA GGTGTCTGCG CCCCTCTTTG 1020
TGGCCCTCAT GCTGTCCATG CCGGGCCGCG TTGGCTTTCC GGAACCTGGG CGCCCTGCTT 1080
CCCGGCTGTC ACCAGCTGTG CTGCGCATG CCCCACACCC TGGCGCGCT CTCTGTGGCT 1140
GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCAGCTGT TTTACACGGA TTTGTGGGC 1200
GAGGGGGCTG ACCAGGAGT GCCCAGAGCT GAGCCGCGCA CCGAGGCCCG GAGACACTAT 1260
GATGAAGGCG TTGCGATGGG CAGCCTGGGG CTGTTCTCTG AGTGGCCCAT CTCCCTGGTC 1320
TTCTCTCTGG TACATGACGA GCTGGTGCA GATTGCGCA CTGAGCAGT CTATTTGGCC 1380
AGTGTGGCAG CTTTCCCTGT GGTGCGCGT GCCACATGCC TGTCACAG TGTTGGCCGTG 1440
GTGACAGCTT CAGCCGCTCT CACCGGGTTC ACCTTCTCAG CCTGCGAGT CTGCGCTTAC 1500
ACACTTGGCT GCCTGTACCA CCGGAGAAAG CAGGTGTTC TGCCCAATA CCGAGGGGAG 1560
ACTGGAGGTG CTAGCAGTGA GGACAGCCCTG ATGACCAGCT TCCTGCGCAG CCTAAGCCCT 1620
GGAGCTCCCT GCTGTCCATG ACAGTGGGT GCTGGAGCA GTGGCTGTCT CCAACTCCA 1680
CCCGCGCTCT GCGGGCCCTC TGCCCTGTAT GTCTCCGTAC GTGTGGTGT GGTGAGCCCT 1740
ACCGAGGCCA GGTGTGTTC GGGCCGCGCG ATCTGCTGAG ACCTGCGCAT CTGGGATAGT 1800
GCCTTCTCTG TGTCCAGGT GGCCTCATCC CTGTTTATGG GCTCCATTGT CCAGCTCAGC 1860
CAGTCTGTCA CTGCTATAT GGTGTCTGCC GCAGGCTGG GTCTGTGCG CATTACTTT 1920
GCTACACAGG TAGTATTGA CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACTTCC 1980
AGCACATTGG GGTGAGGGC CTGCTCACT GGTCCCAGC TCCCCGCTCC TGTAGCCCC 2040
ATGGGGCTGC CCGGCTGGCC GCCAGTTTCT GTTGTGCTCA AAGTAATGTG GCTCTCTGCT 2100
GCCACCTGT GCTGCTGAGG TGCGTAGCTG CACAGCTGGG GGTGCGGCG TCCTCTCTCT 2160
CTCTCCCGAG TCTTAGGGC TGCGTAGCTG GAGGCTTCC AAGGGGTTT CAGTCTGAGC 2220
TTATACAGG AGGCCAGAA GGCTCCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280
ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTGAGAC ACACCTAGAG AAGGGTTTTT 2340
GGGAGCTGAA TAAACTCAGT CACTGTGTTT CCTACTCTA AGCCCCTTAA CCTGAGCTT 2400
CGTTTAAATG AGCTCTTGA TGGAGTTTC TAGGATGAAA CACTCTCCA TGGGATTGA 2460
ACATATGAAA GTTATTTGTA GGGGAGAGT CCTGAGGGGC AACACACAG AACCCAGTCC 2520
CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCTT CTTTACCTT 2580
TT

Al84 Protein sequence:

45
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Gene name: ESTs
Unigene number: Hs.179809
Probeset Accession #: N95796
Protein Accession #: XP_050197
Signal sequence: none
Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401
Cellular Localization: plasma membrane

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60

1 11 21 31 41 51
| | | | |
MVQLWVSR LHRKAQLLL VNLTFGLEV CLAAGITYVP PLLLEVGVSE KFTMTVLIGI 60
PVLGLVCPVL LGSASDHWRG RYGRRRPFIW ALSIGILLSL FLIPRAGWLA GLICPDPRPL 120
ELALLILGVG LIDFQGVCF TPLEALLSDL FRDPDHCRA YSVYAFMISL GGCLGYLLPA 180
IDWDTSALAP YLGTQEELF GLLTLIPLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240
CCPCRRALAP RNLGALLPRL HQLCCRPRT LRLLFVAELC SNMALMTFTL FYTDFVGEOL 300
YQGVPRAEFG TEARRHYDEG VRM3SLGLFL QCAISLVFSL VMDRLVQRF TRAVYLA5VA 360
APFVAAGATC LSHSVAVVTA SAALTGTFTS ALQILPYTLA SLVHREKQVF LPKYRGDTGG 420
ASSEDSLMTS FLPGPKPGAP FPNGHVAGG SGLLPFPFAL CGASACDVSV RVVVGEPTEA 480
RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSIVQLSQSV TAYMVAAGL GLVAIYPATQ 540
VVFDESLAK YSA

Al85 DNA SEQUENCE

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Gene name: ESTs
Unigene number: Hs.11260
Probeset Accession #: R73640
Nucleic Acid Accession #: AK002126
Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

75
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1 11 21 31 41 51
| | | | |
ATGGTTCCGC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GGTGCTCCTC 60
TGCTGTGCTA TCTCTGTCTT GTACATGTTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG 120
CTGGCACTGC CCAGGCGCAA CAGCCCCACG GGAAGGAGG GGTACCAAGC GTCTCTCAG 180
GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240
AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300
GCTGTCTGCC TGCGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCTGGCC 360
TTCTGTCACT CGCAGGTGGA CAAGGCAGAG GTGAATGCTG GCCTCAAGCT GGCCACAGAG 420
TATGAGCAGC TGCCCTTTCA TAGCTTTACT CTACAGAAAG TGTACCAAGT GGAGACTGGC 480
CTTACCCGCC ACCCCAGAGA GAAGCCTGTG AGGAAGGACA AGCGGATGA GTTGGTGGAA 540
GCCATTGAAT CAGCCTTGGA GACCCTGAAC AATCCTGCAG AGAACAGCCC CAATCACCGT 600

5 CCTTACACGG CCTCTGATT CATAGAAGGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAACGGCT CATCTTATTT 720
 CGACCATTCG GCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780
 ATCAATGTGA TCGTGCTCT AGCAAAAAGG GTGGACAAGT TCCGGCAGTT CATGCAGAAT 840
 TTCAGGGAGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACTGTTGT TTACTTTGGG 900
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTTGAAAACA CTTCCAAAGC TGCCAACTTC 960
 AGGAACTTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT 1020
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTTCCTTTTT TCTGTGATGT GGACATCTAC 1080
 TTCACATCTG AATTCCTCAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140
 TATCCAGTTC TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCAGTC 1200
 CCTCCCTTGG AACAGCAGCT GGTCAATAAG AAGGAAACTG GATTTTGAG AGACTTTGGA 1260
 TTTGGGATGA CGTGTGAGTA TCGGTGAGAC TTCAATCAATA TAGGTGGGTT TGATCTGGAC 1320
 ATCAAAGGCT GGGGCGGAGA GGATGTGCAC CTTTATCGCA AGTATCTCCA CAGCAACCTC 1380
 ATAGTGGTAC GGACGCTGT GCGAGGACTC TTCCACCTCT GGCATGAGAA GCGCTGCATG 1440
 GACGAGCTGA CCCCCAGCA GTACAAGATG TGCATGCAGT CCAAGGCCAT GAAOGAGGCA 1500
 TCCACGGGCC AGCTGGGCAT GCTGGTGTTC AGGCACGAGA TAGAGGCTCA CCTTCGCAAA 1560
 CAGAAACAGA AGACAAGTAG CAAAAAACA TGA

20 A186 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 Protein Accession #: NP_060841
 Signal sequence: 1-26
 Transmembrane domains: none found
 Cellular Localization: not determined

30 1 11 21 31 41 51
 MVRRLGLAWI SRVVVLLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60
 EWEDQHRNVY SSLKRQIAQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTOADLLA 120
 FLHSQVDKAE VNAGVKLATE YAAVPFDSFT LQKVYQLETG LTRHPKEKPV RKDKRDELVE 180
 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF 240
 RPFPGIMKVK NEKLNMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300
 KEEINEVKGI LENTSKAANF RNFTFIQLNG EFSRGKGLDV GARFWKGSNV LFFCDVDIY 360
 FTSEPLNTRC LMTQPGKKVP YPVLPSQYNP GIYGHHDVA PPLEQLLVIK KETGFWRDPG 420
 FGMTQCYRSD FINIGGFDDL IKWGSGEDVH LYRKYLSNLT IIVRTFVRGL FHLWHEKRCM 480
 DELTPEQYKM CMQSKAMNEA SHGQLGMLVF RHEIEAHLRK QKQKTSKKT

40 A187 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 ATGATTCTCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGGAGGCC 120
 TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCAGTTTA AAAATCCOCT TATTATGCTG CTTCTGGCCT CTGCACTCAT CAGTGTTTGA 240
 ATGCATCAGT TGTATGATGC CGTCAGTATC ACTGTGGCAA TACTTATGCT TGTTCAGTGT 300
 GCCTTTGTTT CCAAGATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
 CCAGGTGATA CAGTTTGCTT TTCTGTTGGG GATAGAGTTC CTGCTGACTT ACCTTGTGTT 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAAC GCCTTGTCT 540
 AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAGCAAAAGG GTGTGTGCAT TGGAAACAGA 660
 GAAAAATCTG AATTGGGGGA GGTTTTAAAA ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGTGATA 780
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840
 ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTCAAGTGT 900
 ACGCTAGCTC TTGGTGTAT GAGAATGTTG AAGAAAAGGG CCATTGTGAA AAGCTGCTCT 960
 ATTGTTGAAA CTTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGG AACACTGACG 1020
 AAGAATGAAA TGACTGTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTACT 1080
 GGAGTTGGCT TGAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTCT 1140
 TATAACCCAG CTGTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
 AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAAATGCTCT TGCAATGAAG 1260
 ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
 GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
 TGTTTTATGA AAGGTGCTTA CGAACCAAGTA ATTAAGTACT GTACTACATA CCAAGACAAA 1440
 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500
 ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGAACT GGGACAGCTG 1560
 ACATTCTTGT CTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
 ACAACACTCA TTGCCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTCT ACAGGAGACT 1680
 GCAGTTGCAA TCGCAGTCTG TCTGGGATTG TATTCCAAAA CTTCCAGTCT AGTCTCAGGA 1740
 GAAGAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAA GGTTCAGTA 1800
 TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTGGCTACA GAAGAACGGT 1860
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
 ATTGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
 CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040

5 AATAACATTA AAAATTTGCT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100
 ATCTCATTTG CTACATTAAT GAACCTTCTC AATCTCTCTA ATGCCATGCA GATTTTGTGG 2160
 ATCAATATTA TTATGGATGG ACCCCAGCTC CAGAGCCTTG GAGTAGAACC AGTGATAAAA 2220
 GATGTCTATC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTGATA 2280
 CTTAAATATC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTTG CTCTGGCGGT 2340
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
 TTTTGTGACA TGTTCATGTC ACTAAGTTCC AGATCCCGA CCAAGTCTGT GTTTGAGATT 2460
 GGACTCTGCA GTAATAGAAT GTTTTGTCTAT GCAGTCTCTG GATCCATCAT GGGACAATTA 2520
 10 CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
 GATCTGTGTT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
 CTGAAAGTAT GA

A188 Protein sequence:

15 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Protein Accession #: AAP27813
 20 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

25 1 11 21 31 41 51
 MIPVLTSKKA SELPVSEVAS ILQADLQNGL NKCEVSHERRA PHGWNEFDIS EDEPLWKKYI 60
 SQFKNPLIML LLASAVTSVL MHQPDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP 120
 30 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRFP EAVDLSDIES SLTGSTTPCS 180
 KVTAPPAAT NGDLASRSNI AFMGTILVRG KAKGVVIGTG ENSPEGEVFK MMQAEAPKT 240
 PLQKSMDLIG KQLSPYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPPIVTV 300
 TLALGVMRMV KRAIVKQLE IVETLGCNV ICSDKTGLTL KNEMTVTHIF TSDGLHAEVT 360
 GVGYNQFGEV IVDGDVVHGF YNPAVSRIVE AGCVNDDAVI RNNTLMGKPT EGALIALAMK 420
 35 MGLDGLQDDY IRKAEYPPSS EQKMMAVKCV HRTQQDRPEI CPMKAYEQV IKYCTTYQSK 480
 GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASGPGLQQL TFLGLVGIID PPRTGVKEAV 540
 TLLIASGVS I KMITGDSQST AVAIA SRLGL YSKTSQSVSG EEIDAMDVQV LSQIVPKVAV 600
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMQGTGT DVCKEADAMI 660
 LVDDDPQTIM SAIEEGKGIY NNKNFVRFPQ LSTSI AALTL ISLATLNMFP NPLNAMQILW 720
 40 INIIMDGPPA QSLGVPEVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFW 780
 ELRDNVITPR DTTMTPTCFV PFDMPNALSS RSQTSVFEI GLCSNRMFCY AVLGSIMQQL 840
 LVYIFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSRERIKI KHVSTSSSF 900
 LEV

A189 DNA SEQUENCE

45 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 50 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGACGA GAGGATTGCC TTATTCAATG 60
 AAGCAAGCTG GGTTCCTTTT GGGAAATATT CTTTATTTCT GGGTTTCATA TGTTACAGAC 120
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AAACCTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTT TCAGTTTTTG 240
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGTACTTTT GAGCAAAAGT 300
 60 TTTCAAGAA TCCAGAGAGT TGATCCTGAA AACGTGTTA TTGGTCCGCA CTTCATTATT 360
 GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACOGAAATAT AGCAAAAGCT 420
 GGAAAGGTCT CCTCATCTC TACAGGTTA ACAACTCTGA TTCTTGAAT TGTAAATGGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAAACAGAAG ACGCTTGGGT ATTTGCAAAAG 540
 CCCAATGCCA TTCAAGCGGT CGGGGTTATG TCTTTTGCAT TTATTTGCCA CCATAACTCC 600
 65 TTCTTAGTTT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
 ATGTCCATCG TGATTTCTGT ATTATCTGT ATATTCTTTG CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCAAGG GGACTTATT GAAATTAAT GACAGAAATGA TGACTCGGTA 780
 ACATTGGGAA GATTTTGTTA TGGTGTCACT GTCATTTTGA CATACCTAT GGAATGCTTT 840
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTTCCAC 900
 70 ATTGTTGTAA CAGTGATGGT CATCACTGTA GCCACGCTTG TGTCAATTGC GATTGATTGC 960
 CTGGGATAG TTCTAGAAT CAATGGTGTG CTCGTGTCAA CTCCCTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCCGA TAAGATTATG 1080
 TCTTGTGTCA TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTGCT CATGGCTATT 1140
 ACRAATATCT AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTCC TGACAAATTC 1200
 75 TCTCTACAAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAATTTTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

A190 Protein sequence:

80 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 | | | | |
 MGYQRQSPVI PPQRGLPYSM KQAGFPLGIL LLFWVSIVTD FSLVLLIKGG ALSGTDITYQS 60
 LVNKTQFPFG YLLSLVLQPL YPFIAMISYN IIAGDTLSKV PQRIPGVDP NVPIGRHPFI 120
 GLSTVTFTLP LSLYRNIAKL GKVSLSITGL TTLILGIVMA RAISLGHPIH KTEDAWVPAK 180
 PNAIQAVGVM SPAFICHHNS FLVYSSLEEP TVAKWSRLIH MSIVISVPIC IFPATCGVLT 240
 10 FTGTTQDGLF ENYCRNDDL VTFGRPCYGVV VILTYFMECF VTREVIANVF FGNLSSVFR 300
 IVVTVMVITV ATLVSLLIDC LGIVLELNGV LCATPLIPII PSACYLKLSE EPRTHSDKIM 360
 SCVMLPIGAV VMVFGFVMAI TINTQDCTHQQ EMFYCFDFNF SLTNTSESHV QQTTLQLSTLN 420
 ISIFQLE

A191 DNA SEQUENCE

15 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 25 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CGCCCGCAGT TTTCCTTGT TTTATTGATA 60
 AAAGGAGGGG CCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACTTTCGGC 120
 TTTCAGGGT ATCTGCTCCT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
 AGTTACATA TAATAGCTGG AGATACTTTG AGCAAAGTTT TCAGAGAAAT CCCAGGAGTT 240
 GATCCAGAAA ACGTGTATTAT TGGTCGCCAC TTCAATTATT GACTTTCCAC AGTTACCTTT 300
 30 ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
 ACAGGTTTAA CAACCTCGAT TCTTGGAATT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTGCAAAAGC CCAATGCCAT TCAAGCGGTC 480
 GGGGTTATGT CTTTTCGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
 GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCTCGT GATTTCGTGA 600
 35 TTTATCTGTA TATCTTTGTC TACATGTGGA TACTTGACAT TACTGGCTT CACCCAAGGG 660
 GACTTATTG AAAAATCTG CAGAAATGAT GACCTGGTAA CATTGGAAG ATTTTGTAT 720
 GGTGCTACTG TCATTTTGAC ATACCTATG GAATGCTTTG TGACAAGAGA GGAATTGCC 780
 AATGTGTTTT TTGGTGGGAA TCTTTCATCG GTTTTCACA TTGTTGTAAC AGTGATGGTC 840
 ATCACGTAG CCACGCTTGT GTCAATGCTG ATTGATTGCC TCGGATAGT TCTAGAACTC 900
 40 AATGCTGTC TCTGTGCAAC TCCCTCAT TTTATCATC CATCAGCCTG TTATCTGAAA 960
 CTGCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
 GGTGCTGGG TGATGTTTTT TGGATTGCTG ATGGCTATTA CAATATCTCA AGACTGCACC 1080
 CATGGGCAGG AAATGTTCTA CTGCTTCTCT GACAATTCT CTCTCACAAA TACCTCAGAG 1140
 45 TCTCATGTTC AGCAGACAA ACACCTTCT ACITTAATA TTAGTATCT TCAACTCGAG 1200
 TAA

A192 Protein sequence:

50 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: 1-26
 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351
 55 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 60 MGYQRQEPVI PPQFSLVLI KGGALSGTDT YQSLVNKTFG PFGYLLSLV QFLYPFIAMI 60
 SYNIIAGDTL SKVFORIPGV DPENVFIGRH FIIGLSTVTF TLPVSLYRNI AKLGKVSLS 120
 TGLTTILGI VMARAILGP HIPKTEDAV PAFNAIQAV GVMSFAPICH HNSPLVYSSL 180
 EEPVAKWSR LIHMSIVISV PICIFPATCG YLFTGPTQG DLFENYCRND DLVTFGRFCY 240
 GVTVILTYFM ECFVTREVI NVFFGGNLS VPHIVVTVMV ITVATLVSL IDCLGIVLEL 300
 65 NGVLCATPLI PIIPSACYLK LSEPRTHSD KIMSCVMLPI GAVVMVGFV MAITNTQDCT 360
 HGQEMFYCFP DNPSLTNTSE SHVQQTQLS TLNISIFQLE

A193 DNA SEQUENCE

70 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 | | | | |
 80 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CGCCCGCAGG TCAATAAAAC TTTCGGCTTT 60
 CCAGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
 TACAATATA TAGCTGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
 CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240
 CTGCTTTTAT CCTGTACCG AAATATAGCA AAGCTTGGAA AGGTCTCCCT CATCTCTACA 300
 GGTTTAACAA CTCTGATTCT TGGAAATTGA ATGGCAAGGG CAATTTCAC TGGTCCACAC 360
 ATACCAAAA CAGAAGACGC TTGGGTATT GCAAAGCCCA ATGCCATTCA AGCGGTGGG 420

5 GTTATGTCCT TTGCATTTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
 GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
 ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGACATTTA CTGGCTTCAC CCAAGGGGAC 600
 TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAAACAT TTGGAAGATT TTGTTATGGT 660
 10 GTCAGTGTCA TTTTGACATA CCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
 GTGTTTTTGT GTGGGAATCT TTCATCGGTT TTCCACATGT TTGTAACAGT GATGGTCATC 780
 ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCTCG GGATAGTTCT AGAACTCAAT 840
 GGTGTGCTCT GTGCAACTCC CCTCATTTTT ATCATTTCCAT CAGCCTGTTA TCTGAAACTG 900
 TCTGAAGAAC CAAGACACCA CTCCGATAAG ATTATGTCTT GTGTCATGCT TCCCATTTGGT 960
 15 GCTGTGGTGA TGGTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCAACCCAT 1020
 GGGCAGGAAA TGTCTACTG CTTTCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080
 CATGTTTCCG AGACAAACCA ACTTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

15 A194 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 20 Signal sequence: none found
 Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 | | | | |
 MGYQRQEPVI PPQVKNKTPGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIPIVD 60
 PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLKGVSLIST GLTTLILGIV MARAISLQPH 120
 IPKTEDAMVF AKFNAIQAVG VMSFAFICHH NSFVLYSSLE EPTVAKWSRL IHMSIVISVP 180
 30 ICIPFATCGY LTFGTGTQGD LPENYCRNDD LVTFGRFCYV VTVILTYPME CFVTREVIAN 240
 VFPFGLNLSV FHIVVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
 SEEPRTSHDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMPYCFPD NFSLTNTSES 360
 HVQQTQLST LNISIFQLE

35 A195 DNA SEQUENCE:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 40 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | |
 ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CCGCCGAGAG GAGATTTAGA TGACAGAGAA 60
 ACCCTTGTTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180
 GGGTTTCCCT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACAGA CTTTCCCTT 240
 50 GTTTTATTGA TAAAAGGAGG GGCCCTCTCT GGAACAGATA CCTACCAATC TTTGGTCAAT 300
 AAAAATTTGG GCTTTCCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTTT GTATCCTTTT 360
 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAAAT TTTTCAAGA 420
 ATCCCAAGAG TTGATCCTGA AAACGTGTTT ATGGGTGCGC ACTTCATTAT TGGACTTTCC 480
 ACAGTTACCT TTAATCTGCC TTTATCCTTG TACCGAAATA TAGCAAAAGT TGGAAAGGTC 540
 55 TCCTCATCT CTACAGGTTT AACAACTCTG ATTCCTGGAA TTGTAATGGC AAGGGCAATT 600
 TCACCTGGTC CACACATACC AAAAACAGAA GACGCTTGGG TATTTGCAAA GCCCAATGCC 660
 ATTCAGCGGG TCGGGGTAT GTCTTTTGCA TTTATTGACC ACCATAACTC CTCTTAGTT 720
 TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 GTGATTTCTG TATTATCTG TATATCTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
 60 TTCAACCAAG GGGACTTATT TGAATAATAC TGCAGAAATG ATGACCTGGT AACATTTGGA 900
 AGATTTTGTG ATGGTGTGAC TGTCAATTTG ACATACCOCTA TGGAAATGCTT TGTGACRAGA 960
 GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTTCA CGGTTTTCCA CATTGTTGTA 1020
 ACAGTGATGG TCACTACTGT AGCCACGCTT GTGTCATTGC TGATTGATTG CCTCGGGATA 1080
 65 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
 TGTATCTGTA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTGTGTC 1200
 ATGCTTCCCA TTGGTGTGTT GGTGATGGTT TTTGGATTGG TCATGGCTAT TACAAATACT 1260
 CAAGACTGCA CCAATGGGCA GGAAATGTTT TACTGCTTTC CTGACAAATT CTCTCTCACA 1320
 AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACCTT CTACTTTAAA TATTAGTATC 1380
 70 TTTCAATGA

75 A196 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 80 Signal sequence: none found
 Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60

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 15

GFPLGILLLP WVSIVTDFSL VLLIKGALS GTDTYQSLVN KTFGPGYLL LSVLQFLYPP 120
 IAMISVNIIA GDILSRVFPQR IPGVDPENVF IGRHPIIGLS TVTPTLPLSL YRNIARKLKV 180
 SLISTGLTTL ILGIVMARAI SLGPHIPKTB DAMVPAKPNIA IQAVGVMSFA FICHNSFLV 240
 YSSLEPTVA KWSRLIHMSI VISVPICIFF ATCGYLTFTG FTQGDLEFNY CRNDDLVTFG 300
 RFCYGVTVIL TYMECFVTR EVIANVFFGG NLSSVPHIVV TVMVITVATL VSLLLIDCLGI 360
 VLELNGVLCA TPLIFIIPSA CYLKLSEEP THSDKIMSCV MLPIGAVVMV PGFVMAITNT 420
 QDCTHGQEMP YCPPDNFSLT NTSSEHVQQT TQLSTLNIIS FQ

A197 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Nucleic Acid Accession #: NM_017636
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACAGCGATGC ACACACCAAG 60
 GAGAAGCCCA CCGATGCCTA CGGAGAGCTG GACTTCACGG GGGCCGGCCG CAAGCACAGC 120
 AATTTCTCTC GGCCTCTCTG CCGAACCGAT CCAGCTGCAG TTTATAGTCT GGTACACAGC 180
 ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240
 TCCTCTCCAG CCGTGGTGC GGAACCTGCT CCGTGGGGC TGGTGGGGC TGGCCAGAGC 300
 ACAGAGCCTT GGATTGTCTC TGGGGGTCTG CACACGGGCA TCGGCGGCA TGTGGTGTG 360
 GCTGTACGGG ACCATCAGAT GGCCAGCACT GGGGCCACCA AGGTGGTGGC CATGGGTGTG 420
 GCGCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCCAAGGG CTGTTCCCT 480
 GCGAGGTACC GGTGGCGCGG TGACCCGGAG GACGGGGTCC AGTTTCCCT GGACTACAAC 540
 TACTCGGCTC TCTTCCTGGT GGACGAGCGC ACACACGGCT GCTGGGGG CGAGAACCGC 600
 TTCCGCTTGC GCTTGGAGTC CTACATCTCA CAGCAGAAGA CGGGCGTGGG AGGGACTGGA 660
 ATTGACATCC CTGTCTGCT CTTCTGATT GATGTTGATG AGAAGATGTT GACGGAATA 720
 GAGAAGCCCA CCCAGGCTCA GCTCCCATGT CTCTCTGTG CTGGCTCAGG GGGAGCTGG 780
 GACTGCTGG GAGAGACCTT GGAAGACACT CTGGCCCCG GAGTGGGGG AGCCAGGCAA 840
 GGGAGAGCCC GAGATCGAAT CAGGCGTTTC TTCCCAAG GGAACCTTGA GGTCTGCAG 900
 GCGCAGTGG AGAGGATTAT GACCCGGAAG GAGCTCCTGA CAGTCTATTC TTCTGAGGAT 960
 GGGTCTGAGG AATTCTGAGC CATAGTTTGG AAGGCCCTTG TGAAGCCCTG TGGGAGCTCG 1020
 GAGGCCCTAG CCTACCTGGA TGAGCTGGCT TTGGCTGTGG CTGGAACCG CGTGGACATT 1080
 GCGCAGAGG AACTCTTTCG GGGGAGACAT CAATGGCGGT CCTTCCATCT CGAAGCTTCC 1140
 CTATAGGAG CCGTGTGTA TGACCGGCT GAGTTCGTGC GCTTCTCAT TTCCCAAGGC 1200
 CTAGCTGAG GCACTTCTCT GACCCGATG GCGCTGGGCC AACTCTACAG CGCGCGCCG 1260
 TCCAACCTCG TCATCCGCAA CCTTTTGGAC CAGGCGTCCC ACAGCGCAGG CACCAAGGCC 1320
 CCAGCCCTAA AAGGGGGAGC TGCGGAGCTC CGGCCCTCTG ACGTGGGGCA TGTGCTGAG 1380
 ATGCTGCTGG GGAAGATGTG CGCGCGAGG TACCCCTCG GGGGCGCCTG GGACCTCAC 1440
 CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCG ACAAGGCCAC CTCGCGCTC 1500
 TCGCTGAGT GCGCTCTCG GCGAGGCCCG TGGAGCGACC TGCTTCTTG GGCAGTGTG 1560
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCTA 1620
 GCTCTTGGG CCTGTTTGT GCTCCGGGTG ATGGCACGCC TGGAGCCTGA CGCTGAGGAG 1680
 GCAGCACGGA AATCAGAAAG GCGTTCAGG TTTGAGGGGA TGGCGTTGA CTCTTTTGGC 1740
 GAGTGTCTAT GCAGCAGTGA GGTGAGGGCT GCGCGCTCC TCCTCGGTG CTCGCGCTC 1800
 TGGGGGATG AGTCCGCTCG CCAGCTGGCC ATGCAAGCTG ACGCCGTGC CTCTTTGCC 1860
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920
 CCCATCTGGG CCTGGTCTT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CCGCTCATC 1980
 ACCTTCAGGA AATCAGAAAG GGAGCCCA CAAGAGGAGC TAGAGTTTGA CATGGATAGT 2040
 GTCAATTAAT GGAAGAGGCC TGTCGGGAGC GCGGACCCAG CCGAGAAGAC GCGCTGGGG 2100
 GTCCCGCGCC AGTCCGGGCG TCCGGGTTGC TCGGGGGGCC GCTCGGGGG GCGCGGTGC 2160
 CTACGCGCTC GGTTCACATT CTGGGGGCGC CGGTGACCA TCTTCATGGG CAACGTGGTC 2220
 AGCTACCTGC TGTTCCTGCT GCTTTTCTCG CGGTGTCTGC TGTGGATT CTAGCCGCG 2280
 CGCCCGGCT CCTCGAGCT GCTGCTCTAT TTCTGGGCT TCACTGCTG GTGAGGAA 2340
 CTGCGCCAGG GCTGAGCGG AGCGGGGGG AGCTCGCCA GCGGGGGGCC CGGCTGGC 2400
 CATGCTCAT TGAGCCAGCG CTTGCGCTC TACCTCGCG ACAGCTGGA CAGTGCAG 2460
 CTAGTGGCTC TCACCTGCTT CTCTCTGGG GTGGCTGCC GGTGACCCC GGTTTGTAC 2520
 CACCTGGGCC GCATGTCCT CTGCACTGAC TTCATGTTT TCACGTGGG GCTGCTTAC 2580
 ATCTTCAGG TCAACAAACA GCTGGGGCCC AAGATCGTCA TGTGAGCAA GATGATGAAG 2640
 GACGTGTTCT TCTTCTCTT CTCTCTGGG GTGTGGCTGG TAGCCTATGG CGTGGCCAG 2700
 GAGGGGCTCC TGAGGCCAG GACAGTGAC TTCCCAAGTA TCCTGCGCG CGTCTTCTAC 2760
 GGTCCCTACC TGCAATCTT CGGCGAGATT CCCAGGAGG ACATGGAGCT GGCCTCATG 2820
 GAGCACAGCA ACTGCTGTC GGAGCCCGGC TTCTGGGCAC ACCCTCTGG GGGCCAGG 2880
 GGCACCTGG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTG CATCTTCTG 2940
 CTGTGGGCA ACATCTGCT GGTCAACTTG CTCAATGCCA TGTTCAGTTA CACATCGGC 3000
 AAAGTACAG GCAACAGCA TCTCTACTGG AAGGCGCAG GTTACCGCT CATCGGGAA 3060
 TTCACTCTC GCGCCGCGCT GCGCCGCCC TTTATGCTCA TCTCCACTT GCGCTCTG 3120
 CTCAGGCAAT TGTGAGGCG ACCCGGAGC CCCAGCCGT CCTCCCGGC CCTCGAGCAT 3180
 TTCCGGTTT ACCTTCTTAA GGAAGCGAG CGGAAGCTGC TAACGTGGGA ATCGGTGCAT 3240
 AAGGAGAACT TTCTGCTGGC ACGCGTAGG GACAAGCGGG AGAGCGACTC CGAGCGTCTG 3300
 AAGCGCAGT CCAGGAAGT GGACTTGGCA CTGAACAGC TGGGACACAT CCGAGGTAC 3360
 GAACAGCGCC TGAAGTGCT GGAAGCGGAG GTCCAGCAG GTAGCCGCT CCTGGGTGG 3420
 GTGGCCGAG CCTGAGCGG CTCTGCTTG CTGCCCCAG GTGGGCGCC ACCCTCTGAC 3480
 CTGCTGGGT CCAAGAGCTG A

A198 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Protein Accession #: none found

Signal sequence: none found
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MEDAFGAADV TVWDSAMHTT EKPTDAYGEL DFTGAGRKHS NPLRLSDRTD PAAVYSLVTR 60
TWGFRAPNLV VSVLGGSGGP VLQTLWQDLL RRLVRAAQS TGAWIVTGGL HTGIGRHVGV 120
AVRDHQMMAST GGTQKVAMGP APWGVVRNRD TLINPKGSFP ARYRWRGDPE DGVQFPPLDYN 180
YSAFPLVDDG THGCLGGENR FRLRLSEYIS QOKTGVGGTG IDIPVLLLLL DGEKMLTRI 240
ENATQAQLPC LLVAGSGGAA DCLAEITLEDT LAPGSGGARQ GEARDRIRRP PFKGDLEVLQ 300
AQVERIMTRK ELLTVYSSDD GSEEPETIVL KALVKACGSS EASAYLDELK LAVAWNVRDI 360
AQSELPRGDI QWRSPHLEAS LMDALLNDRP EFPVRLISHG LSLGHFLTPM RLAQLYSAAP 420
SNSLIRNLDD QASHSAGTKA FALKGGAAEL RFPDVGHVLR MLLGKMCAPR YPSGGAWDPH 480
PGQGFGBSMY LLGDKATSP LSLDAGLQAP WSDLLWALL LNRAQMAMYF WEMGSAVSS 540
ALGACLLLRV MARLEPDABE AARRKDLAFK FEGMGVDLFG ECTRSSEVRA ARLLLRRCPL 600
WGDATCLQLA MQADARAFPA QDGVQSLTQ KWWGDMASTT PIWALVLAFF CPPLIYTRLI 660
TPRKSEEEPT RESELEPMD S VINGEGPVG T ADPAEKTPLG VPRQSGRPGC CGGRCGGRC 720
LRRWPHFWGA PVITFMGNV SYLLFLLLF S RVLLVDFQPA PPSLELLLY FWAFTLLCBE 780
LRQCLSGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCFLLG VGCRLTPGLY 840
HLGRTVLCID FMVFTVRLH IFTVKNQLGP KIVIVSMMK DVFFFLPFLG VHLVAYGVAT 900
EGLLRPRDSD FPSILRRVFP RPYLQIFGQI PQEDMDVALM EHSNCSEPG FMAHPPGAQA 960
GTCVSQYAMN LVLLLVIFL LVANILLVNL LIAMFSTTFG KVQNSDLYW KAQRYRLIRE 1020
FHSRPAALAP FIVISHLRL LRLQCRPRPS POPSPALEH FRVYLSKEAB RKLLTWESVH 1080
KENFLARAR DKRESDEBL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQCSRVLGW 1140
VAEALSRSAL LPPGGPPFPD LPPGSKD

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A199 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Nucleic Acid Accession #: AA054237
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGAGCGCG GGGCGCTCGT CAOGGCGCTC AGCCTCGGCC TCAGCCTGTG CTCCCTGGGG 60
CTGCTCGTCA CGGCCATCTT CACCGACCAC TGGTACGAGA CCGACCCCGG GCGCCACAAG 120
GAGAGCTGCG AGCCGACGCG CGCGGGCGCC GACCCCGCGG ACCAGAAGAA CCGCCTGATG 180
CCGCTGTGCG ACCTGCGCGT GCGGGAATCG CCCCCTGCTG GCGCGCGGCT GCTCCGCGGC 240
GGCGCGGGGG GCGCGGACCC CGAGTCCTGG CGCTCGCTCC TGGGGCTCGG CGGGCTGGAC 300
GCGGAGTGCG GCCGGCCCTT CTTCGCCACC TACTCGGGCC TCTGGAGGAA GTGCTACTTC 360
CTGGGCGATG ACCGGGACAT CGACACCCCT ATCCTGAAAG GTATTGCGCA GCGATGCAGC 420
GCCATCAAGT ACCACTTTTC TCAGCCCATC OGCTTGCGAA ACATTCCTTT TAATTAAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTTAA GAAGAATCAC TGCTGGCTTC 540
TCGGCATGG CCGTAGCCGT CCTTCTCTGC GGCTGCATIG TGGCCACAGT CAGTTTCTTC 600
TGGGAGGAGA GCTTGACCCA GCACTGTGCT GGACTCCTGT TCCTCATGAC AGGGATATTT 660
TGCACCATTT CCTCTGTGAC TTATGCGGCC AGTATCTCGT ATGATTGAA CCGGCTCCCA 720
AAGCTAATTT ATAGCCTGCC TGCTGATGTG GAACATGTT ACAGCTGTGC CATCTTTTGC 780
GCCTGCTGCA GTTTAGGCTT TATTGTGGCA GCTGGAGGTC TCTGCATCCG TTATCCGTTT 840
ATTAGCCGGA CCAAGATTGC ACAGCTAAG TCTGGCAGAG ACTCCACGCT ATGA

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A200 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Protein Accession #: none found
 Signal sequence: 1-18
 Transmembrane domains: 179-201, 209-231, 257-279
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MEPRALVTAL SLGLSLCSLG LLVTAIFTDH WYETDPRRHK ESCERSRAGA DFPDQKNRLM 60
PLSHLPLRDS PPLGRRLLPF GPGRADPEW RSLGLGLGLD AECGRPLPAT YSGLWRKCYF 120
LGIDRDIIDL ILKGIAQRCT AIKYHFSQPI RLNRNIPNLT KTIQDDEHL LHLRRITAGF 180
LGMVAVLLC GCIVATVSFF WEESLTQVHA GLLFMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISR7KIAQLK SGRDSTV

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A201 DNA SEQUENCE

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGAGGCGCAC TGAATCGGAA AAAAACTTAA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
AAGGTTCCCTG AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120

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TTTACAATA TGGCTTTATT AACCATAAATG GAATTCCTCAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT 240
ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
GTTGCATCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
CAAGATGTGA TATTTAAAGG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
GATGATTCAT CACAGTCTCC AATGTCATGC AGAATTCAATG GCCATCTATA TGTCATATAA 540
GTAGCAGGGA ATTTTCATAT AACAGTGGGC AAGGCAATTC CACATCTCTG TGGTCATGCA 600
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTGATAGAAT AGATCATTTG 660
TCTTTTGGAG AGCTTGTTCG AGCAATATTAT AATCCTTTAG ATGGAACCTGA AAAAAATTGCT 720
ATAGATCACA ACCATGATTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGTA AATATGATCT CAGTTCTCTT 900
ATGGTGACAG TTACTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTGAAG ACTCTGTGGT 960
ATTGTTGGAG GAATCTTTTC AACCAACAGC ATGTTACATG GAATTGGAAG AATTATAGTT 1020
GAAATAAATT GCTGTCGTTT CAGACTTGGG TCCTATAAAC CTGTCAATTC TGTTCTTTT 1080
GAGGATGGCC ACACAGACAA CCACCTACCT CTTTTAGAAA ATAATACAA TTGA
  
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A202 Protein sequence:

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Protein Accession #: NP_057654
 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

1 11 21 31 41 51
 | | | | |
 MRRLNRKKT SLVKELDAFP KVPESEVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
 KYEYEVNDKF SSKLRINIDI TVAMKQYVGV ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
 KEWQRLQLI QSRLOEHSLS QDVIPKSAFK STSTALPPRE DDSSQSPNAC RIHGHLYVNK 180
 VAGNFHITVG KAIPFRGHGA HLAALVNHES YNFSHRIDHL SFGELVPAIL NPLDGTEDIA 240
 IDHNMQFYFP ITVVPTKLET YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSL 300
 MVTVTEEHMP FWQFFVRLCG IVGGIPSTTG MLHGIGKPIV EIIICRFRIG SYKPVNSVPP 360
 EDGHTDNHLP LLENNTH

A203 DNA SEQUENCE

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CGCGGCTCTC CGCGGCCGCG GTGACTCTCG CCTGCGCTCC TTCTCTGAAC GCTCAGTCC 60
GAGGAGACGC CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGCTGCT 120
GCGCTTGTCG CCATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180
ACAGCTGACA GTGCGCAAAAC TTACACTCTA ACTGATTACT TAAAAAATAC TTATAGACTG 240
AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAA 300
ATCTGGTAT TCAATGCTGA ATATGGAAC AGCTCAGTTT TCTTGGAGAA CAGTACATT 360
GATGAGTTTG GACATTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420
TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCCTACA CAGCTTCATA TGACATTAT 480
GATTTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAACAACAC ACAGTGGGTC 540
ACATGGTCA CAGTGGGTCA TAAATTGGCA TATGTTTGGG ACAATGACAT TTATGTTAAA 600
ATTGAACCAA ATTATCCAAG TTACAGAATC ACATGGACGG GGAAGAAGA TATAATATAT 660
AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCCTACTC TGCTCTGTGG 720
TGGTCTCCAA ACGGCACCTT TTTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACCT 780
ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCAGTACC CAAAGACTGT ACGGGTTCCA 840
TATCCAAAGG CAGGAGCTGT GAATCCAAC GTAAAGTTCT TTGTTGTAAA TACAGACTCT 900
CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGTCTTC TATGTTGATA 960
GGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAAG AAAGAATTTT TTTGCAGTGG 1020
CTCAGGAGGA TTCAAGAACTA TTCGGTCAAT GATATTTGTG ACTATGATGA ATCCAGTGGG 1080
AGATGGAATC GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140
AGATTTAGGC CTTCAAGAAC TCATTTTACC CTTGATGGTA ATAGCTTCTA CAAGATCATC 1200
AGCAATGAAG AAGGTTACAG ACACATTTGC TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAAG CTCTAACCAAG TGATTATCTA 1320
TACTACATTA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAATCCAA 1380
CTTATTGACT ATACAAAAGT GACATGCTCT AGTTGTGAGC TGAATCCGGA AAGGTGTCAA 1440
TACTATTCTG TGTCAATCAG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
GGTCTGCCCC TCTATCTCTC ACACAGCAGC GTGAATGATA AAGGCTGAG AGTCTCTGAA 1560
GACAATTCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAAACTGGAC 1620
TTCAATTATT TGAATGAAC AAAATTTTGG TATCAGATGA TCTTGCTCTC TCATTTTGAT 1680
AAATCCAAGA GAATCTCTCT ACTATTAGAT GTGATGACAG GCCCATGTAT TCAAAAAGCA 1740
GACTAGTCTC TCAAGCTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800
GCTAGCTTTG ATGCGAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860
AGAAGACTGG GAACATTGTA AGTTGAAGAT CAAATTGAAG CAGCCAGACA ATTTTCAAAA 1920
ATGGGATTTG TGGACAAACA ACGAATTGCA ATTTGGGGCT GTTCATATAG AGGGTACGTA 1980
ACCTCAATGG TCCTGGGATC GGGAAAGTGGC GTGTTCAAGT GTGGAATAGC CGTGCCGCTC 2040
  
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GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
 CCAGAAGACA ACCTTGACCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAATAATTTT 2160
 AAACAAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAACGTTCA CTTTCAGCAG 2220
 TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
 ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
 AGCCACTTCA TAAAACAATG TTTCTCTTTA CTTAGCACCC TCAAAATACC ATGCCATTTA 2400
 AAGCTTATTA AAATCAATT TGTCTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
 TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGT TACCTTTGTT CCCAAATTTT 2520
 ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCACAACA GATTATTACC TTACAGAAAT 2580
 TTGAATATAT CCGTGGGTTT TTATTGTTTA AAATCAATT TGCATCAGCT GCTGAAACAA 2640
 CAAATAGGAA TTGTTTATAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
 TTTCTAATCT GACTGGTTC AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGTGGGC 2760
 AGTGTATGTA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGGCA 2820
 TGGCTGGGAA CCAAGTCCA AGCATACCAA CACGAGCAGG CTACTGTGAC CTCCCTCGG 2880
 AGAAGAGCTG TTCACCAAGA GACTGGCACA GTTTCTGAG AAAGACTATT CAAACAGTCT 2940
 CAGGAATGCA AATATGAAA GCACTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
 AAAGAAATGT AAGGGAATC GCCAGCAACG CAGCCCCAG GTGCCAGTTA TGGCTATAGG 3060
 TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATA 3120
 TACTGATGTT CCTAGTGAAA GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
 CTGTTAAAGG ATGAAATAT TTGTATCACA AATCTTAAT TGAAGGAGTC CTGCAATCAA 3240
 TTTTCTTAT TTGATTTCTT TGAGTGTCTT AATTAAGA ATATTTAAC TTCCTGGAC 3300
 TCATTTTAAA AAATGGAACA TAAATACAA TGTATGTAT TATTATCCC ATTCTACATA 3360
 CTATGGAATT TCTCCAGTC ATTAAATAA TGTGCTTCA TTTTTC

25

A204 Protein sequence:

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 Protein Accession #: NP_001926.1
 Signal sequence: none found
 Transmembrane domains: 6-28
 DPPIV_N_term domain: 43-557
 Peptidase_S9 domain: 558-635
 Cellular Localization: plasma membrane

35

1 11 21 31 41 51
 MKTPWKILLG LLGAAALVTI ITVPVLLNKG GTDDATDSR KTYTLTDYLK NTYRLKLYSL 60
 RWISDHEYLY KQENNLVFN AEYGNSSVFL ENSTFEFGH SINDYSISPD GQFILLEYN 120
 VKQWRHSYTA SYDIYDLNKR QLITEERIFN NTQWVTWSPV GHKLAYVMNN DIYVKIEPNL 180
 PSYRIWTGK EDIINYNGITD WYEBEEVFSA YSALWNSPFG TFLAYAQFND TEVPLIEYSP 240
 YSDESLQYPK TVRVYPKAG AVNPTVKPFV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDVTWATQER ISLQWLRIQ NYSVMIDICY DESSGRWNCL VARQHIEMST TGMVGRFRPS 360
 EPHPFLDQNS FYKILSNEEG YRHICYFQID KDCCTFITKG TWEVIGIEAL TSDYLYYISN 420
 EYKMPGGRN LYKIQILIDYT KVTCLSCELN PERCQYYSVS FSKEAKYQYL RCGSPGLPLY 480
 TLHSSVNDKG LRVLEDNSAL DKMLQNVQMP SKQLDPIILN ETKFMYQML PPHFDKSKKY 540
 PLLLDVYAGP CSQKADTVFR LNWATYLAST ENIIIVASFPG RGSQVQGDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSGMGFVD NKRIAINGWS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660
 YYDSVYTERY MGLPTPEDNL DHYRNSTVMS RAENPKQVEY LLIHGTADDN VHFQQAQIS 720
 KALVDVGVDV QAMWYTDDEH GIASSTAHQH IYTHMSHFPIK QCFSLP

55

A205 DNA SEQUENCE

Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Nucleic Acid Accession #: none found
 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

60

1 11 21 31 41 51
 ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAATGACA ATGCCATCAG AGTTGACAC 60
 AGAAGTGTGA TTAAGTGGC TGCTAACCAAG TGTTCCTGCG ATGAGGCAGA AAGTGAATCC 120
 AGAAACCCCTC AGGAGCTCTG GATGGGCCCTG CTCCTCTTGA TGGGGTCTCT AGAAGCATGT 180
 GTGGAAATGA GGCCTCTGTC AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240
 CAGCCCCAC TGATGTCTA A

70

A206 Protein sequence:

Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 46-68
 Cellular Localization: not determined

80

1 11 21 31 41 51
 MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHPEASES RNPQELWMGL LLLMGVLEAC 60
 VEMRPLSVWS LRDDKQSPFH QPTLDV

A207 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.222886
Probeset Accession #: AI672225
Nucleic Acid Accession #: none found
Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

```
10 1      11      21      31      41      51
    |      |      |      |      |      |
    ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAAGTCTG 60
    CTCATACTTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
    ATTGATGTAT CTTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
15  ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
    TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTCATGTGGG ATTCCAGAA 300
    AACCTGACTA ATGGTGCOCG TGCTGGCAAT GGTGATGATG GATTAATTCC TCCAAGGAAG 360
    AGCAGAACAC CTGAAAGCCA GCAATTTCC T GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
    GTCAAAGATC AGATAGTTGT AGATATGCGG CGTTATTTC GA
```

A208 Protein sequence:

Gene name: ESTs
Unigene number: Hs.222886
Probeset Accession #: AI672225
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 16-38
Cellular Localization: not determined

```
30 1      11      21      31      41      51
    |      |      |      |      |      |
    MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLLEQN IDVSSQDLDR RPESMLFLVI 60
    IMWTSFVEDN LSMGWGKLED FMAIEEEMKK HGSTHVGFPE NLTNGAAAGN GDDGLIPPRK 120
35  SRTPEQQQFP DTENEYHRF VKDQIVVDMR RYF
```

A209 DNA SEQUENCE

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
Unigene number: Hs.23796
Probeset Accession #: NM_014253
Nucleic Acid Accession #: NM_014253
Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

```
45 1      11      21      31      41      51
    |      |      |      |      |      |
    GACTGCTTGC ATTAAGGAC TTCCTCATCC TTTTTCATCAT GAAACTGAGC TTGCTTAATC 60
    AGAGATGGAG CAAACTGACT GCAAACCCCTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT 120
    GGATCTAGCT TACACCAAGT CTTCTGATGA GAGTGAAGAT GGAAGAAAAC CAAGACAGTC 180
50  ATACAATCTC AGGAGAGCCC TGCAAGAGTA TAACCAAGAG CTGAGGATGA ATTACAATAG 240
    CCAGAGTAGA AAGAGGAAAG AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAAC 300
    CTCTCAGACT CTGTGCTCTG GCTACCAAAC AGACATGCAC AGOGTTTCTC GGCATGGCTA 360
    CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
    TGCACTAGTA ATGTGGATAA GGGGAATGAA ATCAGAGCAT AGTTCTCTGT TGTCCAGCCG 480
55  GGCCAACTCT GCATTATCCT TGAATGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
    TGGTTTCAAA TTCTCTCCTG TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
    TGTGCAGAGC AGCCACACAC ACCAGTTTAC CTTGAGACCC CTCCCACCCG CACCTCCGCC 660
    TCCTCATGCC TGCACTCTGT CCAGGAAGCC ACCCCCTGCA GCGGACTCTC TTCAGAGGAG 720
    ATCAATGACT ACCCGCAGCC AGCCAGCCCC AGCTGCTCCA GCTCCCCCAA CCAGCACGCA 780
60  GGATTCAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCAG 840
    GCATTCCCTG TTCAAACATG GATCTGGTTC CTCTGOGATC TTCAGTCCAG CCAGTCAGAA 900
    CTACCCCTCT ACATCCAATA CGGTGTACTC GCCCCCTCCC AGGCCTCTTC CTCGAAGCAC 960
    CTTTCCCGCA CTGCTCTTTA CCTTTAAACA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
    AGCATTGAGC GCCACTGCAA TCACAGTGAC TTTGGCCTTG TTAAGAGCCT ATGTGATTGC 1080
65  AGTGCATTGT TTGCGCCTGA CTTGGCAGTT GCAACCAATT GAAGGAGAGC TGTATGCAAA 1140
    TGGAGTTAGC AAAGGGAACA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
    AGGAAAAGTT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGGACGGG CGATAGACAC 1260
    TGGAGAAGTT GACATTGGTG CACAGGTCAAT GCAGACCAAT CCACCTGGTT TATTCTGGCG 1320
    TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTTCTT TAGCCAAGGA 1380
70  CTCTCTGCTG GGAATTTATG GCAGAAAGAA CATTCACCTT ACACATACTC AGTTTGATT 1440
    TGTAAACTTA ATGATGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC 1500
    ACAGCACTCC CCTCGGAACC TGATCTTAAC TTGCTTTCAG GAGACAGGTT TCATAGAGTA 1560
    TATGATCAAA GGACCTTGGT ATCTGGCGTT TTACAATGAT GGAAGAAAAG TGGAGCAAGT 1620
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A210 Protein sequence:

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Protein Accession #: NP_055068
 Signal sequence: none found
 Transmembrane domains: 318-340
 Cellular Localization: plasma membrane

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 LVGVNVSPFLH HSDYGFITSR QDGSFDLVAI GGISVILIPD RSPFLPEKRT LWLFWNQFIV 960
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 SSFVRLSYLS SRTPGYKTL RILLTHSTIP VGMIKVHLTV AVEGRLTQKW PPAAINLVYT 1080
 FAWNKTDIY QKWLALAEAL VSVGYEYETC PDIILNEQRT VVLQGFEMDA SNLGDWLSNK 1140
 HHILNPQSGI IHKNGENMF ISQPPVIST IMGNHQRSV ACTNCNGPAH NNKLFAPVAL 1200
 ASGPDGSVYV GDFNFVRRI FSGNSVSILE LSTSPAHKYY LAMPVSESL YLSDTNTTRKV 1260
 YKLKSLVSTK DLSKNFEVVA GTGDQCLPFD QSHCGDGGRA SEASLNSPRG ITVDREGFIY 1320
 FVDGTMIKRI DENAVITTVI GSNGLTSTQP LSCDSGMDIT QVRLWPTDL AVNPMDSNLY 1380
 VLNDNIVLQI SENRRVRIIA GRPIHCQVPG IDHFLVSKVA IHSTLESARA ISVSHSGLLF 1440
 IAEOTFRVNV RIQQVTTTNGE IYIIAGAPT CDCKIDFNCD CFSGDGGYAK DAKMKAPSSL 1500
 AVSPDGTLYV ADLGNVRIRT ISRNQAHND MNIYEIASPA DQELYQFTVN GTHLHTLNL 1560
 TRDYVYNFTY NSEGLDGAIT SSNGNSVHIR RDAGGMPLWL VVPGGQVYWL TISSNGVLKR 1620
 VSAQGYNAL MTPYQNTGLL ATKSNGNGWT TVYEYDPEGH LTNATFPPTGE VSSFHSDLEK 1680
 LTKVELDTSN RENVMSTNL TATSTIYILK QENTQSTYRV NPDGSLRVTF ASGMEIGLSL 1740
 EPHILAGAVN PTIGKCNISL PGEHNNALIE WRQRKBQNGK NVSAFERRLR AHNRNLLSID 1800
 FDIHTRTGKI YDDHRKFTLR ILYDQGTGRPI LWSFVSRYNE VNITYSPSGL VTFIQRGTWN 1860
 EKMEYDQSGK IISRTWADGK IWSYTYLEKS VMLLLHSQRR YIFEYDQSDC LLSVTMPSPV 1920
 RHLGLTMLSV GYRNNTYTPP DSSTSFIDY SRDGRLLQTL HLGTRRRVLY KYTKQARLSE 1980
 VLYDTTQVTL TYEESGVIK TIEHMDGFI CTIRYRQTGP LIGRQIPRPS EBLVNAFDP 2040
 YSVNFRVTS MQAVINETPL PIDLYRYVDV SGRTEQPGKF SVINYDINQV ITTIVMHTK 2100
 IFSANQVIE VQYEILKAIA YWMTIQYDNV GRHGNMCIRV GVDANITRYF YEYDADQLQ 2160
 TVSVNDKTQW RYSYDLNGDI NLLSHGKSAR LTPLRYDLRD RITRLGEIQY KMDGDLFLRQ 2220
 RGNDFPEYNS NGLLQKAYNK ASGNTVQYYY DGLGRRVASK SSLGQHLQFF VDATANPIRV 2280
 THLYNHTSSE ITSLYYDLQG HLIAMELSSG EBYVACDNT GTPLAVFSSR GQWIKELLYT 2340
 PYGDIYHDTY PDPQVIGFH GGLYDFLTKL VHLGQRDYDV VAGRWTYAYH HIWKQLNLLP 2400
 KPFNLYSPEN NYPVGKIQDV AKYTTDIRSW LELPGFQLHN VLPGFPPKPEL ENLELTVELL 2460
 RLQTKTQEWG PGKTIILGIQ ELQQLRNPFI SLDQLPMTPR YNDGRCLGEG KQPRFAAVPS 2520
 VFGKGIKPAI KGIIVTADII GVANEDSRRL AAILNNAHYL ENLHPTIEGR DTHYFIKLS 2580
 LEEDLVLIQN TGGRRILENG VNVTSQMTS LLNGRTRRFA DIQLQHGLGC FNIRYGTIVE 2640
 EEKNVLEIA RQRAVAQANT KEQRRLEQEG EGIRAWTEGE KQQLLSTGRV QGYDGYPVLS 2700
 VEQYLELSDS ANNIHFMRQS EIGRR

A211 DNA SEQUENCE:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Nucleic Acid Accession #: NM_000441
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CTCAGCCTTC CCGGTTCCGG AAAGGGGAAG AATGCAGGAG GGGTAGGATT TCTTTCCTGA 60
 TAGGATCGGT TGGGAAGAC CGCAGCCTGT GTGTGCTCTT CCCTTCGACC AAGGTGTCTG 120
 TTGCTCCGTA AATAAAACGT CCCACTGCTT TCTGAGAGCG CTATAAAGGC AGCGGAAGGG 180
 TAGTCCGCGG GGCATTCCGG GCGGGGCGCG AGCAGAGACA GGTCTATGCA GCGCCAGGCG 240
 GCAGGTCCGA GCGGCGCGAG CTCGCCGAGT ACAGCTGCAG CTACATGGTG TCGCGGCGCG 300
 TCTACAGCGA GCTCGCTTTC CAGCAACAGC ACGAGCGCGC CCTGCAGGAG CGCAAGACGC 360

5 TGCGGGAGAG CCTGGCCAAG TGCTGCAGTT GTTCAAGAAA GAGAGCCTTT GGTGTGCTAA 420
 AGACTCTTGT GCCCATCTTG GAGTGGCTCC CCAATATCCG AGTCAAGGAA TGGCTGCTTA 480
 GTGACGTCAT TTGCGGAGTT AGTACTGGCC TAGTGGCCAC GCTGCAAGGG ATGGCATATG 540
 CCTACTAGC TGCACTTCTG GTGCGATATG GTCTCTACTC TGCTTTTTTC CCTATCCTGA 600
 CATACTTTAT CTTTGGAAACA TCAAGACATA TCTCAGTTGG ACCTTTTCCA GTGGTGAGTT 660
 TAATGGTGGG ATCTGTTGTT CTGAGCATGG CCCCAGACGA ACACCTTCTC GTATCCAGCA 720
 GCAATGGAAC TGTATTAAT ACTACTATGA TAGACACTGC AGCTAGAGAT ACAGCTAGAG 780
 TCCTGATTGC CAGTGCCTCG ACTCTGCTGG TTGGAATTAT ACAGTTGATA TTTGGTGGCT 840
 10 TGCAGATTGG ATTCATAGTG AGGTACTTGG CAGATCCTTT GGTGTGGTGG TTCACAACAG 900
 CTGCTGCCTT CCAAGTGCTG GTCTCACAGC TAAAGATTGT CCTCAATGTT TCAACCAAAA 960
 ACTACAAAGT AGTTCTCTCT ATTATCTATA CGCTGGTTGA GATTTTTCAA AATATTGGTG 1020
 ATACCAATCT TGCTGATTTT ACTGCTGGAT TGCTCACCAT TGCTGCTGTG ATGGCAGTTA 1080
 AGGAATTAAT TGATCGGTTT AGACACAAAA TCCCAGTCCC TATTCCTATA GAAGTAATTG 1140
 15 TGACGATAAT TGCTACTGCC ATTTTCATATG GAGCCAACTT GGAAAAAAT TACAATGCTG 1200
 GCATTGTTAA ATCCATCCCA AGGGGGTTTT TGCTCTCTGA ACTTCCACT GTGAGCTTGT 1260
 TCTCGGAGAT CTGGCTGCTA TCAITTTTCCA TCGCTGTGGT GGCTTATGCT ATTGCACTGT 1320
 CAGTAGGAAA AGTATATGCC ACCAAGTATG ATTACACCAT CGATGGGAAC CAGGAATTCA 1380
 TTGCTTTTGG GATCAGCAAC ATCTTCTCAG GATTTCTTCT TTGTTTTTGG GCCACCACATG 1440
 20 CTCTTTCCCG CACGCGCTGC CAGGAGAGCA CTGGAGGAAA GACACAGGTT GCTGGCATCA 1500
 TCTCTGCTGC GATTGTGATG ATGCGCATTC TTGCGCTGGG GAAGCTTCTG GAACCTTTCG 1560
 AGAAGTGGGT GTTGGCAGCT GTTGTAAATG CCAACCTGAA AGGATGTTT ATGCAGCTGT 1620
 GTGACATTCC TCGTCTGTGG AGACAGAATA AGATTGATGC TGTATCTGG GTGTTTACGT 1680
 GTATAGTGTG CATCATCTG GGGCTGGATC TCGGTTTACT AGCTGGCCTT ATATTGGAC 1740
 25 TGTGTACTGT TGCTCTGAGA GTTCAGTTTC CTCTTTGGAA TGCCCTTGA AGCATCCCTA 1800
 GCACAGATAT CTACAAAAGT ACCAAGAATT ACAAAAACAT TGAAGAACCT CAGGAGTGA 1860
 AGATTCTTAG ATTTTCCAGT CCTATTCTCT ATGGCAATGT CGATGGTTTT AAAAAATGA 1920
 TCAAGTCCAC AGTTGGATTT GATGCCATTA GAGTATATAA TAAGAGGCTG AAAGCGCTGA 1980
 GGAAAAATACA GAACTAATA AAAAGTGAGC AATTAAGAGC AACAAAGAAAT GGATCATATA 2040
 30 GTGATGCTGT TTCAACAAAT AATGCTTTTG AGCCTGATGA GGATATTGAA GATCTGGAGG 2100
 AACTTGATAT CCAACCAAGG GAAATAGAGA TTCAAGTGGG TTGGAACCTC GAGCTTCCAG 2160
 TCAAGATGAA CGTCCCAAA GTGCCAATCC ATAGCCTTGT GCTTGACTGT GGAGCTATAT 2220
 CTTTCTTGGA CGTTGTTGGA GTGAGATCAC TGCGGGTGTG TGTCAAAGAA TTCCAAAGAA 2280
 TTGATGTGAA TGTGTATTTT GCATCACTTC AAGATTATGT GATAGAAAG CTGGAGCAAT 2340
 35 GCGGTTCTGT TGACACCAAC ATTAGAAAGG ACACATTCTT TTTGACGCTC CATGATGCTA 2400
 TACTCTATCT ACAGAACCAA GTGAAATCTC AAGAGGGTCA AGGTTCCATT TTGAAAACGA 2460
 TCACCTCAT CTAGGATTGT AAAGATACCC TTGAATTAAT AGAAACAGAG CTGACGGAAG 2520
 AAGAACTTGA TGTCCAGGAT GAGGCTATGC GTACACTTGC ATCCTGAAAG TGGGTTCCGG 2580
 AGGTCTCTAT GAGCAAGGAA TACAAGACAA AACTTCTCCA ATGCATTGAC TATTTCTTCA 2640
 40 GACTCAAAAC ACTCATCTCT TTTTCTATTA AGCCATTGAA AGAGAAGCAC TAAGACTGCT 2700
 TCTAGGCTTT ATTTATAAAA TAAACACCTT ATCCCTAACA TGGGCAAAAT GGCTAGAAAT 2760
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 TCACAGATTT GCTAATAATG TTCACGTGGG CCCTGGCATA TCTCTGTTC GATTAGAGTA 2880
 GTGCTGACCC AACAGCCTCT GTGGTCAAGC GAGTCAAGAA TGATTAATCA TAAAGAAAAA 2940
 45 TCAGTGTCTG ACTGACCTGG ATATCCATGA GCTGCACTGA TCACCATGTA AGGTACATAT 3000
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 TGGATAATA ATTGGAGTTT TAAAAATGCA AATTTGCTTA GTATCTAATA ATGAAGTGT 3120
 ATTACATATA GCGGAATTTG AGGATCTCTT TGATCCTGGA AATGGTTTAC CTAAAAGCTA 3180
 CAGAACCAAG CCAATATATT TTGAAATATT GATGCAGACA AATGAAATAA TAAAGAGATT 3240
 50 TTCACTGTTT ATAAAAATCT TTTTGTATAT GATAATAATC ATGATCACAA CTGAGATCAA 3300
 AAAAAATAT GACAGATTAT TTTGTTTAAA AATGCAGTTT TAATTATCTT AGTCTATAGA 3360
 AATGATCATT GCATGGAGGC ATGTATAGTT ATGATCTGTG TAAATCTGA CATAAAAAAC 3420
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 TTTATATTTT TTTCTAAAAA TTTTAGCAGT GTGTAAAGTA AGTAATCTTT AACTGAACTC 3540
 55 TGACCACTTA AAAAAAATCT TAAAAATGA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600
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 ATACTGAAAA ATACAGGTTT TTTTGACCAA AAGTTTTTAT ATCTTTTCTT TTTATTTATT 3720
 TTTTCTCTAA GTGCCAACAA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTTGGG 3780
 GACTTTTCCC ATATATTTCA CACTGGAGTG AATGAAGTTG TACTTCAATT CTAGAGAAAA 3840
 60 GTTATACCCA GGTCCCAAT TGAGAAATGC TTGCTTGATT GAAAAAGACA TCATCCCTTG 3900
 GTATACTCCA GGGATTGGTT TCAGGACCCC TGCAATTACC AAAATTGTGT CACACTCAAG 3960
 TCCTGCACTC ACCCTGCTCT AAAGATAAGG TGGCTTCTCT GTTTTCTCTC TGAATATCAA 4020
 CCAGAAACAA TGTGCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTTAAT 4080
 CCTGAATTCT GGTGTAAAT CTGGTTACAG CATAACTAGG ATTATAATGC TGCTCAATT 4140
 65 TCACAGCACT ACTTGCTTAT ATTGACAACA AATCATCTCG CTAAAGAGTG AATGTAGGCC 4200
 AGGCGCGGTG GCTCATGCT GTAAATCCAG CACTTTGGGA GGCGAGGGCG GGTGATCAC 4260
 GAGGTCAAGA GATCGAGACC ATCCTGGCTA ACATGGTAAA ACCCGTCTC TACTAAAAAT 4320
 AGAAAAAAG AAATTAGCCT AGCGTGGTGG CTGGCGGGCG CCTGTAGTCC CAGCTATTTG 4380
 GGAGGCTAAG GCAGGAGAAAT GCGTGAACC CGGGAGGCGG AGCTTGCACT GAGCOGAGGT 4440
 70 CGTGCCACTG CACTCCAGCC TGGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATAA 4500
 AAAAAAATA AGAGTGAATG TAATAGTCTT GCAGAAATG AATGAATACC TTTGTTCAAT 4560
 AAAGGAAATA TGCACTGCTC ACTTTTTTGA AGGAAATGCC AAGTTACGT TTTACACAA 4620
 GGCTAGAGTT TGTAAATCTT GGGTTCAITT GTGATGACAT AAGTCAGCAA ACTGCGGAA 4680
 TACTGTCTCT TCTATGTATT TTGTGAATAG TAAGCATAA TTTAGTTTGT TATTATCAAT 4740
 75 GAAAAATTA CTTGAAATTA AAGCTGCCTT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800
 TCCAGTATTG TATATGAGTT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAATA 4860
 TTTGCACACA TTTAAAAATA AATGTAAAGT TGCTTTTAA ACTACTCGGA TGTGTCTCTT 4920
 CTGAACAAAA

A212 Protein sequence:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Protein Accession #: O43511
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317, 347-369, 386-408, 420-442, 448-470, 486-508
 Cellular Localization: plasma membrane

5

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1      11      21      31      41      51
|      |      |      |      |      |
MAAPGGRSEP PQLPEYSCSY MVSFPVYSEL APQQQHERRL QERKTLRESL AKCCSCSRKR 60
AFGLVLTLPV ILEWLPKYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGGLYSA 120
FFPILTYTYP GTSRHSVSGP FVVSLMVGS VVLSMAPDEH FLVSSSNGTV LNTTMTDIAA 180
RDTARVLIAS ALTLVLGIIQ LIPGGLQIGF IVRYLADPLV GGFTTAAAPQ VLVSQLKIVL 240
NVSTKNYNGV LSIIYTLVEI FQNIQDTNLA DFTAGLLTIV VCMAYKELND RFRHKIPVPI 300
PIEVITVITIA TAISYQANLE KNYNAGIVKS IFRGLPPEL PPVSLFSEML AASPSIAVVA 360
YAIASVGVK YATKYDYTID GNQEFIAFGI SNIFSGFFSC FVATTALSRV AVQESTGGKT 420
QVAGIISAAI VMIAIALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LNRQNKIDAV 480
IWVFTCTVSI ILGLDLGLLA GLIPGLLTVV LRVQPPSWNG LGSIPSTDIY KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LKSGQLRAT 600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKEIEIQVDW NSELVVKVNV PRVPIHSLVL 660
DCGAISFLDV VGVRSRLRVV KEFQRIDVNV YFASLQDYVI EKLEQCGFFD DNIRKDTFFL 720
TVHDAILYLQ NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEBBLDV QDEAMRTLAS 780
QDEAMRTLAS
  
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A213 DNA SEQUENCE:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
 Unigene number: Hs.98280
 Probeset Accession #: AA418000
 Nucleic Acid Accession #: NM_021614
 Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

30

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1      11      21      31      41      51
|      |      |      |      |      |
CGGGGGCAGC AGCCCATGCC TCCGGTGCAA CAGCTGCGCC TCCTCCGGTG CCGCGGCGGC 60
GGGGGGGCGA GATAACCTGT CCTCGCTGCT CGCAGCTGCC TCGCCCGCGG GCGCCTTCCG 120
GACCGCGACC TCCTCGCGCG TGTCGGGCTC GTCTGCTGCT TGCTGCTGCT GCTCGTCCGG 180
CCGGGGCAGC CAGCTCAATG TGAGCGAGCT GACGCGCTCC AGCCATGCCA GTGCGCTCCG 240
CGCAGCAGTAC CGCAGCAGCT CGCGCGAGCA GTCGCGCTCC GCCTCCCACT ACCACCACTG 300
CCACAGCTCG CAGCCCGCGG CCAGCCCGAC GGGCAGCTCC GGCAGTCTGG GCTCCGCGCC 360
CCCGCTCTCG CACCACCACC ACCACCCGCA CCGCGCGCAC CACCAGCACC ACCAGCCCCA 420
GGCGCGCGCG GAGAGCAACC CCTTCACCGA AATAGCCATG AGCAGCTGCA GGTACAAACG 480
GGGCGCTATG CCGCGCTCCA GCAACTTGAG CGCGTCCGCG CGGAACCTCC ACGAGATGGA 540
CTCAGAGGCG CAGCCCTGCG AGCCCCCGCG GTCTGTGGGA GGAGGTGGCG GCGCGTCTCT 600
CCCGTCTGCA GAGCTGCGCG CGCGCGCGCG TGTTTCTGTC TCAGCCCCCG AGATCGTGGT 660
GTCTAAGCCC GAGCACAACA ACTCCAACA CCGTGGGCTC TATGGAACCG GCGCGGAGG 720
CAGCACTGGA GGAGGCGGCG GGGGTGGAGG GAGCGGGCAC GGCAGCAGCA GTGGCACCAA 780
GTCCAGCAAA AAGAAAAACG AGAACATCGG CTACAGCTGG GGCACCGCGC GCGCCCTGTT 840
CGAAAAAGCG AAGCGGCTCA GCGACTACGC GCTCATCTTC GGCATGTTGG GCATCGTGGT 900
CATGTCTATC GAGACCGAGC TGTCGTGGGG CGCTACGAC AAGCGTGGCG TGTTATCTCT 960
AGCTCTGAAA TGCCCTATCA GTCTCTCCAC GATCATCTCG CTCGGTCTGA TCATCGTGTA 1020
CCACGCCAGG GAAATACAGT TGTTCACTGT GGACATGGA GCAGATGACT GGAGAATAGC 1080
CATGACTTAT GAGCGTATTT TCTTCATCTG CTTGGAAATA CTGGTGTGTG CTATTCATCC 1140
CATACCTGGG AATTATACAT TCACATGGAG GCGCGGCGCT GCCTTCTCTC ATGCCCATC 1200
CACAACCAAC GCTGATGTGG ATATTATTTT ATCTATACCA ATGTTCTTAA GACTCTATCT 1260
GATTGCCAGA GTCATGCTTT TACATAGCAA ACTTTTCACT GATGCTCTCT CTAGAAGCAT 1320
TGGAGCACTT AATAAGATAA ACTTCAATAC ACGTTTGTGT ATGAAGACTT TAATGACTAT 1380
ATGCCAGGAA ACTGATCTCT TGGTTTTTAG TATCTCATTA TGGATAATTG CCGCATGGAC 1440
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GATGTGGTTG ATATCAATAA CTTTTCTCTC CATGTGTTAT GGTGACATGG TACCTAACAC 1560
ATACTGTGGA AAAGGAGTCT GCTTACTTAC TGGAAATTAT GGTGCTGGTT GCACAGCCCT 1620
GGTGTGAGCT GTAGTGGCAA GGAAGCTAGA ACTTACCAAA GCAGAAAAAC ACGTGACCAA 1680
TTTCATGATG GATACTCAGC TGAATAAAG AGTAAAAAAT GCAGCTGCCA ATGTACTCAG 1740
GGAAACATGG CTAATTATCA AAAATACAAA GCTAGTGAAG AAGATAGATC ATGCAAAAGT 1800
AAGAAAAACAT CAACGAAAAT TCCTGCAAGC TATTTCATCA TTAAGAAAGT TAAAAATGGA 1860
GCAGAGGAAA CTGAATGACC AAGCAACAC TTTGTGGGAC TTGGCAAGA CCCAGAACAT 1920
CATGTATGAT ATGATTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATTGT 1980
TACCCCTGAA ACAAACTAG AGACTTGTAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT 2040
AAGCCAGACC ATCAGGCGAG AGCAGAGAGA TTTCAATTGAG GCTCAGATGG AGAGCTACGA 2100
CAAGCAGTCT ACTTACAATG CTGAGCGGTC CCGGTCTCTG TCCAGGAGGC GCGGTCTCTC 2160
TTCCACAGCA CCACCAACTT CATCAGAGAG TAGCTAGAAG AGAATAAGTT AACCACAAAA 2220
TAAGACTTTT TGCCATCATA TGGTCAATAT TTTAGCTTTT ATTGTAAAGC CCCTATGGTT 2280
CTAATCAGCG TTATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTAA 2340
GGCCAAATAG AGTGAAGACT CTTTTTTTT CTTCAGATG CACAGGGAAT GCACCTATTA 2400
TTGCTATATA GATTGTTCTC CTGTAAATTT CACTAACTTT TTATTCTATG ACTTCAACA 2460
AACTTTACTA CTACATTATA TGATATATAA TAAAAAAGT TAATTTCGGA
  
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A214 Protein sequence:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
 Unigene number: Hs.98280
 Probeset Accession #: AA418000
 Protein Accession #: NP_067627
 Signal sequence: none found
 Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488
Cellular Localization: plasma membrane

5	1	11	21	31	41	51	
	MSSCRYNGGV	MRPLENLSAS	RRLNHEDMSE	AQPLQPPASV	GGGGGASSPS	ADAAAAAASV	60
	SSAPEIVVSK	PEHNNSNLNA	LYVTGGGGST	GGGGGGGGSG	HGSSSTGKSS	KKKNNQNGYK	120
	LGHRRALPEK	RKRRLSDYALI	PGMFGIVVMV	IETELSWGAY	DKASLYSLAL	KCLISLSTII	180
10	LLGLIIVYHA	REIQFLPMVDN	GADWDRIAMT	YERIFFICLE	ILVCAIHPID	GNYPFWTAR	240
	LAFSYAPSTT	TADVDIILSI	PMFLRLYLYI	RVMLHLSKLF	TDASSRIGKA	LNKNTNPTFR	300
	VKMTLMTICP	GTVLVLLTIS	LWIIAAMTVR	ACERYHDQDD	VTSNFLAGAM	LISITFLSIG	360
	YGDMPNTICY	GKGVCLLTGI	MGAGCTALVV	AVVKAKLELT	KAEKHVENFM	MDTQLTKRVK	420
	NAAANVLRET	WLYIKNTKLV	KIKIDHAKVRK	HQRKFLQAIH	QLRSVKMEQR	KLNDQANTLV	480
15	DLAKTQNIY	DMISDLNERS	EDFEKRIIVTL	EPKLETLIGS	IHALFGLISQ	TIRQQQRDFI	540
	EAOESYDKH	VTYNAERSSR	SSRRRRSSIV	ATTTSSPSSS			

A215 DNA SEQUENCE:

20 ATIS DNA SEQUENCE:
Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
25	CTGCGATCCC	GCAGGGCAGC	GACGCGACTC	TGGTGCGGGC	CGTCTTCTTC	CCCCCGAGCT	60
	GGGCGTGGCG	GGCCGCAATG	AACTGSGAGC	TGCTGTCTGTG	GCTGCTGGTG	CTGTGGCGCG	120
30	TGCTCTCTGT	CTTGGTGCGA	CTGCTGCGCT	TCTTGAGGGC	TGAGCGGCGAC	CTGACGCTAC	180
	TATGGGCGGA	GTGGCAGGAG	CGAGCCGCCAG	AATGGGAGAG	GACTGATATG	GTGTGTGTGG	240
	TGACTGTAGC	CTCAGTGAAG	ATTGGTGAGG	AGCTGGCTTA	CCAGTGTGCT	AAACTAGGAG	300
	TTTCTCTTGT	TGCTGCAGCC	AGAAGAGATG	ATGAGCTGGA	AAGGGTGAAA	AGAGGTATGC	360
35	TAGAGAAATG	CAATTTAAAA	GAAAAAGATA	TACTTGTTTT	GCCCCTTGAC	CTGACCGACA	420
	CTGGTTTCCCA	TGAAGCGGCT	ACCAAAGCTG	TCTTCCAGCA	GTTTGTGTAGA	ATGACCATTC	480
	TGGTCAACAA	TGGTGGAAAT	TCCCAAGCTT	CTCTGTGATC	GGATACACAG	TTCGATGTCT	540
40	ACAGAAAGCT	AATAGAGCTT	AACTACTTTAG	GGAGCGTGTG	CTTGACAAA	TGTGTTCTCG	600
	CTCACATGAT	CGAGAGGAA	CAGGAAAGAT	TGTGTACTGT	GAATAGCATC	CTGGGTATCA	660
	TATCTGTACC	TCTTTCATTT	GGATACTGTG	TAGCAAGCA	TGCTCTCCGT	GGGTTTTTTA	720
	ATGGCCTTGG	AACCAAGACT	GGCCACATACC	CAGGTATAAT	AGTTTCTAAT	ATTTGCCCGG	780
	GACCTGTGCA	ATCAAATATT	GTGGAGAATT	CCCTAGCTGG	AGAAGTCACA	AAGACTATAG	840
	GCAATAATGG	AGACCAGTCC	CACAAGATGA	CAACCAGTGG	TGTGTGCGG	CTGATGTTAA	900
	TCAGCATGGC	CAATGATTTG	AAAGAAGTTT	GGATCTCAGA	ACAACCTTTC	TGTGTATGAA	960
45	CATATTTGTG	GCAATACATG	CCAACTCTGG	CTCGTGGTAG	AACCAACAAC	ATTGGGGAAG	1020
	AAAGGATTGA	GAACTTTGAA	AGTGGCTGTG	ATGCAGACTC	TTCCTATTAT	AAAATCTTAT	1080
	AGACAAAAAC	TGACTTGAAG	AGGACCTGTG	ACTTTTTCAG	CCACTGTGAG	GAGAAATGGA	1140
	AAACATGAAA	ACAGCAATCT	TCTTATGCTT	TGGAATATTC	AAAGACTAAT	TGTGATTTTT	1200
	ACTTTTAAAT	AGATATAGAT	TGTCTTCCAA	CATGGATATG	AATAAAAAAT	AAATAATAAA	1260
	AGATTGCCAT	GACCTTGACA	AA				

A216 Protein sequence:

Gene name:	OGI-86 protein
Unigene number:	Hs.109201
Probeset Accession #:	AW161450
Protein Accession #:	NP_057113
Signal sequence:	1-26
Transmembrane domains:	183-206, 221-243
Cellular Localization:	plasma membrane

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65	MNWEILLWLL	VLCAILLLLV	QLLRFLRADG	DLTLLEWAEQ	GRRPEWELTD	MVVVWTGASS	60
	GIGEELAYQL	SKLGSLVLVS	ARRVHELERV	KRRCELENGL	KEKDILVLPL	DLTDTGSHEA	120
	ATKAVLQEPG	RIDLIVNNGG	MSQRLSDCT	SLDVYRKLIE	LAYLQTVSLT	KCVLFPMHIE	180
	QKGIKIVTVS	ILGIISVPLS	IGYCSAKHAL	GGFFNGRLRE	LATYPGIIVS	NICPGPVQSN	240
	IVENSAGREV	TKTIGNNGDQ	SHIMTTSRCV	RMLISMAAND	LKEVWIESEQ	PLLVTVYLWQY	300
	MPTMAWWTIN	KMGKKRIENF	KSGVDADSSY	FLIKITKHD			

A217 DNA SEQUENCE:

75

Gene name:	Homo sapiens mRNA; cDNA DKFPz56401763 (from clone DKFPz56401763)
Unigene number:	Hs.27373
Probeset Accession #:	FL3036
Nucleic Acid Accession #:	AC012478
Coding sequence:	1-1896 (underlined sequences correspond to start and stop codons)

80

1	11	21	31	41	51	
ATGCGCGCG	TGCGGCTGCC	GGCGCGGCTC	CTGCGCGTGC	TGCTGCTGCG	GCTCCTGGCC	60
GCTCCGCGCG	CCGCGGCCAG	CAGAGCGGAG	TCCGCTCTCG	CGCGGTGGCC	CGAACCCGAG	120
CGCGAGTTCG	GGCCAACGCG	CGCGCGGGGG	CCCGGGAACA	CCACCGCGTT	TGGTCTTGGG	180
GGCGCGGGCG	GCAGCGGCTC	CTCAGCTCC	AACAGCAGTG	GGCAGCGCTT	GATGACCCGC	240

5
 10
 15
 20
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 30

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ATTTCATCC TCCTCCGGGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GCGTTGCGC 300
TTTACCACCC TCCTCATCGC CTGCTGCTGT CTGCGCGTCT TCAGGTGCGG AAAGAGGTGA 360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
TCCTTGCGCG CTGCACTGAG ACCTGAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTT 540
GTGCCCCAC CTCTCATCTT CGACATTGAC CTTCCAGCAA GATGCACTGG AAGGCTGTAT 600
GGTGAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GGCATCTCTG GGAAAGTTGG 660
TCAGCTGCAA CTTGGGGTGT GAAGGACTGG ACCTGGGAAG CCTCTTGCGT CGGAGGTGTT 720
GAAACCAAAA CGAAGCTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGTG AGGCATCTGC 780
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
TTTGGGCATC CTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900
CTGAATCTCA TGGAAAAGCT GGATTCTCTT GCCTTAGCGA GAAACACCCG GGCTCCATCT 960
GCCAGGTGCT TGGCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
CCTTGGTGGC ACTTCAGGCG CACAGGCTCT CCAATAAAAA CCTTTACAC ACAAACCATG 1080
AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCCGCCAGC GGGGCACCTT TTGTGAAGAC 1140
AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTTCTCCA AACAGCTGGC CTGGAAGCCA 1200
GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
ACCAATCCTG TCAGGTTGGC TCGTTTCAGT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
AGGGTGTTC GCGCTCCGGG GCAGTCTCTG CATGGCGGAG GGTCAAGCGG TACCGCAACT 1380
TGCTTTTGG TTTTGAAGAT TCTGTTGAGG CGCCATCTCT ACCTTGACCT CTCTACAAA 1440
ATCTGTCTCC CCGTCTGTGC CGTGAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
GTCTTGTGCT CATTTGAGCA GAGCCACAA AAGGCAGCTG CTGCCACGGG GGAGCCTGTC 1560
AAGAGAGGGC CCAAGTGGGA ATTGACCAA CACATATGCC CTGGCTGGGG GATCACACAT 1620
GGCACTCTGC AGCAATTTC AGATACCCAA GGCCAGGAAG GCCCAAGTGA GGATGTCACT 1680
CACCTGGAG GAGACTTGA TGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
GATGGCAGAT GCCAGAAGAT GGTCTGTATG TCTGAGGAAG GGCCACCTAG TTTGACAGGA 1800
TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860
TCCCCCGAC AGCCCCGTGT TCTGTCCAGG CCCTGA
  
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A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKF2p56401763 (from clone DKF2p56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Protein Accession #: PGENESH predicted
 Signal sequence: 1-27
 Transmembrane domains: 94-115, 448-469
 Cellular Localization: not determined

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 45
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1 11 21 31 41 51
| | | | |
MRVPLPAPL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTRPFGSG 60
AAGSGSSSS NSSGDALVTR ISILLRDLPT LKAAVIVAF FTTLLIACLL LRVFRSGKRL 120
KKTRKYDIIT TPAERVEMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGQTLTLPV 180
VPPFFILDID LPARCSGRPD GGIRPGKTCF PAMWHPVESW SAATWGVKDW TWKPSCVGGV 240
ETKINVMYKT PAPSCVSGIC SDCHWQARFH VTTMELLPPP FGHPPKVPPT STPHGFRQLQ 300
LNLMEKLDSS ALRRNTRAPS ARCLPLVLA EMAAESDLFN PWHFSAATGS PIKTLTYQTM 360
STLGLDVFCG AQORGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHLL RLLRECFPLS 420
THPVRLARSD ARGQASLTGR RVFRPRQSL HGGOSAGTAT CLLVLKILLR RHPHDLDFYK 480
ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHAHEFV KRGPSSQLTR HTCPCGWGITH 540
ANLQTIPTDQ QGEGPREDTV HPGGDLGDVA NFYLEEGFPQ DGRQRMVIM SEEGPPSLTG 600
CERLTGSHHF SSHSKSWFL SPRQPLFLSR P
  
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A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

65
 70
 75
 80

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1 11 21 31 41 51
| | | | |
ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACITTTGGTGC TTCTCATTA AAGAGAGTGA 60
GCCTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
CAGCAAAAGT ACACACACCT GGTGCAATT CAAAACAAAG AAGAGATTGA GTACCTAAAC 180
TCCATATTGA GCTATTTCAC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
GAACCCCAAC ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
GATGTGGGCA TGTGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAACCTG 540
ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGGTTTGCA GTCAACCACT GGGAAACTTC 600
AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
ACCATGCAGT GTATGTCCTC TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCCCTGA 780
AGCTTCCCAT GGAACACAA CTTGTACATT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840
GCCAGAGGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACCTGTAAA 900
GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
CCTGCTGGAG AGTTTACCTT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
TTGCAAGGAC CAGCCAGAGT TGAATGACCC ACTCAAGGGC AGTGGACACA GCAAAATGCCA 1080
GTTTGTGAAG CTTTTCAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140
CTTCCTAGTG CTTCTGGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
GGTTTGTGT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCAAGGGA GTGGGACAC 1260
  
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5 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTTGT TGCTTCAGC 1380
 TGTGAGGAGG GATTTGAAAT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAAG AGGTTCCCTC CTGCCAAGTG GTAAAAATGT CAAGCCTGGC AGTTCCGGGA 1500
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCA CTGTGTGCAA GTTCGCCTGT 1560
 CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 CTTTCTGCTG CTGGACTCTC CCTCCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740
 10 TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A220 Protein sequence:
 15 Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 20 Transmembrane domains: 555-573
 C-lectin domain: 23-139
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 MIAAQFLSAL TLVLLIKESG ANSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKESIEYLN 60
 SILSYSPSY WIGIRKNNV WVMVGTQKPL TEEAKNWAFC BPNRQKDED CVEIYIKREK 120
 DVGWNDERC SKKLLALCYT AACTNTSCSG HGECVETINN YTCKCDPFGS GLKCEQIVNC 180
 30 TALESPHESG LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
 ECDAVTNPAN GFVECFNPNG SPPHNTTCTP DCEEGFELMG AQSLQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSHS PAGEFTPKSS CNFTCEEFGM LQGPQVCT TQGWTOQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSFPRY GSSCEFSCEQ GPVLRGSKRL QCGPTGEWDN 420
 EKPTCEAVRC DAVHQPPKGL VRCASHPIGE FTYKSSCAFS CEEGFELYGS TQLECTSGQG 480
 35 WTEVPSCQV VKCSLAVPQ KINMSCSGEP VPGTVCKPAC PEGWTLNGSA ARTCGATGHW 540
 SGLLPCTEAP TESNIPLVAG LSAAGLSLLT LAPFLLMLRK CLRKAKKFVP ASSCQSLESD 600
 GSYQKPSYIL

Taxol Prostate
 40 A221 DNA SEQUENCE
 Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 Probeset Accession #: N51002
 Nucleic Acid Accession #: N51002
 45 Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60
 50 CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120
 GAAAGGGATC GTCTTCTAGA CACCCCTCGG GAGACCCAGG AAAGCCTCTC ACTTCCCCAG 180
 CAAAGACTTC AGGATGTTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGAGCC 240
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300
 CGGGAATTTG CTGCACTGAC AAAAGAATTA AATGCCTGCA GGGAACTACT TCTAGAAAAG 360
 55 GAAGAAAGAA TCTCTGAACT TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420
 TTGGAGTGCC TTGTGTCAAG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
 GCCCAGTCTC CCTCAGGAGT ATCCAGTGAA GTTGAAGTTC TCAAGGCACT GAAATCTTTG 540
 TTTGAGCACC ACAAGGCCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600
 AGAGTCTCTG CACTGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCTTTGCGT 660
 60 GAACAAAATG TTCATATACA AAGAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
 CATCTTGAGG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTG CAATGGTTCT 780
 ATAGACTCAA CCGATGAAAC TAGTCAAATA GTTGAAGTAC AAGAATTGCT TGAAGAGCAA 840
 AACTATGAAA TGGCCAGAT GAAAGAACGT TTAGCAGCCC TTCTTCCCAG AGTGGGAGAG 900
 GTGGAAACAG AAGCAGAGAC AGCAAGAAAG GATCTCATTG AAACAGAAAG AATGAACACC 960
 65 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAAGAAAT 1020
 ACAACCCCTG AAAAGCGTTA OCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080
 AATGATAAAC TAGAAAATGA GTTAGCAAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140
 AAAAACAGAC AGTTACAAGA AOGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200
 70 AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAAGTGG CTCAGAGAAAT TGCAGCCCTA 1260
 ACCAAGGCTG AAGAGAGACA TGGAAAATAT GAAGAACTGA TGAGACATTG AGAGGTCNA 1320
 CTTGAAGAGA AGAATCAAGA ACTTCAAGA GCTAGGCAAA GAGAGAAAAA GAATGAGGAG 1380
 CATAACAAGA GATTATOGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCCTA 1440
 CAACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA 1500
 TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAG ATTAGCAGAA 1560
 75 GAAATTGAAA AGCTGAGATG TGAAGTTGAC CAATTGAAA TGAGAACTGG CTCTTTAATT 1620
 GAACCCACAA TACCAAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680
 TCCCTAGTGG ACAGCCAGTC TGATTACAGA ACAACTAAAG TAATAAGAAG ACCAAGGAGA 1740
 GGCCGCAATG GTGTGGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800
 AATGAACTC AACAGATTGG AGTACTAAGC AGCCACCCCT TTGAAGTGA CACTGAAATG 1860
 80 TCTGATATG TCGATGATGA CAGAGAAACA ATTTTAGCT CAATGGATCT TCTCTCTCA 1920
 AGTGGTCATT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GATGCCATC 1980
 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGCG TGCTGAAGAA 2040
 ATTGAAAATA GAGTGGCTAG TGTGAGCTC GAAGGCCCTG ATTTGGCAAG GGTCCACCCA 2100

5 GGTACCTCCA TTA CTGCTC TGTTACAGCT TCATCGCTGG CCAGTTTCAT TCCCCCAGT 2160
 GGACACTCAA CTC CAAAGCT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220
 GTCATGACAC TGCCAAAGTA TCTGAGGAAA CATCGGAGAA AGATTGCAGT TGTGGAAGAA 2280
 GATGGTGGAG AGGACAAAGC AACAAATTAA TGTGAAACTT CTCCTCTCTC TACCCCTAGA 2340
 GCCTCAGAA TGA CT CACAC TCTCCCTCTT TCCTACCA CA ATGATGCTCG AAGTAGTTTA 2400
 TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTGTGTAGTG CCAACAGCAG CCAAGACTCT 2460
 CTTCACAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520
 AAAGAAAAAG CTGCACTTGG GCAGCTCOGA GCCTTTATGG AGACTGAAGC TGCAGCTCAG 2580
 GAGTCCCTGG GGTTCAGCAA ACTCGGAAC CAAGCTGAGA AGGATCGAAG ACTAAAGAAA 2640
 10 AAGCATGAAC TTCTTGAAGA AGCTCGGAGA AAGGATTAC CTTTGTCCCA GTGGGATGGG 2700
 CCAACTGTGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
 TGCCGAGCCA ACGTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG 2820
 AGAGAAATGG GAATCAGCAA TCCACTGCAT CGCTTAAAC TTGATTAGC AATCCAGGAG 2880
 ATGGTTTCCC TAACAAGTCC TTCAGCTCCT CCAACATCTC GAACTCCTTC AGGCAACGTT 2940
 15 TGGGTGACTC ATGAAGAAAT GGAAATCTTT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000
 GAAGGAAGCT GGGCCCAAGT TCCGGTTTTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060
 CATGATGGAA TTGGAATAGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
 TTTATGGAAT GCTTGTGAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCCGT 3180
 20 GTCCATTTAA AATGTGTGGA TAGTTTCCAT CGAACAAGTT TACAATATGG AATTATGTGC 3240
 TTAAGAGAGT TGAATATAGA CAGAAAAGAA CTAGAAAGAA GACGGGAAGC AAGCCACAT 3300
 GAAATAAAG ACGTGTGGT GTGGAGCAAT GACCGAATTA TTCCGTGGAT ACAAGCAATT 3360
 GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
 CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480
 25 ACCCAGGCAA GGCAGATTCT TGAAGAGAA TACAATAACC TCTTGGCCCT GGGAACTGAA 3540
 AGGCGACTGG ATGAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAAGCAG 3600
 TTTCTCTCTC GTGAAGTACA TGAATCAGC ATGATGCTCG GGTCTCTAGA AACATTACCA 3660
 GCTGGATTGA GGTTAACCAAC AACCTCTGGG CAATCAAGAA AATGACAAC AGATGTTGCT 3720
 30 TCATCAAGAC TGCAGAGGTT AGACAACCTC ACTGTTGCA CATACTCATG TCTCGAGTAA 3780
 GCGCCGCTT TAA

A222 Protein sequence:

Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 35 Probeset Accession #: N51002
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: none found
 40 AAA domain: 286-539
 SAM domains: 895-964, 1017-1084, 1105-1177
 Cellular Localization: not determined

1 11 21 31 41 51
 45 MMCEVMPTIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDTLR ETQESLSLAQ 60
 QRLQDVIYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEK NACREQLLEK 120
 EEEISELKAE RNNTRILLEH LECLVSRHER SLRMTVVKRO AQSPGVSSE VEVLLKALKSL 180
 FEHHKALDEK VREKRLVSLE RVSALEEEEL AANQEI VALR EQNVHIQRKM ASSEGSTESE 240
 HLEGMEPGQK VHEKRLSNGS IDSTDTSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300
 50 VEQEAETARK DLIKTEEMNT KYQRDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360
 NDKLENELAN KEALLRQME EKNRQLQERLE LAEQKLQQT M RKAETLPEVE AELAQRIALA 420
 TKABERHGN ERMHRHLEGQ LEEKNQELQR ARQREKMN E HNKRLSDTV D RLLTESNERL 480
 QLHLKERRMA LSEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKRLSELD QLMRTGSLI 540
 EPTIFRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRRRPR GRMGVRRDEP KVKSLGDHEW 600
 55 NRTQIGIVLS SHPFESDTEM SDIDDDRET IPSSMDLLSP SGHSDAQTLA MMLQEQLDAI 660
 NKEIRLIQEE KESTELRAEE IENRVAVSLE EGLNLARVHP GTSITASVTA SSLASSSPSP 720
 GHSTPKLTPR SPAREMDRMG VMTLPDLRK HRRKIAVVEE DGREDKATIK CETSPPPTPR 780
 ALRMTHLTPS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKKGI KSSIGRLFGK 840
 60 KEKARLGQLR KGMETAAAAQ ESLGLQKLTG QAEKDRRLK KHELLEEAR KGLPFAQWDG 900
 PTVVWLELW LGMPAWYVAA CRANVKGSAI MSALSDEIQ REIGISNPLH RLKLRLAIQE 960
 MVSILTSPSAP PSTRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCPVP LQTLAYGDMN 1020
 HEWIGNEWLP SLGLPOYRSY FMECLVDARM LDHLTKDLR VHLKMDVSFH RTSLQYGIMC 1080
 LKRLNYDRKE LERRREASQH EIKQVLVWSN DRIIRWQAI GLREYANNIL ESGVHGSLIA 1140
 65 LDENFDYSSL TLLLIQPTON TQARQILERE YNNLLALGTE RRLDBSDDKN FRRGSTWRRQ 1200
 FPPREVHGIS MMPGSSETLP AGFRLTTTSG QSRKMTTDVA SSRLQRLDNS TVRTYSCLE

A223 DNA SEQUENCE

Gene name: CDA14
 Unigene number: Hs.26813
 70 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCTTTTCG 60
 AAGGTTCTCT AGAGCTATGT AGAGACTTCA GCCAGTGGAG GTACAGTTTC TCTAATAGCA 120
 TTTCAACTA TGGCTTTATT AACCATAATG GAATCTCTAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300
 80 GTTGATCTCG CAGATGGTGT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480

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GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCTCG TGGTCATGCA 600
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTTG 660
TCTTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTAG ATGGAACCTGA AAAAATTGCT 720
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAAACAA ACTACATACA 780
TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840
CATGTGCGAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTTCTCTT 900
ATGGTGACAG TTAAGTGGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
ATTGTTGGAG GAATCTTTTC AACAAACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020
GAAATAAATT GCTGTGCTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCCTTTT 1080
GAGGATGGCC ACACAGACAA CCATCTACCT CTTTATAGAAA ATAATACACA TTGA

A224 Protein sequence:

Gene name: CDA14
Unigene number: Hs.26813
Probeset Accession #: N32912
Protein Accession #: NP_057654
Signal sequence: none found
Transmembrane domains: none found
Cellular Localization: nuclear

1 11 21 31 41 51
MRRINRKKTL SLVKELDAPP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
KYEYEVKDF SSKLRINIDI TVAMKQYVG ADVLDLAETM VASADGLVYE PTVFDLSPQQ 120
KEWQRLQLI QSRLEHSL QDVIPKSAFK STSTALPPRE DDSSQSPNAC RINGHLYVNK 180
VAGNPHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SPGELVPAII NPLDGTAKIA 240
IDHNQMFQYF ITVPTKLHT YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
MVTVEEHMP FQPFVRLCG IVGGIFSTTG MLHGIGKPIV EIICCRFRLG SYKPVNSVFP 360
EDGHTDNHLP LLENMTH

Uterine**A225 DNA SEQUENCE:**

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTTA CTGTCACAG TTTCTTCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAGTAA GAAGCCATTA 240
ATGGTTATT ATCAGCTTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGTC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAAATT ATCAGCTGAT GGGCAATATG TGCTAGAAAT CATGTTTGTA 420
GACCTCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAAGAG ATTGTACACA 480
TATGAGCCTC GGGATTTACC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC GATAGAGAT GATAGAAAA AGCCTTCACT TCAAAGAAAG CAAATTTCAT 600
GAAGAAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
TACTATTATA GTTTTITTA TGTGTTTGA ATAGTCTTAT TAAATAAAT GTTTTITTA 720
TCTGAAAAA AAAAAA AAAAAA

A226 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

1 11 21 31 41 51
MLHSLALGLC LLLVTSSNL AIAIKCKRP PQTLRGWGD DITWVQTYEE GLFYAQSKK 60
PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKRLS PDGQYVPRIM 120
FVDPSTLVRA DIAGRYNRL YTYEPRDLPL LIENMKALR LIQSEL

A227 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
Unigene number: Hs.285529
Probeset Accession #: AA460530
Nucleic Acid Accession #: NM_003667
Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GTGGGGGCAA	CGGGCACCTC	AGTCCCGGCC	GGGCTTCTCC	TCGGCGGCCA	CGCCGTGGGG	60
	TCAGGAACGC	GGGCTCTGGC	GCTGCAGACG	CCCGCTGAGT	TGCAGAAGCG	CACGGAGCGG	120
5	CGCCCGGCGC	GCCACGGGCC	GTAGCAGTCC	GGTGTCTCTC	TCGGCCCGCG	TCGGGCTCGT	180
	GGCCCGCTAC	TTGGGGCACC	ATGGACACCT	CCCGGCTCGG	TGTGCTCCCT	TCCTTGCCTG	240
	TGCTGCTGCA	GCTGGCGACC	GGGGGCGAGT	CTCCAGGCTC	TGGTGTGTTG	CTGAGGGGCT	300
	GCCCCACACA	CTGTCAATGC	GAGCCGACG	GCAGGATGTT	GCTCAGGGTG	GACTGTCTCG	360
	ACCTGGGGCT	CTCGAGCTG	CCTTCCAACC	TCAGCGTCTT	CACCTCTTAC	CTAGACCTCA	420
10	GATGAACAA	CATCAGTCAG	CTGCTCCCGA	ATCCCTGCGC	CAGTCTCCGC	TTCTTGGAGG	480
	AGTTACGTCT	TGCGGGAAC	GCTCTGACAT	ACATTCCCAA	GGGAGCATTC	ACTGGCCCTT	540
	ACAGTCTTAA	AGTTCTTATG	CTGCAGAAAT	ATCAGCTAAG	ACACGTACCC	ACAGAAGCTC	600
	TGCAGAAATT	GCGAAGCCTT	CAATCCCTGC	GTCGTGATGC	TAACACATC	AGCTATGTGC	660
	CCCCAAGCTG	TTTCAGTGGC	CTGCAATCCC	TGAGGCACCT	GTGGCTGSGT	GACAATGCGT	720
15	TAACAGAAAT	CCCGTCCAG	GCTTTTAGAA	GTTTATCGCG	ATTGCAAGCC	ATGACCTTGG	780
	CCCTGAACAA	AATACACCAC	ATACCAGACT	ATGCTTTTGG	AAACCTCTCC	AGCTTGGTAG	840
	TTCTACATCT	CCATACCAAT	AGAATCCACT	CCCTGGGAAA	GAAATGCTTT	GATGGGCTCC	900
	ACAGCTTAGA	GACTTTAGAT	TTAAATTACA	ATAACCTTGA	TGAATTCGCC	ACTGCAATTA	960
	GGACACTCTC	CAACCTTAAA	GAACCTAGAT	TTATAGCAAA	CAATATCAGG	TCGATACCTG	1020
20	AGAAAGCAAT	TGTAGGCAAC	CCTTCTCTTA	TTACAATAACA	TTTCTATGAC	AATCCCATCC	1080
	AATTTGTGTG	GAGATCTGCT	TTTCAACATT	TACCTGAACT	AAGAACAAGT	ACTCTGAATG	1140
	GTGCTCTACA	AATAACTGAA	TTTCTGATG	TAACCTGAA	TGCAAACTCG	GAGAGTCTGA	1200
	CTTTAACTGG	AGCAGATGAT	TCATCTCTTC	CTCAAACTCG	CTGCAATCAG	TTACCTAATC	1260
25	TCCAAGTGCT	AGATCTGTCT	TACAACCTAT	TAGAAGATT	ACCCAGTTTT	TCAGTCTGCC	1320
	AAAAAGCTTCA	AAAAATTGAC	CTAAGACATA	ATGAATCTA	CGAAATTAAA	GTTGACACTT	1380
	TCCAGCAATT	GCTTAGCCTC	CGATGCTGTA	ATTTGGCTTG	GAACAAAATT	GCTATTATTC	1440
	ACCCCAATGC	ATTTTCCACT	TTGCCATCCC	TAATAAAGCT	GGACCTATCG	TCCAACCTCC	1500
	TGTGTCTTTT	TCCTATAACT	GGGTACATG	GTTTAACTCA	CTTAAATTA	ACAGGAAATC	1560
30	ATGCCTTACA	GAGCTTGATA	TCATCTGAAA	ACTTTCCAGA	ACTCAAGGTT	ATAGAAATGC	1620
	CTTATGCTTA	CCAAGTCTGT	GCAATTTGAG	TGTGTGAGAA	TGCCTATAAG	ATTTCTAATC	1680
	AATGGAATTA	AGGTGACAA	AGCAGTATGG	ACGACCTTCA	TAAGAAAGAT	GCTGGAATGT	1740
	TTCAAGCTCA	AGATGAACGT	GACCTTGAAG	ATTTCTGCT	TGACTTTGAG	GAAGACCTGA	1800
	AAGCCCTTCA	TTCAAGTGCAG	TGTTCACTT	CCCGAGGCC	CTTCAAAACC	TGTGAACACC	1860
35	TGCTTGATGG	CTGGCTGATC	AGAAATTGGAG	TGTGGACCAT	AGCAGTTCTG	GCACTTACTT	1920
	GTAATGCTTT	GGTGAATCTCA	ACAGTTTCA	GATCCCTCT	GTACATTTC	CCCATTTAAC	1980
	TGTTAATTTG	GGTCACTGCA	GCAGTGAACA	TGCTCAOGGG	AGTCTCCAGT	GCCGTGCTGG	2040
	CTGGTGTGGA	TGCTTCACT	TTTGGCAGCT	TTGCACGACA	TGGTGCCTGG	TGGGAGAATG	2100
	GGGTTGGTTG	CCATGTCAAT	GGTTTTTGT	CCATTTTTC	TTCAAGATCA	TCGTTTTTC	2160
40	TGCTTACTCT	GGCAGCCCTG	GAGCGTGGGT	TCTCTGTGAA	ATATTCTGCA	AAATTTGAAA	2220
	CGAAAGCTCC	ATTTCTAGC	CTGAAAGTAA	TCATTTTGGT	CTGTGCCCTG	CTGGCTTTGA	2280
	CCATGGCCCG	AGTTCCCTCT	CTGGGTGGCA	GCAAGTATGG	CGCCTCCCT	CTGTGCCCTG	2340
	CTTTGCTTTT	TGGGGAGCCC	AGCACCATGG	GCTACATGTT	CGCTCTCATC	TTGCTCAATT	2400
	CCCTTTGCTT	CCTCATGATG	ACCATTGCCT	ACACCAAGCT	CTACTGCAAT	TTGGACAAGG	2460
45	GAGACCTGGA	GAATATTGTC	GACTGCTCTA	TGGTAAACAA	CATTGCCCTG	TTGCTCTTCA	2520
	CCAACTGCAT	CCTTAACTGC	CCTGTGGCTT	TCTTGTCTT	CTCCTCTTTA	ATAAACCTTA	2580
	CATTATATCA	TCCTGAAGTA	ATTAAGTTTA	TCCTTCTGTT	GGTAGTCCCA	CTTCTGCTAT	2640
	GTCTCAATCC	CCTTCTCATC	ATCTTGTTC	ATCCTCACTT	TAAGGAGGAT	CTGGTGAGCC	2700
	TGAGAAAGCA	AACCTACGTC	TGGACAAGAT	CAAAACACCC	AAGCTTGTAT	TCAATTAATC	2760
50	CTGATGATGT	CGAAAACAG	TCCTGTGACT	CAACTCAAGC	CTTGGTAACC	TTTACCAGCT	2820
	CCAGCATCAC	TTTGAACATG	CCTCCCAAGT	CGTGGCCATC	ACCAGCTTAT	CCAGTGACTG	2880
	AGAGCTGCCA	TCCTTCTCT	GTGGCATTG	TCCCATGTCT	CTAATTAAAT	TGTGAAGGAA	2940
	AATGTTTCA	AAGGTGAGA	ACCTGAAAAT	GTGAGATTGA	GTATATCAGA	GCAGTAATTA	3000
	ATAAGAAGAG	CTGAGGTGAA	ACTCGGTTTA	AA			

A228 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
	MDTSRLGVLL	SLPVLLQLAT	GGSSPRSGVL	LRGCPHCHC	EPDGRMLLRV	DCSDLGLSEL	60
	PSNLSVPTSY	LDLSMNNISQ	LLPNPLPSLR	FLEELRLAGN	ALTYIPKGAF	TGLYSLKVLN	120
	LQNNQLRHVP	TEALQNLRSL	QSLRLDANHI	SYVPPSCFSG	LHSLRLRLWD	DNALTEIPVQ	180
	AFRSLSALQA	MTLALNKIHH	IPDYAFGNLS	SLVVLHLNHN	RIHSLGKRCF	DGLHSLLETLD	240
70	LNYNLDEFP	TAIRTLNLK	ELGFHSNNIR	SIPEKAFVGN	PSLTIHFYD	NPIQPVGRSA	300
	FOHLPELRTL	TLNGASQITE	FPDLTGTAHL	ESLTLTGAQI	SSLFQTVCSQ	LPNLQVLDLS	360
	YNLELDLPS	SVQQLKQID	LRHNBIYEIK	VDTFQQLLSL	RLNLAWNKI	AIHPNAPST	420
	LPSLIKLDLS	SNLSSFPIT	GLHGLTHLKL	TGNHALQSLI	SSENFPKLVK	IEMFYAYQCC	480
	APGVCEAYK	ISNQWNKGDN	SSMDLHLKRD	AGMFQAQDER	DLEDPLDFFE	EDLKALHVSQ	540
75	CSFSPGPFKP	CEHLLDGWLI	RIGVWTIAVL	ALCNALVTS	TVFRSPLYIS	PIKLLIGVIA	600
	AVNMLTGVSS	AVLAGVDAFT	FGSPARKGAW	WENGVGCHVI	GFLSIFASES	SVFLTLAAL	660
	ERGPSVKYIA	KPETKAPFSS	LKVIILLCAL	LALTMAAVPL	LGGSKYGASP	LCLFLPFGEF	720
	STMGMVALI	LLNSLCFLMM	TIAYTKLYCN	LDKGDLENIW	DCSMVKHIAL	LLFTNCILNC	780
80	PVAFPLSPSSL	INLTPISEPV	IKPILLVVVP	LPACLNPLLY	ILFNPHFKED	LVSLRKQTVV	840
	WTRSKHPSLM	SINSDVDEKQ	SCDSTQALVT	FTSSSITYDL	PPSSVPSPAY	PVTESCHLSS	900
	VAFVPCIL						

Table 75: See Table 1

Table 76A depicts Seq ID No; UnigenelD; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

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Seq ID No:	PKey:	ExAccn:	UnigenelD:	Unigene Title:	Pred Subcell Loc:
Seq ID No:	Sequence ID No for sequences in table	Unique Eos probe/seq identifier number	Exemplar Accession number, Genbank accession number	Unigene number	Unigene gene title
PKey:	UnigenelD:	Unigene Title:	Pred Subcell Loc:		
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AJ016712	Hs.267797	Integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407835	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracellular
Seq ID 17 & 18	414577	AJ056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.195384	prostaglandin-endoperoxide synthase 2 (p	intracellular
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	perlestin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687	AI905687:IL-BT095-190199-019 BT095 Homo	secreted	
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adican	secreted
Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracellular
Seq ID 63 & 64	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.308201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracellular
Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracellular
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracellular
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracellular
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracellular
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW983419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	intracellular
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 25kD (conn	plasma membrane
Seq ID 119 & 120	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AI357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracellular
Seq ID 127 & 128	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spodoin 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

5	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucin 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
10	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
	Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
15	Seq ID 165	402230			Fgenash predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 166 & 167	402230			Fgenash predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uroplakdn 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uroplakdn 2	plasma membrane
20	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 (Hsa	plasma membrane
	Seq ID 176 & 177	402075			ENSP00000251056*:Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
25	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
30	Seq ID 194 & 195	404875			NM_022819*:Homo sapiens phospholipase A2	intracell
	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
35	Seq ID 204 & 205	420281	AJ623693	Hs.323494	Predicted cation efflux pump	plasma membrane
	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
40	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305:gi3806122[gb]AAC69198.1 (AF0	intracell
	Seq ID 221 & 222	405932			C15000305:gi3806122[gb]AAC69198.1 (AF0	intracell
45	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
50	Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
55	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	delta (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
	Seq ID 252	429466	M85835	Hs.12827	ESTs	
60	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrein Isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
65	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
	Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrein, alpha	secreted
	Seq ID 269 & 270	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
70	Seq ID 271 & 272	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
	Seq ID 273	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 274	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW565360	Hs.4748	adenylate cyclase activating polypeptide	
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	plasma membrane
75	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	secreted
	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-like	plasma membrane
	Seq ID 283 & 284	404049			NM_018937*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018936*:Homo sapiens protocadherin be	plasma membrane
80	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter	plasma membrane
	Seq ID 305 & 306	410407	X66839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
10	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nbcin (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uropod 1B	plasma membrane
20	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035884	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	midkine (neurotrophin growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progestagen-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424587	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	Integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	plasma membrane
	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	plasma membrane
40	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-I	plasma membrane
	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
45	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nbcin (100kD), kalin	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
50	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
60	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188:gi12738842[ref NP_073725.1] p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	plasma membrane
70	Seq ID 435 & 436	407242	M18728		gb:human nonspecific crossreacting anti	plasma membrane
	Seq ID 437 & 438	407242	M18728		gb:human nonspecific crossreacting anti	plasma membrane
	Seq ID 439 & 440	407242	M18728		gb:human nonspecific crossreacting anti	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type 1 transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423585	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
80	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

5	Seq ID 465 & 466	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW369771	Hs.52620	Integrin, beta 8	plasma membrane
10	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
15	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	secreted
	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotrypsin, stratum com	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neurotensin/ovasin) (KLK8)	secreted
20	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446619	AU076543	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	secreted
25	Seq ID 511 & 512	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	intracell
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
30	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (secreted
	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
35	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
40	Seq ID 541 & 542	407792	AJ077715	Hs.39384	putative secreted ligand homologous to f	secreted
	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	plasma membrane
45	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino ac	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino ac	plasma membrane
	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino ac	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino ac	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
50	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418396	AJ765805	Hs.26691	ESTs	plasma membrane
	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
55	Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	X51405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
60	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	plasma membrane
	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656*:Homo sapiens transmembrane pr	plasma membrane
65	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	plasma membrane
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-88 protein	plasma membrane
70	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
75	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.286638	prostate differentiation factor	secreted
80	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
	Seq ID 621 & 622	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.266538	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	clckkopt (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	Intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	Intracell

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Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AAA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW964405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

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Table 76C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NT_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	NT_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29762-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

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Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

	Seq ID No:	Sequence ID No for sequences in table		
5	Pkey:	Unique Eos probe set identifier number		
	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
15	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
20	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
25	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
30	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
35	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
40	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421552	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
	Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
45	Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 79 & 80	451398	breast, ovarian	CTL
50	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
55	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
60	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
	Seq ID 109 & 110	427685	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
65	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
70	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
75	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
80	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452461	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	CTL, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	sm, CTL
25	Seq ID 194 & 195 404875	bladder	Ab, CTL, imaging
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, sm, CTL, diagnostic
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, imaging
	Seq ID 200 & 201 420876	pancreas, bladder	sm, CTL
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	Ab, sm, imaging
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	sm, CTL
	Seq ID 206 & 207 446873	bladder	Ab, CTL, imaging
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	sm
	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, CTL, diagnostic
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, sm, CTL, imaging
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic
	Seq ID 263 & 264 419704	glioblastoma	sm, CTL
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	Ab, sm, CTL, imaging
	Seq ID 267 & 268 409395	glioblastoma	Ab, CTL, diagnostic
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, imaging
	Seq ID 273 458435	glioblastoma	
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
75	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428296	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, sm, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging

	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
10	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 428610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
15	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 438608	lung, bladder, head & neck, cervical	Ab,sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL, diagnostic
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	Ab, sm, imaging
	Seq ID 391 & 392 332180	lung	Ab,sm, CTL, imaging
	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
45	Seq ID 395 & 396 408790	lung	Ab, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, diagnostic
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428488	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, diagnostic
	Seq ID 431 & 432 428547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
	Seq ID 433 & 434 425921	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
70	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
	Seq ID 447 & 448 428392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
75	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 431629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab,sm, CTL, imaging
	Seq ID 469 & 470 452184	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab, diagnostic
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
5	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
20	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, sm, CTL, imaging
	Seq ID 567 & 568 433466	prostate	Ab, CTL, diagnostic
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, CTL, imaging
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, sm, CTL, imaging
	Seq ID 583 & 584 412628	prostate	Ab, CTL, diagnostic
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
70	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, imaging
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, sm, CTL, imaging
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	CTL
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
80	Seq ID 629 & 630 456662	uterine, ovarian	CTL
	Seq ID 631 & 632 418281	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 633 & 634 429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: NM_001400
Coding sequence: 251..1399

5

1	11	21	31	41	51	
TCTAAAGGTC	GGGGGAGCA	GCAAGATGCG	AAGCGAGCGG	TACAGATCCC	GGGCTCTCGG	60
AACGCAACTT	CGCCCTGCTT	GAGCGAGGCT	GCGGTTTCCG	AGGCCCTCTC	CAGCCAAGGA	120
AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	180
CTCGCCCTCG	CCTCTAGCGT	TGCTCTGGAG	TAGCGCCACC	CGGCTTCTCT	GGGGACACAG	240
GGTTGGCACC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCACCGCCA	GCTCGGTCTC	300
TGACTACGTC	AACATATGATA	TCATCGTCCG	GCATTACAAC	TACACGGGAA	AGCTGAATAT	360
CAGCGCGGAC	AAGGAGAACA	GCATTAAACT	GACCTCGGTG	GTGTTCAATC	TCATCTGCTG	420
CTTTATCATC	CTGGAGAACA	TCTTTGTCTT	GCTGACCATT	TGGAAAACCA	AGAAATCCA	480
CCGACCCATG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTTGG	CAGGAGTAGC	540
CTACACAGCT	AACCTGCTCT	TGCTGGGGC	CACCACTTAC	AAGCTCACTC	CCGCCAGTGG	600
GTTTCTCGGG	GAAGGGAGTA	TGTTTGTGGC	CCTGTGAGCC	TCCGTGTTCA	GTCTCTCGC	660
CATCGCCATT	GAGCGCTATA	TCACAATGCT	GAAAATGAAA	CTCCACAACG	GGAGCAATAA	720
CTTCGCGCTC	TTCTTGCTAA	TCAGCGCCTG	CTGGGTCACT	TCCCTCATCC	TGGGTGGCCT	780
GCCTATAGTG	GGCTGGAACT	GCATCAGTGC	GCTGTCCAGC	TGCTCCACCG	TGCTGCCGCT	840
CTACCAACAG	CACATATATC	TCTTCTGCAC	CACGGTCTTC	ACTCTGCTTC	TGCTCTCCAT	900
CGTCATTCTG	TACTGCAGAA	TCTACTCCTT	GGTCAGGACT	CGGAGCGCCG	GCCTGACGTT	960
CCGCAAGAAC	ATTTCCAAGG	CCAGCGCGAG	CTCTGAGAAG	TCGCTGGGCG	TGCTCAAGAC	1020
CGTAATATAT	GTCCCTGAGG	TCTTCATCGC	CTGCTGGGCA	CGGCTCTTCA	TCTCTGCTCT	1080
GCTGGATGTC	GGCTGCAAGG	TGAAGACCTG	TGACATCCTC	TTCAGAGCGG	AGTACTTCTC	1140
GGTGTAGTCT	GTGCTCAACT	CCGGCACCAA	CCCCATCATT	TACACTCTGA	CCAACAAGGA	1200
GATGCGTCCG	GCCTTCATCC	GGATCATGTC	CTGCTGCAAG	TGCGGAGCGG	GAGACTCTGC	1260
TGGCAAAATC	AAGCGAGCCA	TCATGCGCGG	CATGGAATTC	AGCGCGCAGC	AATCGGACAA	1320
TTCTCTCCAC	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1380
CGTCAACTCT	TCTTCTTAGA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTTACTTGG	1440
TGCTGGCCCA	CCCCAGTGT	TGGAAAAAAA	TCTCTGGGCT	TGCACTGCTG	CCAGGGAGGA	1500
GCTGCTGCAA	GCCAGAGGGA	GGAAGGGGGA	GAATACGAA	AGCCTGGTGG	TGTGGGGTGT	1560
TGGTGGGTAG	AGTTAGTTCC	TGTGAACAAT	GCACTGGGAA	GGGTGGAGAT	CAGGTCCCAG	1620
CCTGGAATAT	ATATTCTACC	CCCTCGGAGC	TTTGATTTTG	CATGAGCCCA	AAGGTCTAGC	1680
ATTGTCAAGT	TCTTAAAGGG	TTCAATTGGC	CCCTCTCAAA	AGACTAATGT	CCCATGTGTA	1740
AAGCGTCTCT	TTGTCTGGAG	CTTTGAGGAG	ATGTTTCTCT	TCACTTTAGT	TTCAAAACCA	1800
AGTGAAGTGT	TGCACTTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCCAAC	CCCCACCCTC	1860
CCTCTCCCTC	ATACCCCTCC	TCAACGTTCT	TTTACTTTAT	ACTTTAACTA	CCTGAGAGTT	1920
ATCAGAGCTG	GGGTGTGGGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTTGAGTACG	1980
TAGGCTGTGG	GAAGATGAAG	ATGGTTTGGA	GGTGTAAGAA	AATGTCTCTC	GCTGAGGCCA	2040
AAGTTTCCAT	GTAAGCGGGA	TCCGTTTCTT	GGAATTGTTG	TGAAGTCACT	TTGATTTCTT	2100
TAAAAAACAT	CTTTTCAATG	AAATGTGTTA	CCATTTCATA	TCCATTGAAG	CCGAAATCTG	2160
CATAAGGAAG	CCCACTTTAT	CTAAATGATA	TTAGCCAGGA	TCCTTGGTGT	CCTAGGAGAA	2220
ACAGACAAGC	AAAACAAAGT	GAAAAACGAA	TGGATTAACT	TTTGCAAAAC	AAGGGAGATT	2280
CTTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGTCCTTC	CCACTTTTGT	TGATGTTTAT	2340
TTCAGAATCT	TGTGTGATTC	ATTCAAGACA	ACAACATGTT	GTATTTTGTG	GTGTTAAAG	2400
TACTTTTCTT	GATTTTGTAA	TGTATTTGTT	TCAGGAAGAA	GTCAATTTAT	GGATTTTCT	2460
AAACCGTGT	AACCTTTCTA	GAATCCACCC	TCTTGTGCCC	TGAAGCAATTA	CTTTAACTGG	2520
TAGGGAAAGC	CAGAACTTTT	AAGTCCAGCT	ATTCAATTAGA	TAGTAATTGA	AGATATGTAT	2580
AAATATTAACA	AAGAATAAAA	ATATATTACT	GTCTCTTTAG	TATGGTTTTT	AGTGCAATTA	2640
AACCGAGAGA	TGCTCTGTTT	TTTTAAAAAG	AATAGTATTT	AATAGGTTTC	TGACTTTTGT	2700
GGATCATTTT	GCACATAGCT	TTATCAACTT	TTAAACATTA	ATAAAGTAT	TTTTTTAAAG	

Seq ID NO: 2 Protein sequence
Protein Accession #: NP_001391

60

1	11	21	31	41	51	
MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHYN	YTGKLNISAD	KENSIKLTSV	VFILICCFII	60
LENIFVLLTI	WTKFKFHRFM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
EGSMFVALSA	SVFSLLAIAI	ERYITMLKMK	LHNGSNNFRL	FLNISACWVI	SLILGGLPIM	180
GWNCISALSS	CSTVLPYLYK	HYILFCTTVF	TLLLLSIVIL	YCRIYSLVRT	RSRLTFRKN	240
ISKASRSSEK	SLALLKTVII	VLSVPIACWA	PLFILLLLDV	GCKVKTCDIL	FRARYFLVLA	300
VLSNGTNPII	YTLTNKEMRR	AFIRIMSCCK	CPSGDSAGKF	KRPILAGMEF	SRSKSDNSSH	360
PQKDEGDNFE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence
Nucleic Acid Accession #: NM_002205.1
Coding sequence: 1..3149

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1	11	21	31	41	51	
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CGCCGACCCC	CGCTSSGTGC	GCTGCTGTTG	CTGCTSSGTC	CGCGGCCACC	CAGGGTCGGG	120
GGCTTCAACT	TAGACGGCGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
GGATTCTCAG	TGGAGTTTTA	COGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
CCCAGGCTA	ATACCGACCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGCTCT	300
TGGGGTGCAC	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAGG	CTCTGGGCTC	360
CTGAGTCTCT	CACGTGCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCCCTTGAC	420
TGTTTGGGG	CAACAGTTGG	AGCCCCATGG	TCTCTCATCT	TGGCATGCGC	TCCACTGTAC	480
AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTCAG	CTGGGCAGCA	600

5 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCCAGATTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCAGGAGCAG 720
 ATTGCAGAAAT CTATTATACC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
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 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTCSATCCC TCTACAACCT CTCAGGGGAA 960
 CAGATGGCCT CCTACTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGAAGGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGCTC ATGGATCGGA CCCCTGACGG GCGGCCTCAG 1080
 10 GAGGTGGGCA GGTCTAAGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACC 1140
 CTACCCCTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCCCTGGGG 1200
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 15 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCTGTATC TGATTGTGGG GTCCTTTGGT 1440
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 GGTTCACAG TGGAACTTCA GCTGGACTGG CAGAAGCAGA AGGGAGGGGT ACGCGGGGCA 1680
 CTGTTCTTGG CCTCCAGGCA GGCAACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 20 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCAGACAAA 1800
 CTCTCGCCGA TTCACATCGC TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860
 CAGGCTCTCA CGCCAGCCCT ACATTATCAG AGCAAGAGCC GATAGAGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTG ACCTGCAGCT GGAAGTGTIT 1980
 25 GGGGAGCACA CTTCTAGTGA CTTGGGTGAC AAGAATGCC TGAACCTCAC TTTCCATGCC 2040
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 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280
 30 ATCCAGTTTG CTTCTCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT 2340
 TCCTTTCGCG TCTCGTGGGA GGCTCAGGCC CAGGTCAACC TGAACGGTGT CTCCAAGCCT 2400
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 AGCCAGGGTG TGCTGGAACCT CAGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCTATAT 2580
 35 GTACAGAGAG TTAGGGGACT CAACTGCACC ACCAATCACC CCATTAACCC AAAGGGGCTG 2640
 GAGTTGGATC CGAGGGTTC CCTGCACCAC CAGCAAAAAC GGAAGCTCC AAGCCGACGC 2700
 TGTGCTTCTC CGGAGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTIT CAGGCTGGCG 2760
 TGTGAGCTGC GGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAGTTGCA TTTCCGAGTC 2820
 TGGGCCAAGA CTTTCTTGCA CGGGGAGCAC CAGCCATTTA GCCTGCAGTG TGAGGCTGTG 2880
 40 TACAAGCCCC TGAAGATGCC CTACCGAATC CTGCTCGGC AGCTGCCCA AAAAGAGCGT 2940
 CAGGTGGCCA CAGCTGTGCA ATGGACCAAG GCAGAAGGCA GCTATGGGCT CCCACTGTGG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCCCT CTGCTCCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCATGGA AAAAGCTCAG 3120
 CTCAGGCTC CAGCCACCTC TGATGCCTGA

Seq ID NO: 4 Protein sequence
 Protein Accession #: NP_002196.1

50 1 11 21 31 41 51
 MGSRTPEPFL HAVQLRWGPR RRPPLLPPLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
 GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WNASPTQCTP IEFDSKGSRL 120
 LSSLSSESSEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DFGVTCYLST 180
 DNFTRILEYA PCRSDFSWAA GQGYCOGGFS AEFTKTGRVV LGGPGSYFWQ GQLSATQEQ 240
 55 IAESYYPEYL INLVQQLQT RQASSIYDSS YLGYSVAVGE FSGDDTDEFV AGVPKGNLTY 300
 GVTITLNGSD IRSLYNPFGE QMASYFYGAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
 EGVRYVYVLQ HPAGIEPTPT LTLTGHDFFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
 QQGVVVPVPG GPGGLGSKPS QVLQPLMAAS HTPDFFGSAL RGRDLDDNGN YPDLIVGSFG 480
 60 VDKAVVYRGR FIVSASASLT IPFAMENPEE RSCSLEGNPV ACINLSFCLN ASGKHVADSI 540
 GPTVELQLDW QKQKGGVRRR LPLASRQATL TQTLILQNGA REDCREMKIY LRNESEFRDK 600
 LSPHIALNFP SLDPAQPVDS HGLRPALHYQ SKSRIEDKQA ILLDGCGEDNI CVPDLQLEVF 660
 GBQNHVYLGQ KNALNLTFFA QNVGEGGAYE AELRVTPAPE AEYSGLVRHP GNFSSLSQDY 720
 FAVNQSRLLV CDLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFQILSK MLNNSQSDVV 780
 65 SFRLSVEAQA QVTLNGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QQKREAPSR 900
 SASSGPQILK CPBACFRLR CELGPLHQQE SLSLQLHFRV WAKTFILQREH QPFSLQCEAV 960
 YKALKMPYRI LPRQLPKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
 YKLGFFKRSL FYGTAMEKAQ LKPPATSDA

Seq ID NO: 5 DNA sequence
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1..2397

75 1 11 21 31 41 51
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 GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCCTACT 180
 80 TCTGCACGAT GTGATGATT TGAAGCCTTA AAAAAGAAGG GTTGCCTCC AGATGACATA 240
 GAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CGTAGCAAA 300
 GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA GCAGTTGGTT 360
 TTGCGATTAA GATCAGGGGA GCCACAGACA TTTACATTAA AATTCAAGAG AGCTGAAGAC 420
 TATCCCATTTG ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTGGAG 480
 AATGTAAAAA GTCTTGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGACTTC 540

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AGAATTTGGAT TTGGCTCAAT TGTGGAAAAA ACTGTGATGC CTTACATTAG CACAACACCA 600
GCTAAGCTCA GGAACCCCTTG CACAAGTGAA CAGAACTGCA CCAGCCCATT TAGCTACAAA 660
AATGTGCTCA GTCTTACTATA TAAAGGAGAA GTATTTAATG AACTTGTGTG AAAACAGOGC 720
ATATCTGGAA ATTCTGATTG TCCAGAAAGT GGTTCOGATG CCATCATGCA AGTTGCAATT 780
TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTITTC CACAGATGCC 840
GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAAA TGATGGACAA 900
TGTCACTCGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
CACCTTGTCC AGAAACTGAG TGAAAAATA ATTCAGACAA TTTTTCAGT TACTGAAGAA 1020
TTTCAGCCTG TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
TCTGCAAAAT CTAGCAATGT AATTCAGTTG ATCATTGATG CATACAATTC CCTTTCCTCA 1140
GAAGTCATT TTGAAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
TGCAAGAACG GGTGGAATG AATAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCATT 1260
GGAGATGAGG TTCAATTGTA AATTAGCATA ACTTCAAATA AGTGTCCAAA AAAGGATTCT 1320
GACAGCTTAA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
AATGGGACAT TTGAGTGTGG CGCTGTCAGG TGCAATGAAG GGCCTGTGTG TAGACATTGT 1500
GAATGCAGCA CAGATGAATG TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
AGTTTCAGAA TCTGCAATGA CAATGGAGAG TGCCTCTGCG GACAGTGTGT TTGTAGGAAG 1620
AGGGATATA CAAATGAAT TTATTCTGGC AATTTCTGCG AGTGTGATAA TTTCAACTGT 1680
GATAGATCCA ATGGCTTAAT TTGTGGAGGA AATGGTGTGT GCAAGTGTG TGTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTCTTT TGGATACTAG TACTTGTGAA 1800
GCCAGCAAGC GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGTGTG CTGTAAAGTG 1860
ACAGATCCGA AGTTTCAAGG GCAAACTGTG GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
CTGTGACATA AAGAATGTGT TCAGTGCAGA GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
TGCAACACAG AATGTTCCCTA TTTTAACATT ACCAAGGTAG AAGTCCGGA CAAATTACCC 2040
CAGCCGGTTC AACCTGATCC TGTGTCCCAT TGTAAAGAGA AGGATGTTGA CGACTGTGTG 2100
TTCTATTTTA CGTATTCACT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAT 2160
CCAGATGTGC CCACTGGTCC AGACATCAAT CCAATTGTAG CTGCTGTGTG TGTGGAAATT 2220
GTTCTTATTG GCCTTGCATT ACTGCTGATA TGGAGCTTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAATTGTA AAGAGAGAAA ATGAATGCCA AATGGGACAC GGGTGAATAA 2340
CCTATTATTA AGAGTGGCGT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA

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Seq ID NO: 6 Protein sequence
Protein Accession #: NP_002202.1

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1 11 21 31 41 51
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SARCDLLEAL KKKGCPPDDI ENPRGSKDIK KKNVNTNRSK GTABKLKPED ITQIQPQLV 120
LRLRSGEPQT PTLKFKAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLN NEMRRITSDF 180
RIGPGSPVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTKNGE VFNELVGKRA 240
ISGNLDSPEG GFDALIMQVAV CGSLIGWRNV TRLLVFSFDA GFHFAGDGKL GGIIVLPNDGQ 300
CHLENNMYTM SHYVDYPSIA HLVQKLSENN IQTIFAVTEE PQPVYKELKN LIPKSAVGTL 360
SANSNNIQL IIDAYNSLSS EVILENGKLS EGVITISYKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFBI SI TSNKCPKIDS DSPKIRPLGF TEEVEVILQY ICECEQSEB IPESPKCHEG 480
NGTFECGACR CNEGRVRHRC ECSTDEVNSE DMDAYCRKEN SBEICSNNGE CVCGQCVCRK 540
RDNTNEISYG KPECEDNFCN DRNGLICGG NGVCKCRVCE CNFNYTGSAC DCSLDTSTCE 600
ASNGQICNGR GICECGVCKC TDPKFGQGTQ EMCQTCLGVC AEHKECVQCR APNKEKKDIT 660
CTQECSEYFN LKVESRDKLP QPVQPDVPSH CKKDVDDCW FYFTYSVNGN NEVMVHVVEN 720
PECPGTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIHDR BEFAXFEKEK MNAKNDTGEN 780
PIYKSAVTTV VNPKYEGK

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Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: NM_002425
Coding sequence: 26..1453

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TGCCCGACAA TACCTAGAAA AGTACTACAA CCTCGAAAGG GATGTGAAGC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTG TTAATAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCCTGACGTT GGTCACTTCA GCTCCTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTGT ATTTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGGGAAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACACCTGAAGC 720
TTTGATGTAC CCACTCTACA ACTCATTCAC AGAGCTGGCC CAGTTCGGCC TTTGCAAGA 780
TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCTCT GCTCTACTG AGGAAACCCCT 840
GGTGCCACAA AATCTGTGTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCTCTGCTT 900
GTCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTTCTTAAAG ACAGATATTT 960
TTGGGGAAGA TCCCACTGGA ACCCTGAACC TGAATTTCAT TTGATTTCCT CATTTTGGCC 1020
CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAT AGCAGGGACA CCGTTTTTAT 1080
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TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
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ACAGTTTGAAG TTTGACCCCA ATGCCAGGAT GTGACACAC ATATTAAAG GTAACAGCTG 1440
GTTACATTGC TAGGCAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCTGCAATG TCTGTGACT 1560

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GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCAATGAA GAATGTTTCT GGAATCTTTC 1620
 ACTTGCTTTT GAATGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
 ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCTGTTC 1740
 CTT

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Seq ID NO: 8 Protein sequence
 Protein Accession #: NP_002416

10 1 11 21 31 41 51
 MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVKQF RRDNSNLIVK 60
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 PDLPRDAVDS AIEKALKVWE EVTPLTFSRL YEGEADIMIS PAVKEHGDFY SFDGPGHSLA 180
 HAYPPGPGLY GDIHFDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLYNS 240
 15 FTELAQFRLS QDDVNGIQSL YGPPFASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
 RGEYLPFKDR YFWRSHSWNP EPEPHLISAF WPSLPSYLD AYEVSNSRDTV FIFKGNFMA 360
 IRGNEVQAGY PRGIHTLGFP FTIRKIDAAV SDKEKKKTYF FAADKYWRPD ENSQSMBOGF 420
 PRIADDPFG VEPKVDVILQ AFGFFYFFSG SSQFEFDPNA RMVTHILKSN SWLHC

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Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: XM_058189.2
 Coding sequence: 169..774

25 1 11 21 31 41 51
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 TATGAAGTGA AGGCTCTGA CCCTGGAAAGT GGTCTCAAGC AGGGCAAAAT GGGGTCTCGG 180
 AAGTGTGGAG TGGCTCTAAG TTGTTTGTCT ATTCGCTTG CACTTTGGAG TATAATCGTG 240
 30 AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAACTCACC 300
 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360
 ACAGTCTCTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAAACTGC 420
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCTT 480
 GGATACGACC TGGTCACTCT TGCCTTGGGT CTGTCCCAAG GGCCATATTG CCGCACCCCTT 540
 35 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600
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 CTATAAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720
 TCCAAGATAC TGTGTGGAAG CTATTCAGTG ATCTTCCAGC CTGGAATCAT TTGAATAAGG 780
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 40 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTATTG TTGTAAAAAA 900
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 GAATCTGTAC TAGGGAAGTA AATAAGAATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080
 TGCAACTATTA TTTAATTATC TGGAAAATG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140
 45 AGGATTAAGT AAAGAGTGGT ACATACTGTA AATGTTTCTT GATATTAAAA AAAAAATTAA 1200
 ATAAAAATA AAGAGTACTA CATGGTTGTA AAA

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Seq ID NO: 10 Protein sequence
 Protein Accession #: XP_058189.1

55 1 11 21 31 41 51
 MGSRKGGCL SCLLIPLALW SIIVNILLYF PNGQTSYASS NKLTNYVWYF EGICFSGIMM 60
 LIVTTVLLVL ENNNYKCCQ SENCSSKKIVT LLSIIPSSLG IAPSGYCLVI SALGLVQGPY 120
 CRTLDGHEVA FEETAGRPIT DSSIWIQCLE PAHVVEWNII LFSILITLGS LQVIICLIRV 180
 VMQLSKILCG SYSVIPQPGI I

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Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

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 CCAGGCACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
 TACTACAACC TGAAGAAATG TGGGAGGCAA GTTGAAAGC GGAGAAATAG TGGCCCAAGT 180
 GTTGAAAAAT TGAAGCAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACAGAT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCCTCAGTT 300
 70 GTCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAT 360
 TACAGCCAG ATTGTCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACTC 420
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTTGCTCATG CTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACCTC 660
 75 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGTATGA CCTAGCTAC 720
 ACCTTCAGTG GTGATGTTC GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGAAGTCCC AAAATCCTGT CCAGCCCATC GGCCCAAAA CCCCAGAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 80 TTCTACATGC GCACAAATCC CTCTACCCG GAAGGTGAGC TCAATTTTAT TCTGTTTTC 960
 TGGCCACAA CTTCCAAATGC GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTCAC AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCCTTGTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCCT 1260

GGAATTGGCC ACAAGTTGA TGCAATTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

5

Seq ID NO: 12 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 10 MHSFPPLLLL LFWGVVSHSP PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VERLQMQKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTBGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLSHST DIGALMYPYSY 240
 15 TFSGDVQLAQ DDIDGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRTNPFYP EVELNFIISV WPQLPNGLEA AYEFPADRDEV RFPKGNKYWA VQGNVLRGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSMDFG YPKMLAHDFP 420
 GIGHKVDAVF MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

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Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

1 11 21 31 41 51
 25 ATGCACAGCT TTCCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
 TACTACAAGC TGAAGAATGA TGGGAGGCAA GTTGAAAGAG GGAGAAATAG TGGCCCACTG 180
 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAAGT 240
 30 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCTGATGT GGCTCAGTTT 300
 GTCTCACTG AGGGGAAACC TCGCTGGGAG CAAACATATC TGACCTACAG GATTGAAAAA 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAACCT 420
 TGGAGTAATG TCACACCTCT GACATTCACC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCTTT TTGATGGACC TGGAGGAAAT 540
 35 CTTGCTCATG CTTTTCACCC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTGCGGCG TCATGCCCTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGCTAC 720
 ACCCTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGACGTTCCC AAAATCCTGT CCAGCCCATC GGCCCAACAA CCCCAGGAGC ATGTGACAGT 840
 40 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTTCTACCGG GAAAGTTGAGC TCAATTTTAT TTCTGTTTTC 960
 TGGCCCAACG TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCCAAGGACA TCTACAGCTC CTTTGGCTTC CCTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 45 CTTTCTGAGG AAAACACTGG AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260
 GGAATTGGCC ACAAGTTGA TGCAATTTTC ATGAAAGATG GATTTTCTA TTTCTTTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

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Seq ID NO: 14 Protein sequence
 Protein Accession #: NP_002412.1

1 11 21 31 41 51
 55 MHSFPPLLLL LFWGVVSHSP PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VERLQMQKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTBGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLSHST DIGALMYPYSY 240
 60 TFSGDVQLAQ DDIDGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRTNPFYP EVELNFIISV WPQLPNGLEA AYEFPADRDEV RFPKGNKYWA VQGNVLRGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRY DEYKRSMDFG YPKMLAHDFP 420
 GIGHKVDAVF MKDGFYFFPH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

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Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 141..1580

1 11 21 31 41 51
 70 TCTGCTGTG CCGGGGCTAG GGGCTGGAAG TCCTGGCTCT AGTTGCACCT CGGAAGGAAA 60
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 CTCTACAGGC CTGTGTCTCT ATGGGTTCCC CCGCCGCCCC GGAGGCAGCG CTGGGCTACG 180
 75 TCCGCGAGTT CACTCGCCAC TCCTCCGAGG TGCTGGGCAA CCTCAACGAG CTGCGCCTGC 240
 GCGGGATCCT CACTGACGTC ACGCTGCTGG TTGGCGGGCA ACCCTCAGA GCACACAAGG 300
 CAGTTCTCAT CCGCTGCACT GGCTTCTTCT ATTCAATTTT CCGGGGCGGT GCGGGAGTGG 360
 GGGTGGAGCT GCTCTCTCTG CCGGGGGGTC CCGAAGCGAG AGGCTTCGCC CCTCTATTGG 420
 80 ACTTCATGTA CACTTCGCGC CTGCGCTCTT CTCCAGCCAC TGCAACGACA GTCCTAGCGG 480
 CGGCCACCTA TTTCAGATG GAGCAGGTGG TCCAGGCATG CCACCGCTTC ATCCAGGCCA 540
 GCTATGAACC TCTGGGCATC TCCTTGCGCC CCTTGAAGC AGAACCCCA ACACCCCA 600
 CGGCCCTTCC CCGAGGTAGT CCCAGGCGCT CGAAGGACA CCAAGACCA CCTACTGAAT 660
 CTCGAAGCTG CAGTCAAGGC CCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTGCAACT 720
 GGAAAAAGTA CAAGTACATC GTGCTAAACT CTCAGGCCCT CCAAGCAGG AGCTTGGTGG 780

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GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCCAGTGGG GACGAGGCCT 840
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GCAGGCTCTC TCCAACTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
CCTACCTCCT CACATCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTGCTC 1020
CACTACCGGG AAGTGAATTT TTCAGCTGCC AGAACTGTGA GGCTGTGGCA GGGTGCTCAT 1080
CGGGGCTGGA CTCCTTGGTT CCTGGGGAGC AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
GGTCTTGGTT CCGCTACAAG GGCAACCTTG CCAGTCACTG TACAGTGCAC ACAGGGGAAA 1200
AGCCTTACCA CTGCTCAATC TGCGGAGCCC GTTTTAAACG GCCAGCAAAC CTGAAAACGC 1260
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TACAGGTGGC ACATCTGCGG GCGCAGCTGC TGATCCACAC CGGGAGAGAAG CCCTACCCCT 1380
GCCCTACCTG CGGAACCCGC TTCCGCCACC TGCAGACCCT CAAGAGCCAC GTTCGCATCC 1440
ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGGCCT GCATTTCGG CACAAGAGTC 1500
AAGCTGGGCT GCATCTGCGC CAGAAAACAG GAGCTGTCTC CAACACCAAA GTGCACTACC 1560
ACATTCTCGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCC CACTTGCTTC CTGGGGTGG 1620
GAAAGCTGCA GGGCCAGGCC TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGGC 1680
CACTTTGGTA TCAGAAATTT CCACCTCTCT AATTTCTCAC TGGGAGAGC AGGGGTGGCA 1740
GATCCTGGCT AGATCTGCCT CTGTTTGTCT GGTCAAAACC TCTTCCCAAC AAGCCAGATT 1800
GTTTCTGAGG AGAGAGCTAG CTAGGGGCTG GGAAGAGGGA GAGATTGGAG TCCTGTCTC 1860
CCTAAGGGAAG TAGCTCTGCT CTTGTGGCCC CCATTGCATT CAGTTTATCT GTAATATAA 1920
TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTCAATCGA TTGCATTTC CACTCCCTC 1980
TTCCACAAGT GTGATTAATA GTGACCAGAA ACACAGAAGG TGAGATCACA GCTCTGTCTG 2040
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TAACTTTTAT CTTTGAATTT GTTCTTTCTC CTGTTTGTCT GCTTGTAGT TTGTTTAAAA 2160
TGGAAAAGG GATTCTCTGT GTTCTGCCCT TGTAACTCTA GGTCTGGAAC CTTTATTGT 2220
TCTAGGCGAG CTCTGGGAAC ATGCGGGATT GTGGAATTGG GTCAGGAACC CTCTCTGTA 2280
TTCTGGATGT TGTAGTTTCT CTAGCAGTCT AGAAATGGAT ACAGACATT CTCTGTCTT 2340
CAAGGGTGAT AGGAACCATC ATGTTGAGCC CAAAATGGAA GTAATAATAA ATGCTCTCTG 2400
GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCGGTA TCATCCCAAC TGGAGGCTGT 2460
GGGTGTGGGG GATCTGTAT CTGGATTCCG TATCACTCCA AGTGGAGGCT GGCAGGTTT 2520
TCTGCAAGAT GGTCCAGAAT CTAAAATGTC CCATTAATCT GGTCACTTGG GTTTGGCTCT 2580
GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCTCTC 2640
CACGGGTAGC TGTCTTAGC ACTGAGTTGA TCGCTCCATG GGGAGAGAT CAGACATTC 2700
TTATCAGAGA TGATGTGACC TTTTCTGACT CTGCCAGTCT TCTATGAATG TTATGGCCTA 2760
GGGAAGAGG ATGAACCTCT TTAGCTTGAT TAGATGGTAA ACAGTGTAA CCCATCCTT 2820
ACTACAGAGG CATATGGGTT TGAATGTAC CTGGGTTCT CTCTATTGAG TTGAGCCCT 2880
TCTTCTTTA GTGGGTTTTG GACATCTTCT GGCAAGTGT CAGATGCCAG AACCTTCTT 2940
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TCTTCCATC CTGCACTTCC TGTCTGGAAC CAGTGAATGC ATTAGAACC TCCATAGGAA 3060
AAGAAAAGGG GCTGAGTTCC ATTCTGGGTT TGCTGTAGTT TGGTTGGGAT TATTGTTGGC 3120
ATTACAGATG TAAAAGATTG ACTAGCCCAT AGGCCAAAGG CCTGTCTAG TTGACCAAGT 3180
TTCAAGTAGG ATTAAGAGGT TGGTTGAGGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA 3240
GAAAGTGAGG AACAGGGTTG CCTCTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC 3300
GCTGAAGCCT TGATGTAGAT TTCTGCCCT TGTGTCCCTG GGGCTTATCT GATTATGGGA 3360
CGAGGGTAGA AAGTGAAGAG CACTTTTGAA TTTGTGGGT AGAACTTCAA CAATAAGTCA 3420
GTTCTAGTGG CTGTGCGCTG GGGACTAGTG AGAAAGCTAC TCTTCTCCCT CTTCCTCTT 3480
TCTCCCATG GCCCCACTGC AGAATTAAGG AAGGAAGAAG GGAAGGCGGA GGAAGTCTATA 3540
AGAAAGGATC ATGATTTCTA TTTAGCAGAT TGGATGGGCA GGTGGAGAAAT CCCTGGGGT 3600
AGAAATGTTA GATCTGCAA CATCAGATCC TTGGAATAAA GAAGCCTCTC TGTGCAAAAA 3660
AAAAA

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Seq ID NO: 16 Protein sequence
Protein Accession #: FGENESH predicted

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1 11 21 31 41 51
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GFFYSIFRGR AGVGVLDVLSL PGGPEARQFA PLLDFMYTSR LRLSPATAPA VLAATYQLQM 120
EHVQACHRF IQASYEPLGI SLRPLEAEPP TPPTAPPPGS PRRSEGHDP PTERSCSOG 180
PPSPASPDFK ACNWKYKYI VLNSQASQAG SLVGERSSQG PCPQARLPSS DEASSSSSSS 240
SSSSEGGPIP GPQSRLSPTA ATVQFKGAP ASTPYLLTSQ AQDTSGSPSE RARPLPGSEF 300
FSCQNCRAVA GCSSGLDSL PVGDEKPYKC QLCRSSFRYK GNLAHRTVH TGEKPYHCSI 360
CGARFNRNPN LKTHSRHSG EKPYKCETCG SRFVQVAHLR AHVLIHTGEK PYPCPTCGTR 420
PRHLQTLKSH VRIHTGEKPY HCDPCGLHFR HKSQRLRLHLR QKHGAATNTK VHYHILGGP

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Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: XM_039209
Coding sequence: 1..2049

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AATGGGAACC CCCCAGAGCG OCTGAAAAGG AGAGACAGGA GGATGATGTC CCAGCTGGAG 180
CTGCTGAGTG GGGGAGAGAT GCTGTGCGGT GGCCTTCTACC CTCGGCTGTC CTGCTGCCTG 240
CGGATGTGCA GCCCGGGGCT AGGGCGCCTG GAGAATAAGA TATTTTCTGT TACCAACAAC 300
ACAGAAATGT GGAAGTTACT GGAGGAAATC AAATGTGCAC TTTGCTCTCC ACATTCTCAA 360
AGCCTGTGCC ACTCACCTGA GAGAGAAGTC TTGGAAGAG ACCTAGTACT TCCTCTGCTC 420
TGCAAGACT ATTGCAAGA ATTCTTTTAC ACTTGCAGAG GCCATATTCC AGGTTTCCTT 480
CAAAACAATG CGGATGAGTT TTGCTTTTAC TATGCAAGAA AAGATGCTG GTTGTGCTTT 540
CCAGATTTTC CAGAGAAAACA AGTCAGAGGA CCAGCATCTA ACTACTTGA CCAGATGGAA 600
GAATATGACA AAGTGAAGA GATCAGCAGA AAGCACAAC ACAACTGCTT CTGTATTGAG 660
GAGGTGTGGA GTGGGCTGCG GCAGCCCGTT GGTGCCCTGC ATAGTGGGGA TGGCTCGCAA 720
CGTCTCTTCA TTCTGAAAAA AGAAGGTTAT GTGAAGATAC TTACCCCTCA AGGAGAAATT 780
TTCAAGGAGC CTTATTGGA CATTACAAA CTTGTTTCAA GTGGAATAAA GGGAGGAGAT 840

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GAAAGAGGAC TGCTAAGCCT CGCATTCCAT CCCAATTACA AGAAAAATGG AAAGTTGTAT 900
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GTGTGTGAAT ACACAGTATC CAGAAAAAAT CCACACCAAG TTGATTGTAG AACAGCCAGA 1020
GTCTTTCTTG AAGTTTGAGA ACTCCACAGA AAGCATCTGG GAGGACAACT GCTCTTTGGC 1080
CCTGAOGGCT TTTTGTACAT CATTCTTGGT GATGGGATGA TTACTCTGGA TGATATGGAA 1140
GAAATGGATG GGTAAAGTGA TTTACAGGCC TCAGTGCTAC GGTGGATGT GGACACAGAC 1200
ATGTGTAAAG TGCCCTTATTC CATACCAAGG AGCAACCCAC ACTTCAACAG CACCAACCAAG 1260
CCCCCGAAG TGTTTGCTCA TGGGCTCCAC GATCCAGGCA GATGTGCTGT GGATAGACAT 1320
CCCACTGATA TAAACATCAA TTTAACGATA CTGTGTTTCA ACTCCAATGG AAAAAACAGA 1380
TCATCAGCCA GAAATTCTACA GATAATAAAG GGGAAAGATT ATGAAAGTGA GCCATCACTT 1440
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CAGTCAGAAA GATTGTATGG AAGCTACGTG TTTGGAGATC GTAATGGGAA TTTCTTAAC 1560
CTCCAGCAAA GTCCCTGTGAC AAAGCAGTGG CAAGAAAAAC CACTCTGTCT CGGCACTAGT 1620
GGGTCTCTGA GAGGCTACTT TTCCGGTCAC ATCTTGGGAT TTGGAGAAGA TGAACCTAGT 1680
GAACTTTACA TTTTATCAAG CAGTAAAAGT ATGACCCAGA CTCACAATGG AAACTCTTAC 1740
AAAAATTAG ATCCCAAAG ACCTTTAATG CCTGAGGAAT GCAGAGCCAC GGTACACCT 1800
GCACAGACAC TGACTTCAGA GTGCTCCAGG CTCTGTCGAA ACGGCTACTG CACCCCAAG 1860
GGAAAGTGCT GCTGCAGTCC AGGCTGGGAG GGGGACTTCT GCAGAACTGC AAAATGTGAG 1920
CCAGCATGTC TGCTATGGAG TGCTGTGTT AGACCGAACA AGTGCTCTG TAAAAAGGA 1980
TATCTTGGTC CTCATGTGA ACAAGTGGAC AGAAACATCC GCAGAGTGAC CAGGCGAGAC 2040
ATCACCTAG

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25 Seq ID NO: 18 Protein sequence
Protein Accession #: XP_039209

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1 11 21 31 41 51
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LLSGGEMLOG GFYPRLSCL RSDSPGLGRL ENKIFSVTNM TECGKLLLEE KCALCSPHSQ 120
SLFHSPEVER LERDLVLP LL CKDYCKEPPY TCRGHIPGFL QTTADEFCFY YARKDGGLCF 180
PDPFRKQREV PASNYLDQME EYDKVEBISR KHKHNCFCIQ EVVSGLRQPV GALHSGDGSQ 240
RLFLILEKEGY VKILTPGEI FKEPYLDIHK LVQSGIKGGD ERGLLSLAHF PNYKKNKRLY 300
VSYTTNQERW AIGPHDHLR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
PDGLFYIILG DGMITLDDME EMDGLSDPTG SVLRLLDVTD MCNVFYSIPR SNPHFNSTNQ 420
PPEVFAHGLH DPGRCVDRH PTDININLTI LCSDSNGKNR SSARILQIHK GKDYSESEPSL 480
LEFKFPNSNG LVGGFVYRGC QSERLYGSYV FGDRNGNFLT LQSPFVTKQW QEKPLCLGTS 540
GSCRGYFSGH ILGFGEDELG EYILSSSKS MTQTHNGKLY KIVDPKRPLM FEECRATVQP 600
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YLGPOCEQVD RNIRRVTRAD IT

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45 Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: NM_014331.2
Coding sequence: 1..1506

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1 11 21 31 41 51
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AACGGGAGGC TGCCCTTCCCT GGGCAACAAG GAGCCACCTG GGCAGAGAAA AGTCAGCTG 120
AAGAGGAAA TCACITTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTGGAGCA 180
GGAATCTTCA TCTCTCTTAA GGGCGTGCTC CAGAACAACG GCAGCGTGGG CATGTCTCTG 240
ACCATCTGGA OGGTGTGTGG GTTCCTGTCA CTATTGTGAG CTTTGTCTTA TGCTGAATTG 300
GGAACAACCTA TAAAGAAATC TGGAGGT CAT TACACATATA TTTTGAAGT CTTTGTGCTCA 360
TTACCACTCT TTGTACGAGT CTGGGTGGAA CTCCTCATAA TACGCCCTGC AGCTACTGCT 420
GTGATATCCC TGGCATTTGG ACGCTACATT CTGGAACCAT TTTTATTCA ATGTGAAATC 480
CCTGAACCTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTATG GGTCTCTAAT 540
AGCATGAGTG TCAGCTGGAG OGCCCGGATC CAGATTCTCT TAACCTTTTG CAAGCTCACA 600
GCAATCTCTA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCA AACCGAGAAC 660
TTTAAGACG CGTTTTCAGG AAGAGATTCA AGTATTACGC GGTGTCCACT GGCTTTTAT 720
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AACCCTGAAA AAACCATTTCC CCTTGCAATA TGTATATCCA TGGCCATTGT CACCATTTGC 840
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AATGCAGTGG CAGTGACCTT TTCTGAGCGG CTACTGGGAA ATTTCTCATT AGCAGTTCCG 960
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GGGCTGGCAG TTGCTGGGCT GATTATCTT CGATACAAAT GCCCAGATAT GCATCGTCT 1260
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TTTTCAATTC TGAAAAAAG CATACATCAT GATTATGGCA AAGAGGAGAG AAAGAAATTT 1980
ATTTTACATT GACATTGCTT TGCTTCCCT TAGATACCA TTTAGATAAC AAACACTCAT 2040
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TTAAAGAGGA GTTCTAGGG GCTACTGTT ATGAGACACA TCCAGGAGTT ATGTTTAAAT 2160
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GCTGGTAATC TCAGCTATAG AGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CCGGAGGCG 3060
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Seq ID NO: 20 Protein sequence
 Protein Accession #: NP_055146.1

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GIPISPKGVL QNTGSGVMSL TIWTVCGVLS LFGALSYAEL GTTIKKSGGH YTYILEVFGP 120
LPAFVRVWVE LLIIRPAATA VISLAFGRYI LEPPFIQCEI PELAIKLITA VGITVVMVLN 180
SMVSVWSARI QIFLTPECKLT AILIIIVPGV MQLIKGQTQN FKDAFSGRDS SITRLPLAFY 240
YGMAYAGWVF YLNFVTEEEVE NPEKTIPLAI CISMAITIGV YVLTNVAYPT TINAEELLS 300
NAVAVTFSSR LLGNFSLAVP IFVALSCFSG MNGGVFAVSR LFPYVASREGH LPBILSMIHV 360
RKHTFLPAVI VLHPLMTIML PFGDLDSLNL PLSFARWLPF GLAVAGLIYL RYKCPDMHRP 420
FKVPLFIPAL PSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYYLFIIW DKKPRWFRIM 480
SEKITRITLIQ ILEVVPEDK L
  
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Seq ID NO: 21 DNA sequence
 Nucleic Acid Accession #: NM_002422.2
 Coding sequence: 64..1497

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1 11 21 31 41 51
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Seq ID NO: 22 Protein sequence
 Protein Accession #: NP_002413

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YTPDLPKDAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYPPDGPQNV 180
LAHAYAPGPG INGDAHPDDD EQWTKDTTGT NLPLVAAHEI GHSLGLFHSA NTEALMYPLY 240
HSLTDLTRFR LSDDDIINGIQ SLYGPPFPDSP ETPLVPTFEP PEPGTPANC DPALSFDAVS 300
TLRGEILIFK DRHFWKSLR KLEPELHLIS SFWPSPSGV DAAVEVTSKD LVFIPKGNQF 360
WARGNEVRA GYPRGHTLIG FPPTVRKIDA AISDKERKMT YPFVEDKYWR FDEKRNMEP 420
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Nucleic Acid Accession #: NM_006528
Coding sequence: 57..764

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Seq ID NO: 24 Protein sequence
Protein Accession #: NP_006519

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TCEKPFSGGC	HRNRIENRFP	DEATCMGFCA	PKKIPSPCYL	PKDEGLCSAN	VTRYFFNFRY	180
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: NM_005458.1
Coding sequence: 1..2825

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CTCATGCGCC	TCACCAAGGA	GGTGGCCAAG	GGCAGCATCG	CGCGCGGTGT	GCTCCCCGCC	240
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AAAAAGCTGA	AGGGGAATGA	TGTGCGGATC	ATCCTTGGCC	AGTTTGACCA	GAATATGGCA	780
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5	AATCCCCAGC	TACAGTGGAA	CACACAGAG	CCCTCTCGAA	CATGCAAGA	TCCTATAGAA	2640
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	CACGCCCTACC	TCCCATCCAT	CGGAGGCGTG	GACGCCAGCT	GTGTCAGCCC	CTGCCGTCAGC	2760
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	IKYGNHLMV	PGGVCPSVTS	IIAELQGW	LVQLSPAATT	PVLADKKKYP	YFRTVPBDN	180
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	KKLKGNDVRI	ILGQFDQDMA	AKVFCCAYBE	NMYGSKYQWI	IPGWYBPSWW	EQVHTEANSS	300
20	RCLRKNLLAA	MEGYIGVDPE	PLSSKQIKTI	SGKTPQQYER	EYNKRSGVGV	PSKFRGYAYD	360
	GIWVIARTLQ	RAMETLHASS	RHQRIQDFNY	TDHTLGRILL	NAMNETNPFQ	VTGQVVRNFG	420
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	LYSILSALT	LGMIMASAF	PFNIKRRNQK	LIKMSSPYMN	NLIILGGMLS	YASIFLPLGLD	540
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25	VGGMLLIDL	ILICWQAVDP	LRRTVKYSYM	EPDPAGRDIS	IRPLLEHCEN	THMTIHLGIV	660
	YAYKGLMLF	GCPLAWETRN	VSPALNDSK	YIGMSVYNVG	IMCIIGAAVS	FLTRDQPNVQ	720
	FCIVALVILP	CSITITCLVP	VPKLITLRTN	PDAATQNRFP	QPTQNKKEED	SKTSTSVTSV	780
	NQASTSRLEG	LQSENHRLRM	KITELDKDLE	EVTMLQDTP	EKTTYIKQNH	YQELNDILNL	840
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Seq ID NO: 28 Protein sequence
Protein Accession #: NP_000441.1

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Seq ID NO: 29 DNA sequence
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Coding sequence: 56..610

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CACAGCCAAC ATTTTAGGAA CTTTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT 720
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TCTTTGACTT TGATGTACAT TAATGTTGGG ATATGGAATG AAGACTTAAG AGCAGGAGAA 1020
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AGTATTTACC TGATTTTAT TCTTGAAGTT GGCCACAGA GTTGTGAATG TGTGTGGAAG 1920
GCCTTTGAAT GTAAAGCTGC ATAAGCTGTT AGGTTTTGTT TTAAGAGGAC ATGTTTATTA 1980
TTGTTCAATA AAAAGAACA AGATAC

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Seq ID NO: 30 Protein sequence
Protein Accession #: NP_008967.1

80

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1 11 21 31 41 51
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RGHTCYRTVS GMDGKCGPG LRCQPSNGED PFGEEFGICK DCPYGTFGMD CRETNCQSG 120
ICDRGTGKCL KPPFPQYSVT KSSNRPVSLT EHDMSGDGN IVREBVKEN AAGSPVWRKN 180

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LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM_000963

Coding sequence: 135..1949

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ATACAGCAAA	TCCTTGCTGT	TCCCACCCAT	GTCAAAACCG	AGGTGTATGT	ATGAGTGTGG	240
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GAGCCCTTCC	TCCTGTGCTC	GATGATTGCC	CGACTCCCTT	GGGTGTCAAA	GGTAAAAAGC	600
AGCTTCTCGA	TTCAAAATGAG	ATTGTGGAAA	AATTGCTTCT	AAGAAGAAAG	TTATCCCTG	660
ATCCCGCTGG	CTCAACATG	ATGTTTGCA	TCTTTGCCCA	GCACTTCAAG	CATCAGTTT	720
TCAGACAGCA	TCATAAGCGA	GGGCCAGCTT	TCACCAACGG	GCTGGGCCAT	GGGGTGGAGT	780
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Seq ID NO: 32 Protein sequence
Protein Accession #: NP_000954

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NMMFAPPAQH FTHQPFKTDH KRGPFTNGL GHGVDLNHIY GETLARQRKL RLFKDGGRMY 240
10 QIIDGEMVPP TVKDPTQAEI YPPQVPEHLR FAVGQEVFGL VPGLMYATI WLREHNRVCD 300
VLKQHEPENG DEQLPQTSRL ILIGETIKIV IEDYVQHLSE YHFLKFDPE LLFNKQFYQ 360
NRIAAEFNTL YHWHPLLPDT FQIHDQKYNQ QQFIYNNLSL LEHGITQFVE SPTQRIAGRV 420
AGGRNVPPAV QKVQSASIDQ SRQMKYQSFN EYRKRPMLEP YESFEELTGE KEMSAEAL 480
YGDIDAVELY PALLVEKPRP DAIFGETMVE VGAPFSLKGL MGNVICSPAY WKPSTFGGEV 540
15 GFQINTASI QSLICNNVKG CPPTSFSVPD PELIKVTIN ASSSRSLDD INPTVLLKER 600
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Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: NM_001508.1
Coding sequence: 1..1361

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AAGGATACT TGCAGAGGA GGTGACAGAC CACATGGTGA GTTTGGCTG CTGGACATC 240
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30 GCTACGCTG TGCAGTGTG GACGCTCAGC TTTGAGCGCT ACATCGCAT CTGTCACTCC 420
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ACCAACGAGA GCGCCGCTT TGTGACGCG CCGTGTCTCT TCGGTCCCG GCGCCAGTCC 1200
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Seq ID NO: 34 Protein sequence
Protein Accession #: NP_001499.1

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VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTFV QSSIFGAFV YLVVLLSVAF 240
MCMNMQVLM SQKQSLAGG TRPPQLRKSE SEESRTARRQ TIIFRLIVV TLAVCMWNP 300
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Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_006475.1
Coding sequence: 28..2538

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TTGGGGCTTT TCATTAAACA TTATCTTAAT GGGGTGTGCA CTGTAAATG TGCTCGAATC 660
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80 CAAATTGGTA CCTCAATTCA AGACTTCATT GAAGCAGAAG ATGACCTTTC ATCTTTTAGA 780
GCAGCTGCCA TCACATCGGA CATATTGGAG GCCCTTGGAA GAGACGGTCA CTTACACTC 840
TTTGCTCCCA CCAATTGAGG TTTTGAGAAA CTTCCACGAG GTGTCTTACA AAGGTTTATG 900
GGAGACAAAG TGCTTCCGA AGCTCTTATG AAGTACCACA TCTTAAATAC TCTCCAGTGT 960
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	GGCTTGGCAT	CTGCTCTGAG	GCCAGATGGA	GAATACACTT	TGCTGGCACC	TGTGAATAAT	1260
	GCATTTTCTG	ATGATACTCT	CAGCATGGTT	CAGCGCCTCC	TAAATTAAT	TCTGCAGAA	1320
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	CACCTTACAC	CCTTTTTTCAT	CTTGACATTA	AAAGTTCTGG	CTAACTTTGG	AATCCATTAG	2820
	AGAAAAATCC	TTGTCAACAG	ATTCAATTACA	ATTCAAAATCG	AAGAGTTGTG	AACCTGTTATC	2880
	CCATTGAAAA	GACCGAGCCT	TGTATGTATG	TTATGGATAC	ATAAAATGCA	CGCAAGCCAT	2940
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35	TCAAAAGGCT	TTGACAGATT	CTATATGAGT	GGGTTTACTG	GTAATTTATG	TTATTTTTTA	3060
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	TCTCAACAGT	TTCAATAAAA	CCATTTTTCA	GATATAAAGA	GAATTACTTC	AAATTGAGTA	3180
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Seq ID NO: 36 Protein sequence
Protein Accession #: NP_006466.1

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	NGMIIPSMYN	NLGLFINHYP	NGVVTVNCAR	IIHGNQIATN	GVVHVIVDRVL	TQIGTSIQDF	240
	IEAEDDLSSF	RAAITSIDIL	EALGRDGHFT	LFAPTNEAPE	KLPRGVLERF	MGDKVASEAL	300
50	MKYHILNTLQ	CSBILMGGAV	PETLEGNTIE	IGCDGDSITV	NGIKMVNKID	IVTNVGIHL	360
	IDQVLIPDSA	KQVIELAGKQ	QTTFTDLVAQ	LGLASALRPD	GEYTLAPVN	NAPSDDTLSP	420
	VQRLLKLILQ	NHILKVKVLG	NELYNGQILE	TIGGKQLRVP	VYRTAVCIEN	SCMRKSGSKQ	480
	NRGAIHIFRE	IIKPAEKSLH	EKLKQDKRFS	TPLSLLEAAD	LKELLTPQGD	WTLFVPTINDA	540
	FKGMTSEESK	ILIRDKNALQ	NIILYHLTPG	VFIGKGFEPG	VTNLIKTTQG	SKIFLKEVND	600
55	TLNVNELKSK	ESDITMTNGV	IHVVDKLLVP	ADTFVGNDDQ	LEILNKLIKY	IQIKFVRGST	660
	FKIIPVTVYT	TKIITKVVEP	KIKVIEGSLQ	PIIKTEGPTL	TKVKIDGEP	FRLIKEGETI	720
	TEVIGHGEPI	KYTKIIDGV	PVEITEKETR	BERIITGPEI	KYTRISTGGG	ETBETILKRL	780
	QEEVTKVTKF	IEGGDGHLEF	DEBIKRLQGG	DTPVRKLQAN	KKVQGSRRRL	REGRSQ	

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

65	1	11	21	31	41	51	
	ATCCAAATACA	GGAGTGACTT	GGAACCTCCAT	TCTATCACTA	TGAAGAAAAG	TGGTGTCTCT	60
	TTCTCTCTGG	GCATCATCTT	GCTGGTCTCTG	ATTGGAGTGC	AAGGAACCCC	AGTAGTGAGA	120
	AAGGGTGGCT	GTTCTCTGAT	CAGCACCAAC	CAAGGGACTA	TCCACCTACA	ATCCTTGAAA	180
	GACCTTAAAC	AATTTGCCCC	AAGCCCTTCC	TGCGAGAAAA	TTGAATCAT	TGCTACACTG	240
	AAGAATGGAG	TTCAAAACATG	TCTAAACCCA	GATTACAGAG	ATGTGAAGGA	ACTGATTAAA	300
70	AAGTGGGAGA	AACAGGTGAG	CCAAAAGAAA	AAGCAAAGGA	ATGGGAAAAA	ACATCAAAAA	360
	AAGAAAGTTC	TGAAAGTTCC	AAAATCTCAA	CGTTCTCGTC	AAAAGAAAGAC	TACATAAGAG	420
	ACCACTCTAC	CAATAAGTAT	TCTGTGTTAA	AAATGTTCTA	TTTAAATTAAT	ACCGCTATCA	480
	TTCCAAAGGA	GGATGGCATA	TAATACAAAG	GCTTATTAAT	TTGACTAGAA	AATTTAAAC	540
75	ATTACTCTGA	AATTGTAACT	AAAGTTAGAA	AGTTGATTTT	AAGAATCCAA	ACGTTAAGAA	600
	TTGTAAAGG	CTATGATTGT	CTTTGTCTCT	CTACCAACCA	CCAGTTGAAT	TTATCATATGC	660
	TTAAGGCCAT	GATTTTATGCA	ATACCCATGT	CTACACAGAT	GTTCAACCAA	CCACATCCCA	720
	CTACAAACAG	CTGCCCTGGA	GAGCAGCCCT	AGGCTTCCAC	GTACTGCAGC	CTCCAGAGAG	780
	TATCTGAGGC	ACATGTCAGC	AAGTCCCTAAG	CCTGTTAGCA	TGCTGGTGAG	CCAAGCAGTT	840
80	TGAAATTTAG	CTGGACCTCA	CCAAGCTGCT	GTGGCCATCA	ACCTCTGTAT	TTGAATCAGC	900
	CTACAGGCCCT	CACACACAA	GTGTCTGAGA	GATTTCAGCT	GATTGTTATT	GGGTATCACC	960
	ACTGGAGATC	ACCAGTGTGT	GGCTTTTCTG	GCCTCTCTTC	TGGCTTTGGA	AGCCATGTGA	1020
	TTCCATCTTG	CCCGCTCAGG	CTGACCACTT	TATTTCTTTT	TGTTCCCTCT	TGCTTCATTC	1080
	AAGTCAGCTC	TTCTCCATCC	TACCAACAATG	CAGTGCCTTT	CTTCTCTCCA	GTGCACTGT	1140
	CATATGCTCT	GATTTATCTG	AGTCAACTCC	TTTCTCATCT	TGTCCCAAC	ACCCACAGA	1200

5 AGTGCTTTCT TCTCCCAATT CATCTCACT CAGTCCAGCT TAGTTCAGT CCTGCCTCTT 1260
 AAATAAACCT TTTTGGACAC ACAAATTATC TTAATACTCC TGTTCACCTT GGTTCAGTAC 1320
 CACATGGGTG AACACTCAAT GGTTAACATA TTCTTGGGTG TTTATCCTAT CTCTCCAACC 1380
 AGATTGTGAG CTCCTTGAGG GCAAGAGCCA CAGTATATTT CCCTGTTTCT TCCACAGTGC 1440
 CTAAATAATC TGTGGAACTA GGTTTTAATA ATTTTAAAT TGATGTGTGT ATGGGCAGGA 1500
 TGGCAACCG ACCATTGTCT CAGAGCAGGT GCTGGCTCTT TCCTGGCTAC TCCATGTTGG 1560
 CTAGCCTCTG GTAACTCTCT ACTTATTATC TTCAGGACAC TCACTACAGG GACCAGGGAT 1620
 GATGCAACAT CCTTGTCTTT TTATGACAGG ATGTTTGCTC AGCTTCTCCA ACAATAAGAA 1680
 10 GCAOCTGGTA AAACACTTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
 AAAATCATAT AATCTTACAA TGAAAAGGAC TTTATAGATC AGCCAGTGAC CAACCTTTTC 1800
 CCAACCATAC AAAAATTCCT TTTCCCGAAG GAAAAGGCT TTCTCAATAA GCTCAGCTT 1860
 TCTAAGATCT AACCAAGATAG CCACCGAGAT CCTTATCGAA ACTCATTTTA GGCAAAATATG 1920
 AGTTTATTATG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 15 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
 TAGTGAAGC ATGATTGGTG CCCAGTTAGC CTCTGCAGGA TGTGGAACCC TCCTTCCAGG 2100
 GGAGGTTTCAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
 CTTTCCCAAA TTGAATCACT GCTCACACTG CTGATGATTT AGAGTGCTGT CCGGTGGAGA 2220
 TCCCAACCGA ACCTCTTATC TAATCATGAA ACTCCCTAGT TCCTTCATGT AACTTCCCTG 2280
 20 AAAAACTGTA GTGTTTCTA AATTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
 GTAGACAGTA TATACTAAC AACCAAGAC TACATATTGT CACTGACACA CACGTATATA 2400
 TCATTATCA TATATATACA TACATGCATA CACTCTCAA GCAATAAAT TTTCACTTCA 2460
 AACAGTATT GACTGTGATA CCTTGTAAAT TGAAATATTT TCTTTGTAA AATAGAATGG 2520
 TATCAATAAA TAGACCATA ATCAG

25 Seq ID NO: 38 Protein sequence
 Protein Accession #: NP_002407

30 1 11 21 31 41 51
 MKKSGVLFLI GYILLVLIGV QGTPVVRKGR CSCISTNQGT IHLQSLKDLK QFAPSPSCSEK 60
 IEIILATLKNQ VQTCLNPDFA DVKELIKKWE KQVSQKKKQK NGKXHQKKV LKVRKSQRSR 120
 QKKT

35 Seq ID NO: 39 DNA sequence
 Nucleic Acid Accession #: NM_006670
 Coding sequence: 85..1347

40 1 11 21 31 41 51
 CCGGCTCGCG CCCTCCGGGC CAGCCTTCCC GAGCCTTCGG AGCGGGGCCC GTCCAGCCCC 60
 AGCTCCGGGG AAACGCGAGC CGCGATGCCT GGGGGGTGCT CCGGGGCCCC CGCGCGCGGG 120
 GACGGGGGTC TCGGGCTGCG GCGACTAGCG CTGGTACTCC TGGGCTGGGT CTCTCGTCT 180
 TCTCCCACTT CCTCGGCATC CTCTCTTCCC TCCTCGGGCG CGTTCCTGGC TTCGCGGTG 240
 TCGCGCCAGC CCGCGCTGCC GGAACAGTGC CCGCGCTGT GCGAGTGTCT CGAGGCAGCG 300
 45 CGCAGAGTCA AGTGCCTTAA CGCAATCTG ACCGAGGTGC CCACGGACCT GCCCGCTTAC 360
 GTGCGCAACC TCTTCTTAC CGGCAACGAG CTGGCGGTGC TCCTGCGCG CGCCTTCCGC 420
 CGCGCGCGGC CGCTGGCGGA GCTGGCGCG CTCAACCTCA GCGGCAGCGG CCTGGACGAG 480
 GTGCGCGCGG GCGCCTTCCA GCATCTGCC AGCCTGCGCC AGCTCGACCT CAGCCACAAC 540
 CCACTGGCGC ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCT CTGCGCCCC 600
 50 AGTCCCCCTG TGAACCTGAT CCGGAACAC ATCGTGCCCC CTGAAGATGA GCGGCAGAAC 660
 CGGAGCTTGG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCGGTGCACT GCAGGGGCTC 720
 CGCGCTTGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGATGT GCTGGCCCAA 780
 CTGCCAGGCC TCAGGCACCT GACTTAAAT AATAATTGCG TGGTGAGCCT GACTTACGCT 840
 55 TCCTTCGCGA ACCTCACACA TCTAGAAAGC CTCCACCTGG AGGACAATGC CCTCAAGTCC 900
 CTTCACAATG GCACCTTGGC TGAATTGCAA GGTCTACCCC ACATTAGGGT TTTCTGGAC 960
 AACATCCCT GGGTCTGCGA CTGCCACATG GCAGACATGG TGACCTGGCT CAAGGAAACA 1020
 GAGGTAGTGC AGGGCAAGAA CGGCTCACCC TGTGCATATC CGGAAAAAAT GAGGAATCGG 1080
 GTCTCTTGG AACTCAACAG TGCTGACCTG GACTGTGACC CGATTCTTCC CCCATCCCTG 1140
 60 CAAACCTCTT ATGTCTTCTT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCTCTG 1200
 GTTTTGTATT TGAACCGCAA GGGGATAAAA AAGTGGATGC ATAACATCAG AGATGCCTGC 1260
 AGGGATCACA TGAAGGGGTA TCATTACAGA TATGAAATCA ATGCGGACCC CAGATTAACA 1320
 AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
 CATGAGATGT AGACTTAAGC TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
 65 TAGATACAAC GGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCTTGT TTATGTAAAG 1500
 TTTCTCGGTG TGTCTGTGTA ATGTAAGAGG ATGAACAGTT GTGTATAGTG TTTTACCCTC 1560
 TTCTTTTCTT TGAACCTCCT CAACAGTATG GGAGGGATT TTAGGTTTC AGCATGAACA 1620
 TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
 ACAGATAGCA TTCAACAAA GCTGCTCAA CTTTTCGAG AAAAAACTT TATTCAATAA 1740
 70 TATCAGTTT ATTCTCATGT ACCTAAGTTG TGGAGAAAAT AATTGCATCC TATAAACTGC 1800
 CTGCAGAGT TAGCAGGCTC TTCAAAATAA CTCATGCTG CACAGGAGCA CCTGCATCCA 1860
 AGAGCATGCT TACATTTTAC TGTCTGCAAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
 TCTTTGACA AAGTAAATTA CTTTTTGTAT TGCAGTTTAT ATGAAAAATG ACTGATTTT 1980
 TTTTATAAAA CTGCATCGAG ATCCAACCGA CTGAATTGTT AAAAAAATAA AAAAAATAAG 2040
 ATTCTTAAAA GAA

75 Seq ID NO: 40 Protein sequence
 Protein Accession #: NP_006661

80 1 11 21 31 41 51
 MPGGCSRGP AAGDRLRLAR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60
 QCPALCECSE AARTVKCVNR NLTEVPDLE AYVRNLFITG NQLAVLPAGA FARRPPLAEL 120
 AALNLGGSLR DEVRAGAFEH LPSLRQLDLS HNPLADLSPF APSGSNASVS APSPLVELIL 180
 NHIVPEDER QNRSPFGMVV AALLAGRALQ GLRRLKELASN HFLYLPRLVD AQLPSLRHLD 240

LSNNSLVSLT YVSPRNLTHL ESLHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDCD 300
 HMADMVTLWK ETEVVOGKDR LTCAYPEKMR NRVLLELNSA DLDCDPLPF SLQTSYVFLG 360
 IVLALIGAIF LVLVLYLNRKG IKWMNRNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

5

Seq ID NO: 41 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..927

10 1 11 21 31 41 51
 | | | | | |
 ATGCGCTGGG GGTGCTCCCG GGGCCCCGCC GCGGGGAGCG GGCGTCTGCG GCTGGCGCGA 60
 CTAGCGCTGG TACTCTCTGG CTGGGTCTCC TCGTCTTCTC CCACCTCTCC GGCATCTCTC 120
 TTCTCTCTCT CGCGCGCGGT CCTGGCTTCC GCGGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
 15 CAGTGCCCCG CGCTGTGCGA GTGCTCOGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
 AATCTGACCG AGGTGCCACG GGACCTGCCG GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 AACCACTGGG CCAGCAACCA CTCCTTTTAC CTGCGCGCGG ATGTGCTGGC CCAACTGCCG 360
 AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCTCTC 420
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480
 20 AATGGCACCC TGGCTGAGTT GCAAGGTCTA CCCACATTA GGGTTTTCCT GGACAACAAT 540
 CCCTGGGTCT GCGACTGCCA CATGCGAGAC ATGGTGAAGT GGCTCAAGGA AACAGAGGTA 600
 GTGCAAGGCA AAGACCGGCT CACCTGTGCA TATCGGAAA AAATGAGGAA TCGGTCTCTC 660
 TTGGAAGTCA ACAGTCTGTA CTTGGACTGT GACCCGATTC TTCCCCATC CTGCAAAACC 720
 TCTTATGTCT TCTTGGGTAT TGTTTTAGCC CTGATAGCGG CTATTTTCCT CTGGTCTTTG 780
 25 TATTGAACCC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
 AGTTCTAACT CGGATGTCTC CGAGTGA

Seq ID NO: 42 Protein sequence
 Protein Accession #: Eos sequence

30

1 11 21 31 41 51
 | | | | | |
 MPGGCSRQPA AGDGRRLRLR LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPPLPD 60
 QCPALCEBSE AARTVKCVNR NLTEVPTDLP AYVRNLFITG NQLASNHFLY LPRDVLALQLP 120
 35 SLRHLDLSEN SLVSLTYVSF RNLTHLESLH LEDNALKVLH NGTLAELOGL PHIRVFLDNN 180
 FWVCDCHMAD MVTWLKETEV VQGRDLRTCA YPEKMRNRVL LELNSADLDC DPILPPSLQT 240
 SYVFLGIPLA LIGAIPLVLV YLNRKGIKWM MNINRDACRD HMEGYHYRYE INADPRLTNL 300
 SSNSDVLE

40

Seq ID NO: 43 DNA sequence
 Nucleic Acid Accession #: NM_058173
 Coding sequence: 68..340

45 1 11 21 31 41 51
 | | | | | |
 AGCGCCTTGC CTCTCTTAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT 60
 CACCACCATG AAGTCTCTAG CAGTCTGGGT ACTCTTGGGA GTTTCATCT TTCTGGTCTC 120
 TGCCCAAGAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTGTA 180
 50 TGATGAAGCC CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240
 TACCACTGCA ACCACCGCTG CTCTACCACT TGCTCGTAAA GACATTCCAG TTTTACCCAA 300
 ATGGGTGGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCTTGAGTCT 360
 TCTGCAATTG GGTCACAACT ATTCATGCTT CCTGTGATTT CATCCAATA CTTACCTTGC 420
 CTACGATATC CCCTTTATCT CTAATCAGTT TATTTTCTTT CAAATAAAAA ATAACATGA 480
 55 GCGAGCTAAC AT

Seq ID NO: 44 Protein sequence
 Protein Accession #: NP_477521

60 1 11 21 31 41 51
 | | | | | |
 MKFLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETAAAA TTATTAAPT 60
 ATTAASTTAR KDIFVLPKWV GDLENGRVCP

65 Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26..2299

70 1 11 21 31 41 51
 | | | | | |
 CAGCACCCAG CTCCCCGCCA CGGCCATGGT CCCGACACCC GCCTGCGTTC TTCTGCTCAC 60
 CCTGGCTGCC CTGCGCGCGT CGGACAGGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
 GCAGATGCTT CGGGAACCTG AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
 CGCGCAGCAG GTCAAGGAGA TCACGTTCTT GAAAAACAG GTGATGAGT GTGACGCGTG 240
 75 CGGATGACAG CAGTCAGTAC GCACCGGCTT ACCAGCGTGC CGGCCCTGTC TCCACTGCGC 300
 GCGCGGCTTC TGCTTCCCGG GCGTGGCCTG CATCCAGACG GAGAGCGCGG GCGCTGCGCG 360
 CCCCTGCCCC GCGGGCTTCA CGGGCAACGG CTGCACTGTC ACCAGCTCA ACAGTGCAG 420
 GCGCCACCCC TGCTTCCCGG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCGCTGCGCA 480
 GGCTTGGCGG CGGGGTACCA CGGGCCACAC CCACCAAGGC GTGGGGCTGG CTTTGCCCAA 540
 80 GGCACACGAG CAGTTTTCGA CGGACATCAA CGAGTGTGAG ACCGGGCAAC ATAACTGCGT 600
 CCCCACCTCC GTGTGATCA ACACCCGGGG CTCCTTCCAG TGGGGCCCGT GCCAGCCCGG 660
 CTGCTGGGGC GACCAAGCGT CGGGCTGCCA GCGGGGCGCA CAGCGCTTCT GCGCCGACCG 720
 CTGCGCCAGC GAGTGCACAG AGCATGCAGA CTGCTTCTTA GAGCGGATG CTGCGGGTTC 780
 GTGCGTGTGT CGCGTGGGCT GGGCCGGCAA CGGGATCTCT TGTGGTCTGC ACACCTGACT 840
 AGACGGCTTC CCGACGAGA AGCTGCGCTG CCGGAGCCG CAGTGCCTGA AGGACAACTG 900

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COTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCCTG 960
CGATCCGGAT GCGGACGGGG ACGGGGTCCC CAATGAAAAG GACAACTGCC CGCTGGTGGG 1020
GAAACCCAGC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAAATGCCG 1080
GTCCCAAGAG AACGACGACC AAAAGGACAC AGACCAGGAC GGCCGGGGCG ATGCGTGCGA 1140
CGACGACATC GACGCGGACC GGATCCGCAA CCAGGCGGAC AACTGCCCTA GGGTACCCAA 1200
CTCAGACGAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCACGACTTT GTGGGAGATG CTTGTGACAG 1320
CGATCAAGAC CAGGATGGAG ACGGACATCA GGAATCTCGG GACAACTGTC CCACGGTGCC 1380
TAACAGTGCC CAGGAGGACT CAGACCAAGA TGGCCAGGGT GATGCGTGCG ACGACGACGA 1440
CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCCTA ACCCCGGCCA 1500
GGAGGAGCGG GACAGGGGAG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTCAACGTC CAAGACTTCAG 1620
GGCCTTCCAG ACAGTCGTGC TGGACCCGGA GGGTGAACCG CAGATTGACC CCAACTGGGT 1680
GGTGTCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCACG TTCCATGTGA ACACGGTCAC 1800
GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCAAGGAC AGCTCCAGCT TCTACGTGGT 1860
CATGTGGGAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG CTGTGGCCGA 1920
GGCTGGCATC CAACTCAAGG CTGTGAAGTC TTCCACAGGC CCCGGGGAAC AGCTGCGGAA 1980
CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCGCGG 2040
AAAAGTGGGT TGGGAAGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GGGCCCAAGT 2100
GGGCTACATC AGGGTGGGAT TCTATGAGGG CCCTGAGCTG GTGGCCGACA GCAAGGTGGT 2160
CTTGGACACA CAGATCGGGG GTGGCCGCGT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
CATCTGGGCC AACCTCGGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
TCAGCTGCGG CAGGCTAGG GACCAAGGTG AGGACCCGCC GGATGACAGC CACCTCACC 2340
GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGGAAATGAG 2400
AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG
  
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Seq ID NO: 46 Protein sequence
 Protein Accession #: NP_000086.1

30
 35
 40
 45

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1 11 21 31 41 51
| | | | |
MVPDTACVLL LTLAALGASG OGQSPGLGSDL GPOMLRELQE TNAALQDVDR WLRQQVREIT 60
FLKRTVMCED ACGMQQSVRT GLPSVRPLLH CAPGFCFFGV ACIQTESGGR CGPCPAGFTG 120
NGSHCTDVNE CNARHPCFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
INCBCTGQHN CVPNSVCINT RGSFQCGPCQ PGFVGDAQSG CQRAQARPCP DGSPSECEHE 240
ADCVLERDGS RSCVCRVWNA GNGILCGRDT DLDGFPDEKL RCPFQCRKD NCVTVPNSSG 300
EDVDRGIGD ACDPDAADGG VPNEKDNCLP VRNPDQRNTD EDKMGDADCN CRSQRNDQK 360
DTDQDGRGDA CDDDDIGDRI RNQADNCFRV PNSDQKDSGD DGIQDADCN POKSNPDQAD 420
VDHDFVGDAC DSDQDQDGGD HQDSRDNCPT VFNQAQEDSD HDGQGDACDD DDDNDGVFDS 480
RDNCRLVFPN QGEDADRQDV GDVCQDDFDA DKVVDKIDVC PENAEVLTLD PRAPQTVVLD 540
PEGDAQIDPN VVVLNQGREI VQTMNSDFGL AVGYTAFNGV DFBGTFFHVT VTDDEYAGFI 600
PGYQDSSSPY VVMKQMEQT VYQANPFRPV AEPGIQLKAV KSSTGPGEOL RNALWHTGDT 660
ESQVRLWLD PRNVGWKDKK SYRWFLQHRP QVGYIRVRPY EGPVLVADSN VVLDTTMRGG 720
RLGVFCFSQE NIIWANLRYR CNDTIPEDYE THQLRQA
  
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Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67..363

50
 55
 60
 65
 70

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1 11 21 31 41 51
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GAGACATTCC TCAATTGCTT AGACATATTC TGAGCCTACA CGAGAGGAAC CTCAGTCTC 60
AGCACCATGA ATCAAAGTGC GATTCTGATT TGCTGCCCTA TCTTTCTGAC TCTAAGTGGC 120
ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
CCTGTTAATC CAAGGTCTTT AGAAAAAAGT GAAATTAATC CTGCAAGCCA ATTTGTGCTA 240
CGTGTGAGA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
TCGAAGGCCA TCAGAATTT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCCT 360
TAAACACAGA GGGGAGCAAA ATCGATCGAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTT TTAGTTTGCA 480
GTTACATAAA AAGGTGACCA ATGATGGTCA CCAATACAGC TGCTACTACT CCTGTAGGAA 540
GGTTAATGTT CATCATCCTA AGCTATTGAG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
GCTCTACTGA GGTGCTATGT TCTTAGTGGA TGTTCGACC CTGCTTCAA TATTTCCTC 660
ACCTTTCCCA TCTTCCAAGG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAAITC 720
TCAGAAATCTC AAATAACTAA AAGGTATGCA ATCAAACTCG CTTTITAAAG AATGCTCTTT 780
ACTTCATGGA CTTCACATGC CATCTCCCA AGGGGCCCAA ATCTTTTCAG TGGCTACCTA 840
CATACAATTC CAAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAATATT 900
CTTATTTAAT GAAAGACTGT ACAAAGTATA AGTCITAGAT GTATATATTT CCTATATTGT 960
TTTCAGTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
TTTTCAAATA AAAATGAGGT ACTCTCCTGG AAATATTAAAG
  
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Seq ID NO: 48 Protein sequence
 Protein Accession #: NP_001556.1

75
 80

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1 11 21 31 41 51
| | | | |
MNQTALICC LIPLTLGSIQ GVPLSRTVRC TCISISNPQV NPSLEKLEI IPASQPCPRV 60
EIIATMKKKG EKRLNPESK AIKNLLKAVS KEMSKRSP
  
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Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: XM_057014
 Coding sequence: 143..874

1 11 21 31 41 51
 5 GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCTCGGT CTCTCCGCC TCCAGCTCCG 120
 CGCTGCCGCG CAGCGCGGAG CCATGCGACC CCAGGGCCCC GCGCGCTCCC CGCAGCGGCT 180
 CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCCGAGC CCTCTGAGAT 240
 CCCCAGGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGCTCGAGAC GGGAGCCCTG GGGCCAATGG 360
 10 CATTCCGGGT ACACCTGGGA TCCCAGGTCC GGATGGATTG AAAGGAGAAA AGGGGGAATG 420
 TCTGAGGGAA AGCTTTGAGG AGTCTGGAC ACCCACTAC AAGCAGTGT CATGGAGTTC 480
 ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCCGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCACTGG CTCACITCGG CTAAAAATGCA GAAATGCATG 600
 CTGTGACGCT TGGTATTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTA 660
 15 AGCTATAATT TATTTGGACC AAGGAAGCCC TGAATGAAT TCAACAATTA ATATTTCATG 720
 CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGTCTAT 780
 TTGGGTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
 TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCA TTGCTACCTC 900
 TTTTATTATT ATGCTTTGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
 20 CATCTGAATG AAAGCAAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCATAT TTTTITTAGT 1080
 TGGTTAGAAT ACTTCTTCTA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTGTT 1140
 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAAA ATATAAAGC TACCAATCTT 1200
 25 TGACAAATT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
 CAACCTTAAA AAAAAA AAAA

Seq ID NO: 50 Protein sequence
 Protein Accession #: XP_057014

30 1 11 21 31 41 51
 MRPQGPAAASP QRLRGLLLLL LLQLPAPSSA SEIPKGGKKA QLRQREVVLD YNGMCLQGPA 60
 GVPRDGGSPG ANGIPGTPGI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNLYGIDL 120
 GKIAECTFTK MRSNSALRLV FSGSLRLKCR NACQQRWYFT FNGABCSGPL PIEAIIYLDQ 180
 35 GSPENNSTIN IHRSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
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Seq ID NO: 51 DNA sequence
 Nucleic Acid Accession #: NM_020974
 Coding sequence: 81..3080

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	TCCTCTGCC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
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	CCAGGTCAAA	GAAGCTGTGG	ATTCAAGTTCA	AGTCCAATGA	AGGGAACAGC	GCTAGAGGGT	2820
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	CCGGCCCTCT	CTAAGGGAGC	CCTCTGCACT	CGTGTGCAGG	CTCTGACCAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCCTGACGG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
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Seq ID NO: 52 Protein sequence

Protein Accession #: NP_066025

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	HDGHNCLVD	ECLENNGGCQ	HTCVNVMGSY	ECCKEKGFFL	SDNQHTCIHR	SEEGLSMNMK	180
	DHGCSSHCKE	APRGSVACBC	RPGFELAKNQ	RDCILTCNHG	NGGQHSCHDD	TADGPECSCH	240
	PQYQMTDGR	CSCLEREDTVL	EVTESNTTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300
	STGVESCSPV	GFTLQLDQKT	CKDIDECQTR	NGGCDHFCKN	IVGSPDCGCK	KGFKLITDEK	360
35	SCQDVDECSL	DRTCDHSCIN	HPGTFFACACN	RGYTLYGFTH	CGDTNECSIN	NGGQQQVCVN	420
	TVGSYECQCH	PGYKLHWNKK	DCVEVKGLLP	TSVSPRVSLH	CGKSGGGDGC	FLRCHSGIHL	480
	SSDVTITRTS	VTFKLNEGKC	SLKNAELFPE	GLRPLALPEKH	SSVKESPRYV	NLTCSGSKQV	540
	PGAPGRPSTP	KEMFITVEFE	LETNQKEVTA	SCDLSICVKR	TEKRLRKAIR	TLRKAVHREQ	600
	FHLQLSGMNL	DVAKKPPRTS	ERQAESCQVG	QGHAEHQVSV	CRAQTYDGA	RERCILCPNG	660
40	TFQNEEGQMT	CEPCPRPGNS	GALKTPPEAWN	MSECCGGLQCF	GEYSADGFAP	COLCALGTFQ	720
	PEAGRTSCFP	CGGGLATKHQ	GATSPQDCET	RVQCSFGHFY	NTTTHRCIRC	PVGTYPQPEFG	780
	KNNVCSPQVN	TTTDFDGSIN	ITQCKNRRCG	SELGDFGTGYI	ESPNYPGNYP	ANTECTWTIN	840
	PPPKRILIVL	WPEIFLPIED	DCGDYLVMRK	TSSNSVTTY	ETQTYERPI	AFTSRSKLW	900
	IQPKSNEGNS	ARGFQVPYVT	YDEDYQELIS	DIVRDGRLYA	SENHQEILKD	KKLIKALFDV	960
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Seq ID NO: 53 DNA sequence

Nucleic Acid Accession #: NM_014211

Coding sequence: 157..1479

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55	CCTACTCTCAG	CCCCTTGCTG	TGAGCAGCTT	CTCAACATGA	ACTACAGCCT	CCACTTGGCC	180
	TTCTGTGTCT	TGAGTCTCTT	CACTGAGAGG	ATGTGCATCC	AGGGAGATCA	GTTCAACGTC	240
	GAGGTCCGGC	GAAGTGACAA	GCTTTCCCTG	CCTGGCTTTG	AGAACCTCAC	AGCAGGATAT	300
	AACAAATTTT	TCAGGCCCAA	TTTGTGTGGA	GAACCCGTAC	AGATAGCGCT	GACTCTGGAC	360
	ATTGCAAGTA	TCTCTAGCAT	TTCAAGAGAGT	AACATGGACT	ACACAGCCAC	CATATACTTC	420
60	CGACAGCGCT	GGATGAGACCA	GCGGCTGGTG	TTTGAAGGCA	ACAAGAGCTT	CACTCTGGAT	480
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	ATGACACAC	AGACATGCAA	GTTGACAGTG	GAAAGCTGGG	GCTATGATGG	AAATGATGTG	720
65	GAGTTACCT	GGCTGAGAGG	GAAACGACTCT	GTGCGTGGAC	TGGAACACCT	GCGGCTTGCT	780
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	ACCTACGTTT	CTTCCACTTT	CCTGGTGGTG	TTGTCTGGGG	TTTCATTTTG	GATCTCTCTC	960
	GATTCACTCC	CTGCAAGAAC	CTGCATTGGA	GTGACGACCG	TGTTATCAAT	GACCACTAGT	1020
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Seq ID NO: 54 Protein sequence
 Protein Accession #: NP_055026

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WGYDGNDSVR TWLRGNDSVR GLEHLRLAQY TIERYFTLV T RSQQTGNIT RLVLQFELRR 240
NVLYFILETY VPSTFLVLS WVSFWISLDS VPARTCIGVT TVLSMTLMI GSRTSLPNTN 300
CFIKAIIDVYL GICPSFVFGA LLEYAVAHYS SLQQMAAKDR GTTKEVEEVS ITNIISSSIS 360
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20 Seq ID NO: 56 Protein sequence
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 EHSDDHDSH HHNHAASGN KRKALCPDHD SDSSGKDPFN SQGKAHRPE HASGRRNVKD 180
 SVSASEVTST VYNTVSEGH FLETIETPR GKLFPKDVSS STPPSVTSKS RVSRLGRKT 240
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 30 RSLIHTSEK KABIPPKTYS LQIAWVGFP AISIISFLSL LGVILVPLMN RVFFKPLLSF 360
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40 Seq ID NO: 57 DNA sequence
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Seq ID NO: 60 Protein sequence
 Protein Accession #: Eos sequence

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 40 PNTFFPTPR LSNLEQSPS PILETLLELP WMVCSLGNAI FSKSGPQTGE AMDLTFKPSSL 240
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 Coding sequence: 128..1237

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 Protein Accession #: NP_073580

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 WKWEQLVLANC QAIISNSER LPDINIYQLK VLDCAWDACI NLGLLEALP YGTRTMEPYR 300
 25 IFFPGSHFVR GVQVMKVGKL QHQGMFPQA MNLRLAFDI MRVTHGREHS LIEDLILLE 360
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 Coding sequence: 238..648

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Seq ID NO: 64 Protein sequence
 Protein Accession #: NP_003005.1

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SSQCCHILP	QODVLIMCYE	WRSRMMLLEN	CLVERKWRDL	SKRSIQWEER	LQEQRRTVQD	300
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 Coding sequence: 248..1780

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CAAAACAGCC	ATGAACCAAT	TTGTTTCAGGA	GAATGGGACC	CTACGGGCCA	AGCCACCGGG	1740
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CTAGGCCCTG	CTCCTTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GGCTCCTTAA	1860
ACACCCCATC	TTCTTGGCGA	AGATGTCTCC	CATCCCACTG	ACTGCTTGAC	CTTTACTCTC	1920
AACCCCTCTG	TTCTTGGCGA	GGGCTCCACC	AATTGAGTCT	CTCCCACTAT	GCATGCAAGT	1980
CACGTGTGCT	GTGCATGTGT	GCCTGTGTGA	GTGTTGACTG	ACTGTGTGTG	TGTGGAGGGG	2040
TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGATCT	2100
AAGTGAAGCT	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACGTGTCAG	2160
GTGTTGGCGT	TGTGTCAATG	GGCTGTGTGT	GACCTCTGCG	TGAAAAGACA	GGTATTTTCT	2220
CAGACCCAGG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
CAGACCCAGG	TGTGCGGGCA	TAGCTGGAGC	TGGAATCTGC	CTCGGTGTGT	AGGGAACCTG	2340
TCTCTACCA	CTTCGGAGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCCA	2400
GAGGCTTGAA	CTGTTACAGA	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
ACATATTTTC	TGTAAATATA	CATGCGCGCG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
ACTTTTAAAT	TTTTTCTTTT	TTTTTCTTTG	CCCTTTCCAT	TAGTGTGTAT	TTTTATTAT	2580
TTTTATTTTT	ATTTTTTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTCTG	2640
CTGTAAAAAA	ACCAAAACCC	AAAAAAACCC	AAAAAAACCC			

Seq ID NO: 66 Protein sequence
 Protein Accession #: AAH10423

65
 70
 75
 80

MPLSLGAEMW	GPRAWLLLLL	LLASFTGRCP	AGELETSDDV	TVVLGQDAKL	PCFYRGDSGE	60
QVGQVAVARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
DEGEYECRVS	TYPAGSFQAR	LRLRVLVPLP	PSLNPGPALE	EQGLTLAAS	CTAEGSPAPS	180
VTDTEVKG	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHFGL	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMLC	LSEGGPPPSY	NWTRLDGPLP	SGVRVDGDTL	300
GFPPPLTTEHS	GIYVCHVSNE	PSSRDSQVTV	DVLDPQEDSG	KQVDLVSASV	VVVGVIALLL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDLSKDN	SSCSVMSEEP	EGRSYSTLTT	VREIETQTEL	LSPSGRAABE	EEDQDEGIKQ	480
AMNHPVQENG	TLRAKPTGNG	IYINGRGLHV				

Seq ID NO: 67 DNA sequence
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274..1782

80

CGCGGGGCGC	GGAGTCGGCG	GGGCTCGCG	GGACGCGGGC	AGTGCGGAGA	CGCGGGCGCT	60
GAGGACGCGG	GAGCCGGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCTACTC	TTTCTTAGAT	120
GTGAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180

	CATAACCATT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTTAAA	CTTACAAGCC	240
	TGCCATAAGT	GAGAAGCAAA	CTTCCTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAAAATTA	300
	AATGTGGGCA	CCAAGAAAGA	GGATGGTGA	AGTACAGCCC	CCACCCCCCG	TCCAAAGGTC	360
5	TTGCGTTGTA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TTGCAGCACA	420
	GACGGATATT	GTTTCAACAT	GATAGAAGAG	GATGACTCTG	GGTTGCGTGT	GGTCACCTCT	480
	GGTTGCCTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTCCGG	ACACTCCCAT	TCCTCATCAA	540
	AGAAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAAGACCT	ACACCCCTACA	600
	CTGCCTCCAT	TGAAAAACAG	AGATTTTGTG	GATGGACCTA	TACACCACAG	GGCTTTACTT	660
10	ATATCTGTGA	CTGTCTGTAG	TTTGCTCTTG	GTCTTATCA	TAATTATTTG	TTACTTCCGG	720
	TATAAAGAC	AGAAACCCAG	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACCTTAC	780
	ATTCCTCTCTG	GAGAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGA	840
	TCAGGCCTCC	CTCTCTGTGT	CCAAAGGACT	ATAGCTAAGC	AGATTGAGAT	GGTGAACAG	900
	ATTGGAAAG	GTGCTATG	GGAGTTTGG	ATGGGAAAGT	GGCGTGGCGA	AAAGGTAGCT	960
15	GTGAAGTGT	TCTTACCAC	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
	ACAGTGTGA	TGAGGCATGA	AAACATTTTG	GGTTTCATTG	CTGCAGATAT	CAAAGGGACA	1080
	GGGTCTCTGA	CCCAAGTTGA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
	TATCTGAAGT	CCACCACCT	AGACGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
	AGTGGCTTAT	GTCATTTACA	CACAGAAATC	TTTAGTACTC	AAGGCAAAAC	AGCAATTGCC	1260
	CATCGAGATC	TGAAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACTTG	CTGTATTGCT	1320
20	GACCTGGGCC	TGGCTGTTAA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
	ACTCGAGTTG	GCACCAAAAG	CTATATGCCT	CCAGAAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
	AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCCTCAT	CCTTTGGGAG	1500
	GTGCTAGAGA	GATGTGTATC	AGGAGGTATA	GTGGAAGAAT	ACCAGCTTCC	TTATCATGAC	1560
25	CTAGTGCCTA	GTACCCCTCT	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAAGAAGTTA	1620
	CGCCCTCAT	TCCCAAACCG	GTGGAGCAGT	GATGAGTGTG	TAAGGCAGAT	GGGAAAATC	1680
	ATGACAGAAAT	GCTGGGCTCA	CAATCTTGCA	TCAAGGCTGA	CAGCCCTGCG	GGTTAAGAAA	1740
	ACACTTGCCTA	AAATGTCAAG	GTCCAGGAC	ATTAACCTCT	GATAGGAGAG	GAAAAGTAAG	1800
	CATCTCTGCA	GAAAGCAAC	AGGTACTCTT	CTGTTGTGGS	GCAGAGCAAA	AGACATCAAA	1860
30	TAAGCATCCA	GTGCAACAGC	CTTGAACATC	GTCTGCTTCC	CCAGTGGGTT	CAGACCTCAC	1920
	CTTTCAAGGA	GGACCTGGG	CAAAGACAGA	GAAGCTCCCA	GAAGGAGAGA	TTGATCOGTG	1980
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Seq ID NO: 68 Protein sequence
Protein Accession #: NP_001194

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	MLLSRAGKLN	VGTKKEDGES	TAPTPRPKVL	RCKCHHCPE	DSVNNICSTD	GYCPTMIEED	60
	DSGLPVVTS	CLGLESDQFQ	CRDTPIPHQR	RSIECCTERN	ECNKLHPTL	PPLKNRDFVD	120
40	GPIHHRALLI	SVTVCSLLLV	LILFLCYFRY	KRQSTRPRYS	IGLEQDETYI	PGESLRDLI	180
	EQSSSSGSGS	GLPLLQRTI	AKQIQMWKQI	GKGRYGEVWM	GKWRGEKAVV	KVFFTTSEAS	240
	WFRREIYQT	VLMRHENILG	FIAADIKGTG	SWTQLYLITD	YHENGSLYDY	LKSTTLDAKS	300
	MLKLAYSSVS	GLCHLHTEIF	STQKGPAIAH	RDLSKSNILV	KKNGTCCIAI	LGLAVKFISD	360
	TNEVDIPPT	RVGTGRYMPF	EVLDESINRN	HFQSYIMADM	YSFGLILWEV	ARRCVSGGIV	420
45	EEYQLPYHDL	VPSDPSYEDM	REIVCIKKLR	PSFPNRWSSD	ECLRQMGKLM	TECWAHNPAS	480
	RLTALRVKKT	LAKMSESQDI	KL				

Seq ID NO: 69 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 166..1737

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	TCCTCCCAAC	TCAGCCACCC	AAGTGGCTGG	GACTACAGAT	TAAGAATGAC	CCAAAATAAA	180
	TTAAAGCTTT	GTTCCAAAGC	CAATGTGTAT	ACTGAAGTGC	CTGATGGAGG	ATGGGGCTGG	240
	GGGCTAGCTG	TTTCATTTTT	CTTGTGTGAA	GTCTTCACTT	ACGGCATCAT	CAAGACATTT	300
	GGTGTCTTCT	TTAATGACTT	AATGGACAGT	TTTAATGAAT	CCAATAGCAG	GATCTCATGG	360
60	ATAATCTCAA	TCTGTGTGTT	TGTCTTAACT	TTTTCAGCTC	CCCTCGCCAC	AGTCTGAGC	420
	AATGTTTTCG	GACACCGTCT	GGTAGTGATG	TTGGGGGGGC	TACTTGTGAG	CACCGGAGTG	480
	GTGGCGCGCT	CCTTCTCACA	AGAGGTTTCT	CATATGTACG	TGCGCATCGG	CATCATCTCT	540
	GGTCTGGGAT	ACTGCTTTAG	TTTTCTCCCA	ACTGTAAACA	TCCTATCACA	ATATTTTGGC	600
65	AAAAGACGTT	CCATAGTCAC	TGCAGTTGCT	TCCACAGGAG	AATGTTTTCG	TGTGTTTGCT	660
	TTGCGCACC	CAATCATGGC	TCTGAAGGAG	CGCATTGGCT	GGAGATACAG	CCTCTCTTTC	720
	GTGGCCCTAC	TACAGTTAAA	CATTGTCTATC	TTGGAGGCAC	TGCTCAGACC	CATCTTTATC	780
	AGAGGAGACC	CGTCAACGAA	AATAGTCATC	CAGGAAATATC	GGAAAGAAGC	GCAGTATATG	840
	CTTGAATGAT	AGAAACACAG	AACCTCAATA	GACTCCATTG	ACTCAGGAGT	AGAACTAACT	900
	ACCTCACCTA	AAAATGTGCC	TACTCACACT	AACCTGGAAC	TGGAGCGGAA	GGCGGACATG	960
70	CAGCAGGTCC	RVGTTGAAGC	CAGCCCCAGG	CCAAGCGAAA	AGAAAGCCCC	GCTATTAGAC	1020
	TTCTCCATTT	TGAAAGAGAA	AAGTTTATT	TGTTATGCAT	TATTTGGTCT	CTTTGCAACA	1080
	CTGGGATCTT	TTGCACTTTC	CTGTACATC	ATTCTCTGCG	GCATTAGTCT	GGGCATTGAC	1140
	CAGGACCGCG	CTGCTTTTTT	ATTATCTACG	ATGGCCATTG	CAGAAGTTT	CGGAAGGATC	1200
	GGAGCTGGTT	TTGTCTCTCA	CAGGGAGCCC	ATTCTTAAGA	TTTACATTGA	GCTCATCTGC	1260
75	GTCACTTTAT	TGCTGTGTC	TTTACTTTTG	CTACTGAATT	CTGGGCTCTA	CTGGGCTCTA	1320
	ATGTCATGCA	GCATATTTTT	TGGGTTTATG	GTGGAACAA	TAGGAGGGAG	TCACATTCCA	1380
	CTGCTTGTCT	AGGATGATGT	CGTGGGCATT	GAGAAGATGT	CTTCTGCAGC	TGGGGTCTAC	1440
	ATCTTCAATC	AGAGCATAGC	AGGACTGGCT	GGACCGCCCC	TTGCAGGTTT	GTGTGTGGAC	1500
80	CAAAGTAAGA	TCTACAGCAG	GGCCTTCTAC	TCCTGCGCAG	CTGCGATGGC	CCTGGCTGCT	1560
	GTGTGCTTCC	CCCTGGTGAG	ACCGTGTGAG	ATGGGACTGT	GCCAGCATCA	TCACCTAGGT	1620
	GAAACAAAGG	TAGTGAGCCA	TCGTGGGAGG	ACTTTACAGG	ACATACCTGA	AGACTTTCTG	1680
	GAAATGGATC	TTGCAAAAAA	TGAGCACAGA	GTTCACGTGC	AAATGGAGCC	GGTATGACAC	1740
	ACTTTCTTAC	AACCAACGCC	ACTGTGTTGG	CTGGAGAGGG	ATGGGGTGGG	CCCAACGGGG	1800
	ACACAAGGAG	GCAGAGGAGC	TAACCCCTCT	ACTCCACTTT	CAAACTACA	TTTTAAAGGG	1860

AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAGC 1920
 TTTTITTTTT TGCTTGTGTT TAAAGCCAAA ACAAAAAACA ACCAAGCACT CTTCATATA 1980
 TAAATCTGGC TGTATTCAGT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTCACA 2040
 5 TCCGATATT AAAATAGTGA CATGAACCTG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100
 TAAATGATTT TCTTTTITTC TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACCTACTCT 2160
 CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAAATGAA ATTGGCCAGT C

Seq ID NO: 70 Protein sequence
 Protein Accession #: Bos sequence

10
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 MTQNKLLKCS KANVYTEVPD GGNWNAVAVS PFFVEVFTYG IIKTFGVFFN DLMDSFNESN 60
 15 SRISWIISIC VFVLTSPAPL ATVLNRRFGH RLVVMLGGLL VSTGMVAASP SQEVSHMYVA 120
 IGIISGLGYC PSFLPTVTIL SQYFGKRRSI VTAVASTGEC PAVFAPAPAI MALKERIGWR 180
 YSLLFVGLLQ LNIIVFGALL RPIPIRGPAS PKIVIQENRK EAQYMLENEK TRTSIDSIDS 240
 GVELTTPSPN VPTHNLELE PKADMQQVLV KTSRPPSEKK AFLDPSILK EKSFCYALF 300
 GLPATLGFPA PSLYIIPPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
 20 IELICVILLT VSLPFTFAT EFWGLMSCSI PFGPMVGTIG GTHIPLLAED DVVGIEKMSS 420
 AAGVYFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
 HHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 71 DNA sequence
 Nucleic Acid Accession #: NM_004694
 Coding sequence: 166..1737

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 TTAAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAAGTC CTGATGGAGG ATGGGGCTGG 240
 GGGTAGCTTG TTTTCTTTT CTTCGTTGAA GTCTTCACT ACGGCATCAT CAAGACATTT 300
 35 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
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 40 AAAAGACGTT CCATAGTCAC TGCAGTTGCT TCCACAGGAG AATGTTTCGC TGTGTTTGCT 660
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 GTGGCCCTAC TACAGTTAAA CATTGTCATC TTCGGAGCAC TGCTCAGACC CATCATTATC 780
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 45 ACCTCACCTA AAAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960
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 50 GGAGCTGGTT TGTCTCTCAA CAGGAGGCC ATTCTGAAGA TTTACATTGA GCTCATCTGC 1260
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 ATGTCATGCA GCATATTTTT TGGGTTTATG GTTGGAAACA TAGGAGGACT CACATTCCAC 1380
 TGCTTGCTGA AGATGATGTC GTGGGCATTG CAGAAGATGT CTCTGCAGC TGGGCTCTAC 1440
 ATCTTCATTC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
 CAAAGTAAGA TCTACAGCAG GGCTTCTAC TCCTGCGCAG CTGGCATGGC CTTGGCTGCT 1560
 55 GTGTGCTCG CCTGTGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCTCA TCACTCAGGT 1620
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 GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCAGTGC AAATGGAGCC GGTATGACAC 1740
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 TCCGATATT AAAATAGTGA CATGAACCTG CAAAGTGGTT TTAAGAGCTT TCACGTGGGA 2100
 65 TAAATGATTT TCTTTTITTC TTTTCTTTCT TCCTATGGTC TTGTCTGAAT AAACCTACTCT 2160
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Seq ID NO: 72 Protein sequence
 Protein Accession #: NP_004685

70
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 75 SRISWIISIC VFVLTSPAPL ATVLNRRFGH RLVVMLGGLL VSTGMVAASP SQEVSHMYVA 120
 IGIISGLGYC PSFLPTVTIL SQYFGKRRSI VTAVASTGEC PAVFAPAPAI MALKERIGWR 180
 YSLLFVGLLQ LNIIVFGALL RPIIIRGPAS PRIVIQENRK EAQYMLENEK TRTSIDSIDS 240
 GVELTTPSPN VPTHNLELE PKADMQQVLV KTSRPPSEKK AFLDPSILK EKSFCYALF 300
 GLPATLGFPA PSLYIIPPLGI SLGIDQDRAA FLLSTMAIAE VFGRIGAGFV LNREPIRKIY 360
 IELICVILLT VSLPFTFAT EFWGLMSCSI PFGPMVGTIG GLTFHCLLKM MSWALQKMSS 420
 80 AAGVYFIQS IAGLAGPPLA GLLVDQSKIY SRAFYSCAAG MALAAVCLAL VRPCKMGLCQ 480
 RHHSGETKVV SHRGKTLQDI PEDFLEMDLA KNEHRVHVQM EPV

Seq ID NO: 73 DNA sequence
 Nucleic Acid Accession #: NM_002184.1
 Coding sequence: 256..3012

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AGACGGGAG GGTGAGGCG GCGCGGCGCT AGTGAAACCC AATGGAAGAA GCATGACATT 180
TAGAAGTAGA AGACTTAGCT TCAATCCCT ACTCCTTCAC TTACTAATT TTGTGATTGG 240
AAATATCCGC GCAAGATGTT GACGTTGCAG ACTTGGGTAG TGCAAGCCTT GTTTATTTTC 300
CTCACCACCTG AATCTACAGG TGAACCTCTA GATCCATGTG GTTATATCAG TCCTGAATCT 360
CCAGTTGTAC AACTTCATT TAATTTCACT GCAGTTTGTG TGCTAAAGGA AAAATGTATG 420
10 GATTATTTTC ATGTAATGTC TAATTACATT GTCTGGAAAA CAAACCAATT TACTATTCTC 480
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15 ACAACTTCA CTTTAAAAAT TGAATGGGCA ACACAAGAT TTGCTGATTG CAAAGCAAAA 780
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20 CTGTCTAGT TCTTAAAAAT GACATGGACC AACCCAAGTA TTAAGAGTGT TATAATACTA 1020
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30 GAGTGTGTG TGTATTCAGA TAAAGCACCC TGTATCAGC ACTGSCAACA AGAAGATGGT 1680
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40 CCAGATCCTT CAAAGAGTCA TATTGCCAG TGGTCACTC ACATCTCTCC AAGGCACAAT 2280
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50 ATTTCAAAAT CCTGTGGATC TGGGCAAAAT AAAATGTTTC AGGAAGTTTC TGCAAGAGAT 2880
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ATGCTCAGT GAAGGACTAG TAGTTCCTGC TACAACCTCA GCAGTACCTA TAAAGTAAAG 3060
55 CTAATATGAT TTTATCTGTG AATTC

Seq ID NO: 74 Protein sequence
Protein Accession #: NP_002175.1

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ISGLPFEPKP NLSCIVNEGK KMRCEWDGGR ETHLENTFTL KSEWATHKFA DCKAKRDTPT 180
SCTVDYSTVY FVNIEVVEA ENALGKVTSD HINFPVYKV KPNFPNLSV INSEELSSIL 240
65 KLTWNPSIK SVILKYNIQ YRTKDASTWS QIPPEDTAST RSSFTVQDLK PFTEYVFRIR 300
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YLRGNLAESK CYLITVTPVY ADGPGSPESI KAVLKQAPPK KGPTVRTKKV GKNEAVLEWD 540
70 QLFVDVQNGF IRNYTIFPYR IIGNETAVNV DSSHTETLS SLTSDTLVMV RMAAYTDEG 600
KDGPEFTFT PKPAQGEIEA IVPVCLAPL LTTLLGLVLC FNKRDLIKKH IWPNVDPDSK 660
SHIAQWSPHT PPRHFNFSKD QMYSNGNFTD VSVVEIEND KKPFPDLKS LDLFKKEKIN 720
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ESTQPLDSE ERFEDQLVD HVDGGDILP RQYQFKQNC QHSSPDISH PERSKQVSSV 840
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Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_022131
Coding sequence: 11..2878

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Seq ID NO: 76 Protein sequence
 Protein Accession #: NP_071414

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 TFLIQAYDQ AGPHETAWKK SHKAVVHIQV KDVNEPAPTF KEPAYKAVVT EGKIYDSILQ 180
 VEAIDEDCSF QYSQICNYEI VTIDVPPAID RGNIRNTEK LSYDKQHQB LVTAYDCQG 240
 KPAAQDTLVQ VDKVPVCKPG QDWTKRIEY QPGSGSNPLF PSIHLETCDG AVSSLQIVTE 300

5 LQTNVIGKGC DRETYSEKSL QKLCGASSGI IDLLPSPSAA TNWTAGLLVD SSEMIPKFDG 360
 RQGAIPDGI VPKNLTQDFT ITMMKHGKPS PGVRAEKETI LCNSDKTEKN RHHYALVYHN 420
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 CKEGLDINSL ESIGQGIKYH FNPSSQILVM EGDDIGNINR ALQKVSYINS RQFPFAGVRR 600
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 DIKIVSTFAK TEAPGDVKT DPKSEVLEEM LHNLDPCDIL VIGGDLDPRQ ECLLEINHSEL 720
 HQRHLDATNS TAGYSIYGVG SMSRYEQVLH HIRYRNWRPA SLEARRPRIK CSEINGRYTS 780
 10 NEFNLEVSIL HEDQVSDKEH VNLIVQPPF LQSVHHPESR SSIQHSVVP SIATVVIIS 840
 VCNLVEVWAM GYRVRIAHO HFIQETBAK ESEMWDSDA LTITVNPMEK HEGPGHGEDE 900
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Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482..3007

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 25 CTTTATGAAG CTATGGGACT TGACAAAAGT TGATATTGGA GAAGAAAGTA CGCAGTGTT 360
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Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

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5 PPQNPRKILY AGNIIHSLMK SDLVEYFTLE MLHLGNRIE VLEEGSFMNL TRIQLKLYLNG 420
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Seq ID NO: 79 DNA sequence
 Nucleic Acid Accession #: NM_016640.2
 Coding sequence: 39..1358

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TGGCCTCCAT	GACAGCCGAC	AGCAAGCTG	CACGGCTGCG	GCGGATCGAG	CGCTGGCAGG	240
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Seq ID NO: 80 Protein sequence
 Protein Accession #: NP_057724.1

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VSTLVGLLSP	HNPALAAAL	DYRCPVHFYV	VRGEIIPRG	HRRGRIDDLR	YQIDDKPNQ	240
IRISKQLAEF	VPLOYSVPIE	IPTIRCKPDK	LPLPKRQVEN	HIPVGSKTAD	PCCYGHQTQH	300
LLPKLRLRER	LLRQNCADQI	EVVFRANAIA	SLPAWTGAQA	MYQGFNSEAD	VTRPFVSQAV	360
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Seq ID NO: 81 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
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CCTGTATGCC	AACCCAGTGG	GTACAGGTTT	TGGGGGACCT	GGACAGATGC	CGCTACCTCT	480
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15 Seq ID NO: 82 Protein sequence
 Protein Accession #: FGENESH predicted

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35 Seq ID NO: 83 DNA sequence
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Seq ID NO: 84 Protein sequence
 Protein Accession #: NM_005264.1

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Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: XM_027172.1

Coding sequence: 143..1405

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	AAGCCTGCCA	CGCTTGCAAT	TATTTAGTAC	AGATGTAAAT	ACAAAGGCTT	AAAGCAAAAT	4260
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55	GAGGTGGGTC	TTGGAGAGGA	AGGACTTAGG	GAGGCAGAGT	GGAGGAAGTG	AGAGGACACC	4740
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	AGCACTTTGG	GAGGCTGAGG	CGGGCGGATG	GCTTGAAGGT	AGGAGTTTGA	AACCGGCTGT	6060
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Seq ID NO: 88 Protein sequence
Protein Accession #: BAA32297.1

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    ILLAGNMKKE AQMLCQRHRR KSSVTDSESS LVNRPDLGQF TEEIHAIEVC YAECLLQRAA 180
    LTFLOQSSHG GAVRPRALHD PSHACSCPPG PGRQHLFLQ DENMVSFIKG GIKVRNSYQT 240
    YKELDSLVSQ SQYCKGENHP HFEGGVKLGV GAFNLTLML PTRILRLLEF VGFSGNKDYG 300
    LLQLEBEGASG HSFRSVLCVM LLLCYHTFLT FVLGTGNVNI EEAEKLLKPY LNRYPKGAIF 360
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Seq ID NO: 89 DNA sequence

Nucleic Acid Accession #: AF007170

Coding sequence: 73..1725

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    CTGGAGATGC AGCCCATGAT GACCTTTGAC CCTCAGGACA TCTGCTTGC CGGCAACATG 240
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25 GAGGTCTGCT ATGCAGAGTG CCTGTGCGAG CGAGCAGCCC TGACCTTCTT GCAGGACGAG 420
    AACATGGTGA GCTTTCATCA AGGCGGCATC AAGTTGCGAA ACAGCTACCA GACCTACAAG 480
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    GAAGGAGAGG TGAAGCTTGG TGTAGGGGCC TTCAACCTGA CACTGTCCAT GCTTCCTACT 600
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30 CAGCTGGAGG AGGGAGCGTC AGGGCAGCAG TTCGCTCTG TGCTCTGTGT CATGCTCCTG 720
    CTGTGCTACC ACACCTTCTT CACCTTCTGT CTCGCTACTG GGAACGTCAC ATCGAGGAG 780
    CCGAGAGAAG TCTTGAAGCC CTACCTGAAC CGGTACCCCTA AGGGTGCCAT CTTCTCTGTC 840
    TTTGACGGGA GGATTTGAAG CATTAAGGCG AACATTGATG CAGCCATCCG GCGTTTCGAG 900
    GAGTGCTGTG AGGCCGAGCA GCACTGGAAG CAGTTTCACC ACATGTGCTA CTGGGAGCTG 960
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Seq ID NO: 90 Protein sequence

Protein Accession #: AAC39582.1

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    EVCYAECLLQ RAALFLQDE NMVSFIKGI KVRNSYQTYK BLDSLVSQSSQ YCKGENHPFP 180
    EGGVILGVGA FNLTLSMLPT RILRLLEFVG FSGNKDYGLL QLEEGASGHS FRSVLCVMLL 240
    LCVHTFLTFV LGTGNVNIEE AEKLLKPYLN RYPKGAIFL FAGRIEVIKG NIDAAIRRPF 300
75 ECCEAQGHWK QPHHMCYWEI MWCFTYKQW RMYSPYADLL SKENCWSKAT YIYKKAAYLS 360
    MFGKEDHKFP GDEVELFPA VPGLKLIAG KSLPTEKFAT RKSRYPSSN PISLPVPALE 420
    MMYINWYAV IGKQPKLTDG ILEITKAE MLEKGPENEY SVDDDECLVL LKGLCLKYLG 480
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Seq ID NO: 91 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 31..906

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Seq ID NO: 92 Protein sequence
 Protein Accession #: Eos sequence

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Seq ID NO: 94 Protein sequence

Protein Accession #: NP_219487.1

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1 11 21 31 41 51
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MKDVGPEPCG QPTPCWPSPA LESVLGKASQ HLGLESQQPL YLLELNWGGT ECALSSSTGRT 60
AACFLPISLL PTSPAAMLGP EALCLPGRPG TTGLRDTGGP LLLPPPTLLQ DTRWCNMLV 120
LWPAKVHGDG PHGILRDQAA GIGKEFHPDH CPSQVPRRPH HTPFQGGSS KPRARILCCC 180
LVBSLPPCVG SVGQAECIGD RAVSMGLGVC ELRPRCAVNR RVLSGKRCGP KVCVCRGWVC

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Seq ID NO: 95 DNA sequence

Nucleic Acid Accession #: XM_090469

Coding sequence:

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1 11 21 31 41 51
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TGCCGCGTGC TGGACAGGAC GCAGGTGAAC AAGCCCTGCC TGCTGGAGGC TGCCAAGCAC 120
AGCCACACCC CCTTGCATGG ACAGTCCGTC AACAGCCACC CATCAGGTGC TCATCAGAAA 180
CCACCTGAAG TGAATAATGT TGGAGCCAGT CAAGGTTTGC TGACAATGGA AACAAACAG 240
TCCCTGGCAC AAGGCACAGG CTGCTCAGTG TGCTGGGAGG TGAACGGCCC AGGGTTGGAA 300
ATGCTCTTTC CTGGAGTGCT CAGTGTGAT GCTGGCCAGG TGGAGCACAG AAGACAAATG 360
AACTCCGAG ATACTGACTG GGGAACTGAG GAGGGACCAG GAAGTCTAGA TTTCCCGGTG 420
GCTGCCACCC AGGAAGACAC TTTCTTTTG AAAGACATCA AGCACACAAG TACGTTTCCG 480
CAATCAGTTC AGCAGCAGAA TTGCATTAC AGCCCCAGAG AAAAAACCTG TGGGAATGTC 540
AGGGCACCTT GCGGCGCAC AAGGCGAGAG GCCCGGCTTG CCTCAGCAG GCCCTGGCGG 600
CTCAGCCGCA GCGGCGCGC GTCCCCAGT ACACCCATG GCGCCTTCCC GACCTCTGAC 660
CGGAGCTAG ACGCGCCAGG CCGCCCCCCC GGGCTGCGGA GCTCGGCAGC AGCCCTCAC 720
TGCTTCCCG CCGCTCCAGA AGCCAGAAA CTCTTCTTCC TGCTGCCCTT TTATCCAGAT 780
GGCAGCCAC CACCTAAGCA CATCTTGCA AGCTCCAGC ACAAGGCACC TGGGAAGAGA 840
CTGCATCAAG AATCACCAGG TTCAATTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900
TGATATCAAG GGGCTCTGGG TGTGCTGCT GAAGCAGCAT TTCATTACA GTTTTCCAGT 960
GAATGA

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Seq ID NO: 96 Protein sequence

Protein Accession #: XP_090469

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1 11 21 31 41 51
| | | | |
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PPEVKMFGAS QGLLTMETNQ SLAQGTGCSV CNEVNGPLE MSLPGVLSAD AGQVEHRRQM 120
NSADTMDGTE EDPGSLDFAV AAHQEDTFFL KDIKHTSTFR QSVQQNCIY SPREKPGQNV 180
RAPCAPPRRE AFLALSRPWR LSRSPAPSPR TPMAPFTSD RBLDAPGPPP GLRSSAAAPH 240
CLPAAPPAQK LFFLLPLYPD GSPPPKDILQ TLQHKAPGR LHQESPGSFP IGLCNRTAEP 300
CIKALGVAA EAAPHLQFSS E

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Seq ID NO: 97 DNA sequence

Nucleic Acid Accession #: NM_003474.2

Coding sequence: 37..3036

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1 11 21 31 41 51
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TCAAGGCTGG CTTGTGCCAG AACGGCGCGC GCGGACGCA CGCACACACA CGGGGGGAAA 120
CTTTTAA AATGAAAGGC TAGAAGAGCT CAGCGCGCGC GCGGGCCGTG CGCAGGGCT 180
CCGGAGCTGA CTCGCGGAGG CAGGAAATCC CTCGGTCTGC GACGCCCGGC CCGCTCGGC 240
GCCCGGTGG GATGTTGAG CGCTGCGCGC CGGGCCCGAG AGCTGCTGCA CTGAAGGCGG 300

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	GCGAGGATGG	CAGCGCGCCC	GCTGCCCGTG	TCCCCCGCCC	GCGCCCTGCT	GCTCGCCCTG	360
	GCCGGTGCTC	TGCTCGCGCC	CTGCGAGGCC	CGAGGGGTGA	GCTTATGGAA	CGAAGGAAGA	420
	GCTGATGAAG	TTGTGAGTGC	CTCTGTTGCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
5	TTGACTCCA	AGAAATCATCC	AGAAGTGCTG	AATATTGAC	TACAAACGGA	AAGCAAAGAA	540
	CTGATCATAA	ATCTGGAAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
	TATCTGCAAG	ACGGTACTGA	TGTTCCCTC	GCTCGAAATT	ACAGSGTAAT	TCTGGGTCAC	660
	TGTTACTACC	ATGGACATGT	ACGGGGATAT	TCTGATTGAG	CAGTCAGTCT	CAGCACTGT	720
	TCTGGTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGTCTTAGA	ACCAATGAAA	780
10	AGTGCAACCA	ACAGATACAA	ACTCTTCCCA	GCGAAGAGC	TGAAAAGGT	CCGGGGATCA	840
	TGTGGATCAC	ATCAACACAC	ACCAACCTC	GCTGCAAGAA	ATGTGTTTCC	ACCAACCTCT	900
	CAGACATGGG	CAAGAAGGCA	TAAAAGAGAG	ACCTCAAGG	CACTAAGTA	TGTGGAGCTG	960
	GTGATCGTGG	CAGACAACCG	AGAGTTTCAG	AGGCAAGGAA	AAGATCTGGA	AAAAGTTAAG	1020
	CAGCGATTAA	TAGAGATTGC	TAATCACTGT	GACAAGTTT	ACAGACCACT	GAACATTGCG	1080
	ATCGTGTGG	TAGGCGTGGG	AGTGTGGAAT	GACATGGACA	AATGCTCTGT	AAGTCAGGAC	1140
15	CCATTACCCA	GCCTCCATGA	ATTCTGGAC	TGGAGGAAGA	TGAAGCTTCT	ACCTCGCAAA	1200
	TCCCATGACA	ATGCGCAGCT	TGTCAGTGGG	GTTTATTTC	AAGGGACCAC	CATCGGCATG	1260
	GCCCCAATCA	TGAGCATGTG	CACGGCAGAC	CAGTCTGGGG	GAATTGTCT	GGACCATTTCA	1320
	GACAAATCCCC	TTGGTGACGC	CGTGACCCCTG	GCACATGAGC	TGGGCCACAA	TTTCGGGATG	1380
20	AATCATGACA	CTGTGGACAG	GGGCTGTAGC	TGTCAAATGG	CGGTTGAGAA	AGGAGGCTGC	1440
	ATCATGAAAG	CTTCCACCGG	GTACCCATT	CCCATGGTGT	TCAGCAGTTG	CAGCAGGAAG	1500
	GACTTGGAGA	CCAGCCTGGA	GAAGGAATG	GGGGTGTGCC	TGTTTAACT	GCCGGAAGTC	1560
	AGGGAGTCTT	TGCGGGGCCA	GAAGTGTGGG	AACAGATTTG	TGGAAGAAGG	AGAGGAGTGT	1620
	GACTGTGGGG	AGCCAGAGGA	ATGTATGAAT	CGCTGTGCA	ATGCCACCAC	CTGTACCCCTG	1680
25	AAGCGGACG	GTGTGTGGC	ACATGGGCTG	TGCTGTGAAG	ACTGCCAGCT	GAAGCCTGCA	1740
	GGAAACAGGT	GCAGGAGCTC	CAGCAACTCC	TGTGACCTCC	CAGAGTTCTG	CACAGGGGCC	1800
	AGCCCTCACT	GCCCAGCCAA	CGTGTACCTG	CACGATGGGC	ACTCATGTCA	GGATGTGGAC	1860
	GGCTACTGCT	ACAAATGGCAT	CTGCCAGACT	CACGAGCAGC	AGTGTGTGAC	ACTCTGGGGA	1920
	CCAGGTGCTA	AACTGCCCC	TGGGATCTGC	TTTGAGAGAG	TCAATTCTGC	AGGTGATCTC	1980
30	TATGGCAACT	GTGGCAAGGT	CTCGAAGAGT	TCCTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
	AAATGTGGAA	AAATCCAGTG	TCAAGGAGGT	GCCAGCCGGC	CAGTCATTGG	TACCAATGCC	2100
	GTTTCCATAG	AAACAAACAT	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGAGCC	2160
	CAGGTGTACT	TGGGCGATGA	CATGCCGGAC	CCAGGGCTTG	TGCTTGCAAG	CACAAAGTGT	2220
	GCAGATGGAA	AAATCTGCCT	GAATCGTCAA	TGTCAAATA	TTAGTGTCTT	TGGGGTTTCA	2280
35	GAGTGTGCAA	TGCGATGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
	GAGGCCCACT	GGGCACTCC	CTTCTGTGAC	AAGTTTGGCT	TTGGAGGAAG	CACAGACAGC	2400
	GGCCCCATCC	GGCAAGCAGA	TAACCAAGGT	TTAACCATAG	GAATCTGCT	GACCATCTCT	2460
	TGCTCTCTGT	TGCCCCGATT	TGTGGTTTAT	CTCAAAAGGA	AGACCTTGAT	ACGACTGTCT	2520
	TTTCAAAATA	AGAAAGCCAC	CATTGAAAAA	CTAAGGTGTG	TGCGCCCTTC	CCGGCCACCC	2580
40	CGTGGCACT	ACCCTCTCC	GGCTCACCTC	GGCCACCTTG	GAAGAGGCTT	GATGAGGAAG	2640
	CCGCCAGATT	CCTACCCACC	GAAGGACAAT	CCCAGGAGAT	TGCTGCAGTG	TCAGAATGTT	2700
	GACATCAGCA	GACCCCTCAA	CGGCTGAAAT	GTCCCTCAGC	CCCAGTCAAC	TCAGCGAGTG	2760
	CTTCTCTCCC	TCCACCGGGC	CCACCGTGCA	CCTAGCGTCC	CTGCCAGACC	CCTGCCAGCC	2820
	AAGCCTGCAC	TTAGGCGAGC	CCAGGGGACC	TGTAAGCCAA	ACCCCTCTCA	GAAGCCTCTG	2880
45	CCTGCAGCAT	CTCTGGCCAG	AACAACTCGG	CTCACTCATG	CCTTGGCCAG	GACCCACAGG	2940
	CAATGGGAGA	CTGGGCTCCG	CCTGGCACCC	CTCAGACCTG	CTCCACAATA	TCCACACCAA	3000
	GTGCCAGAGT	CCACCCACAC	CGCCTATATT	AAGTGAGAAG	CCGACACCTT	TTTTCAACAG	3060
	TGAAGACAGA	AGTTTGCACT	ATCTTTGAGC	TCCAGTTGGA	GTTTTTTGTA	CCAACTTTTA	3120
	GGATTTTTTT	TAATGTTTAA	AACATCATTA	CTATAAGAAC	TTTGAGCTAC	TGCCGTGAGT	3180
50	GCTGTGCTGT	TCTGTGCTG	TCTGTCTACT	TGCACAGGTA	CTTGTAATTT	ATTAATTTAT	3240
	GCAGAATGTT	GATTACAGTG	CAGTGGCGTG	TAGTAGGCAT	TTTTACCATC	ACTGAGTTTT	3300
	CCATGGCAGG	AAGGCTTGTT	GTGCTTTTAG	TATTTTAGTG	AACCTGAAAT	ATCCTGCTTG	3360
	ATGGGATGTT	GGACAGGATG	TGTTTGCTTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
	CCAATCAACC	CCAGCTGTGC	TTATGTTACC	AGATGCAGCT	CAAGAGATCC	CAAGTAGAAT	3480
55	CTCAGTGTAT	TTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
	TGTGTTTGGC	TTTCAGGGAG	GGCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCACGGG	3600
	ACACCTGGGA	GAATCTGGC	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
	AGGAATCTTA	AGGTGTAGCC	ACACCAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCCTGAG	CTGACCAGCC	GTGAGCATGT	TTGGAAGGGG	TCTGTAGTGT	CACCTAAGGC	3780
60	GGTGCTTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTGCTG	TCCTTTCTAG	AGCACTGCCA	3840
	CCAGTAGGTT	ATTTAGCTTG	GGAAAGGTGG	TGTTTCTGTA	AGAAACCTAC	TGCCCAGGCA	3900
	CTGCAAAACG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCACCACA	AACGTATAAT	3960
	CAATGATCCT	GTAATCAGAC	AGATGAGGAC	TTTCCATGGG	ACCACAACTA	TTTTTCAGATG	4020
	TGAACCATTA	ACCAAGCTCA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTCA	ACTTATTAAAC	4080
65	AAATAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TGTTTCATGGG	4140
	TATAGTTCAT	GTCTGCTATC	ATTATTCTGA	GATATTGGAC	AAAGAACCCT	CTCTATGGGG	4200
	CATCTCTTTT	TTCCAACTTG	GCTGCAGGAA	TCCTTAAAGG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTCTT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAATGTG	ATAAGGAAAT	4320
	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTTGAA	4380
70	CTCTTCACTC	TTCAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGCTTT	TAAAGTGACT	4440
	AATGGCATGA	GAAATACAAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGACTGGT	TTTCAATTA	GAAGACAATT	GACAACAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTTCTTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCTTCCAGA	AAACAAAAC	GCATTTCAC	TTCCCGGTGT	4680
75	TCCCACTGTT	ATCTAGGCAA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAAGGGGAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAAAG	TCTTTAAAT	GTAAGCCAT	GCTGGAAAAT	AATACTGCTG	4860
	AGATACATAC	AGAAATTAAG	TAACTGATTA	CACCTTGGTA	TTGTAATAAA	GCCAAACATA	4920
	TATATACTAT	TAAAAGGTTT	TACAGATTTT	TATGGTGCAT	TACGTGGGCA	TTGTCTTTT	4980
80	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCTC	CCAATTATAA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAATAAA	AA				

Seq ID NO: 98 Protein sequence
Protein Accession #: NP_003465

1 11 21 31 41 51
 5 MAARPLPVSP ARALLLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSR DLNIPVKSFD 60
 SKNHPEVLNI RLQRESKELI INLERNEGLI ASSPTETHYL QDGTDSVSLAR NYTVILGHCI 120
 YHGHVRGYSO SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRKLFPAK KLKSVRSGSG 180
 SHHNTFNLA KNVFPFSSQT WARRHKRETL KATKYVELVI VADNREFQRK GKDLKVKQR 240
 LIEIANHVDK FYRPLNIRIV LVGVEVWDM DKCSVSQDPF TSLHEFLDWR RMKLLPRKSH 300
 DNAQLVSGVY FQGTITGMAP IMSMCTADQS GGIWMDHSDN PLGAAVTLAH BLGHNFGMNH 360
 10 DTLDRGCSQ MAVKGGCICM NASTGYPPFM VFSSCSRKDL ETSLEKGMV CLFNLPEVRE 420
 SPGGQKQNR FVEEGECDC GEPEECMNR CNATTCTLPK DAVCAHLCC EDCQLKPAQT 480
 ACRSSNSCD LPEFCTGASR RCPANVYLHD GHSQDQVDGY CYNIGCQTHE QQCVTLWGP 540
 AKPAPGICFE RVNSAGDPYG NCGKVSXSS AKCEMRDAK GKIQCQGGAS RPIVGTNAVS 600
 IETNIPLOQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRCQ NISVFGVHEC 660
 15 AMQCHGRGVC NNRKNCHEA HWAPPPCDKF GFGGSTDSP IRQADNGLT IGLVTLICL 720
 LAAGFVVYLK RKLIRLLFT NKTITIEKLR CVRPSRPPRG FQPCQAHLG LGKGLMRKPP 780
 DSYPPKDNFR RLLQCNVDI SRPLNGLNVP QPQSTQVLP FLHRAPRAPS VPARPLPAK 840
 ALRQAGCTCK PNFPQKPLPA DPLARTTRLT HALARTPGQW ETGLRLAPLR PAPQYPHQVP 900
 RSTHTAYIK

20 Seq ID NO: 99 DNA sequence
 Nucleic Acid Accession #: NM_003714
 Coding sequence: 135..1043

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 25 GAGGAGGAGG GAAAAGGCGA GCAAAAAGGA AGAGTGGGAG GAGGAGGGA AGCGGCGAAG 60
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 30 TGGCCACCTT TGACCCGGG CGGGGAGCCG AGCCACCAA CCCACCGAG GGTCCCCAAG 240
 ACAGGAGCTC CCAGCAGAAA GGCCGCCCTGT CCTCGAGAA TACAGCGGAG ATCCAGCACT 300
 GTTTGTGCAA CGCTGGCGAT GTGGGTGTG CGGTGTTGA ATGTTTCGAG AACAACTCTT 360
 GTGAGATTCC GGGCTTACAT GGGATTGCA TGACTTTTCT GCACAAAGCT GGAATAATTG 420
 ATGCCAGGG CAAGTCATT ATCAAAGACG CCTTGAAATG TAAGGCCAC GCTCTGCGGC 480
 35 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCATCAG GGAAATGGTG TCCAGTTGC 540
 AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGTGCG CCAGGAGAAC ACCCGGGTGA 600
 TAGTGAGAT GATCAATTTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660
 ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGGTTT 720
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 40 AGAAGCTCC CACGGCGGCC CCGAGCGGCC AGCCCCAGGT GGACAGAAC AAGCTCTCCA 840
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 45 GTCCATTTTC TTATCTATGG ACATTCCAAA ACATTACCA TTAGAGAGGG GGGATGTAC 1140
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 55 TGTCTGGGCT GGGGGGGA CA TGTCCAAGG GAGTGGCCCC TATGAGTTTA TATTTAACC 1740
 ACTGCTTCAA ATCTCGATTT CACTTTTTTT ATTTATCCAG TTATATCTAC ATATCTGTCA 1800
 TCTAAATAAA TGGCTTTTCA ACAGAGCAAC TGGGTCTATTA AAACAGCTC AAAGGGGTT 1860
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 TTAAAGAGTA TCAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCTCTGC 1980
 60 CACTTGGGGG AAACCTTATA CCCAGAGGAA AATACACACC TGGGGAGTAC ATTGACAAA 2040
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 GAAAGAAGAG AATGAAGACT ACTTAGTAAT TCCCATCAGG AAATGCTGAC CTTTATCATA 2220
 65 AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTGGAAG 2280
 TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAAATAAAGG CAGAGAGAGA GAGAGAGAGA 2340
 GGGAGAGGAA GAAAGAGAG AGAGAAAAGA GCCTCGTGCC

Seq ID NO: 100 Protein sequence
 Protein Accession #: NP_003705

70 1 11 21 31 41 51
 MCAERLGQFM TLALVLATFD PARGTDATNP PEGPQDRSSQ QKGRSLQNT ABEIQHCLVNA 60
 GDVGGGVPEC FENNSCEIRG LHGICMTFLH NAGKPDAGK SPIKDALKCK AHALRHRFGC 120
 75 ISKCPAIRE MVSQLRRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVKBAIT HSQVQCEQN WGSLSILSF CTSAIQKPT APPERQPOVD RTKLSRAHEG 240
 EAGHHLPEPS SRETGRGAKG ERGSKSHFNA HARGRVGGLO AQGPSGSSEW EDEQSEYSDI 300
 RR

80 Seq ID NO: 101 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

1 11 21 31 41 51

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AAGCCAGCA GCGCCGGGG GGTGGCTCC GCGCGCTGG CTCCGAGCG CGGCGGCGG 60
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TCTGCCGCG GAGCTCCACC ACCTCCATGC CGAGAGAGG GGGCCACAG CCTGGCATG 180
AGCCCTGCCC AGTAGCCCG CACCTGCCCC TGCCACGCG GAAGCCCCC GGCCTGCCAG 240
CAGCCTCAGG CCCCCCGCT GTGGCGTGCC CGACCCATCT GATGGCTGA GTGCCCGCA 300
CGACAGAAG AGGTTCTGTC TTTCTGGCG GCGCTGGAG AAGACGGACC TCACCTACAG 360
GATCCTTCGG TTCCCATGGC AGTTGGTGCA GAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
CCTAAAGGTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCAG AGGCCCGTGC 480
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TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
CGACTATGAT GAGACTTGGG CTATCGGGGA TGACCGGGC ACAGACCTGC TGCAGGTGGC 660
AGCCCATGAA TTTGGCCAGG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
GTCCGCCCTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGATGACT GCAGGGGCGT 780
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CCCCGACCCC CTCACCGAGC TGGGCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200
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CTCTGAGATC GAGCGTGCTT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGCGCGGCCG 1380
CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGTCTCGT 1440
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GTAGACCACT GGCAGACTG GGGGAACCTG AGTGTCTTG CTGTATCCCT GTTGTGAGT 1860
TCCTTCCAGG GGTGGCCTC GAAGCAAGGG TGCTGGGGCC CCATGGCCTT CAGCCCTGGC 1920
TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCCTGC 1980
ATCTGTCTGC CTCTTGGCTG ACAATCCCTG AAATCTGTT TCCAGAAATC AGGCCAAAA 2040
GTTACAGTC AAATGGGGAG GGGTATTCT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
CAACATACCT CAATCTCTG CCAGGCCGGA TCCTCTGAA GCGCTTTTC CAGCACTGCT 2160
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TTTTAACT GAGGATTGTC ATTAACACA GTTGTTTTCT
  
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Seq ID NO: 102 Protein sequence

Protein Accession #: NP_005931

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1 11 21 31 41 51
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PAPATQEA PR PASSLRPPRC GVPDPDSGLS ARNRQKRFV SGRNWKTDL TYRILRPFQ 120
LVQEQVRQ TM AEARLVHSDV TPLTFTEVHE GRADIMIDFA RYWHGDDL PF DPGGILAH 180
FPFKTHRESD VHPDYDETW IGDDQGTDL QVAHEFGHV LGLQHTTAAK ALMSAFYTF 240
YPLSLSPDDC RGVGHLYGQP WPTVTSRTPA LGPQAGIDTN EIALEPDAP PDACEASFDA 300
VSTRGLLEFP FKAGFVWLRL GGQLQPGYPA LASHWQGLP SPVDAAPEDA QGHINFPQGA 360
QYVYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPBKNI YPFRGRDYWR FHPSTRVDS 420
PVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDP VKVKALEGFP RLVGPDPPGC 480
AEPANTFL
  
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Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM_033151.2

Coding sequence: 351..4499

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GCAGTGGGGA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTTG 1860
65 CCTCAGCTTC CCCAGTAGT GGGACCACAG GTGCCCGCCA CCACACCCAA CTAATTTTGT 1920
TATTTTGTAG AGAGACAGGG TTTCACCATG TTGGCCAGGC TGCTCTCAAA CCCCTGACCT 1980
CAAAATGATG GCTCTGTTCA GCTTCCACA GTGCTGGGAT TACAGGCATG GGCCACCACG 2040
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GCGGCCCTTC CCACTGTGCC ATCTGTTTTC CTCTCCAGGG GTCTTGCAA ATTCTGAGC 2160
70 AGATAAGCAG TTATGTGACC TCACGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
CCAGCCGAGA AGTGACAGAC TGACGTCACT GCACGTTTTC ATCTCTAGGG ACCAGAACCA 2280
AACCACCCCT TTCTACTTCC AAGACTTATT TTCACATGTG GGGAGGTAA TCTAGGAATG 2340
ACTCGTTTAA GCGCTATTTT CATGATTTCT TTGTAGCATT TGGTGTCTGA CGTATTATTG 2400
75 TCCTTTGATT CCAATAATA TGTTCCTTC CCTCAAAAAA AAAAAAATA AAAAAAATA 2460
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Seq ID NO: 108 Protein sequence
Protein Accession #: NP_076927

1 11 21 31 41 51
80 MGENDPFAVE APFSFRLSPG LDDLKISFVA PDADAVAAQI LSLLPLKFFP IIVIGIALI 60
LALAIGLGIH PDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GQGNALQVP 120
TAASWKTMCB DDWKGHYANV ACAQLGFPFY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
VTALHHSVYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQWPN QASLQFGYH 240

LCGGSVITPL WIITAACHVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPCLFNSE NFPDGVKCHT SGWQATEDGG DASPLVLAHA 360
 VPLISNKICN HRDVYGGIIS PSMLCAGYLT GGVDSQGGDS GGPLVQERR LWKLVGATSF 420
 GIGCAEVNKP GVTYTRVTSFL DWIHEQMERD LKT

Seq ID NO: 109 DNA sequence
 Nucleic Acid Accession #: NM_000493.2
 Coding sequence: 97..2139

1 11 21 31 41 51
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 CTGCTAGTAT CCTTGAACCT GGTTCATGGA GTGTTTACG CTGAACGATA CCAATGCCCC 180
 ACAGGCATAA AAGGCCCACT ACCCAACACC AAGACACAGT TCTTCATTCC CTACACCATA 240
 AAGAGTAAAG GTATATCACT AAGAGGAGAG CAAGGTACTC CTGGTCCACC AGGCCCTGCT 300
 GGACCTCGAG GGCACCCAGG TCCTTCTGGA CCACCCAGGAA AACCCAGGCTA CGGAAGTCCT 360
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 GGTGTGCCAG GACTCCGAGG AAAACCCAGG GAGAGAGGAC CATATGGACC AAAAGGAGAT 480
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 GGTGCCAG GACTCCGAGG CCCTCCTGGA GTGGGAAAAA GAGGTGAAAA TGGGGTTCCA 780
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 GCTGGAGCCC CAGGCCAGCC AGGGATTCCA GGAACMAAG GTCTCCCTGG GCTCCAGGA 960
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 GAAAGAGGAG CTGAGTTGG TCCTGGGGGT CCAGGTGCCA AAGGGGAACA AGGCCAGCA 1080
 GGTCTTCTG GGAAGCCAGG TCTGACTGGA CCCCCTGGGA ATATGGGACC CCAAGGACCA 1140
 AAAGGATCC CGSGTAGCCA TGGTCTCCA GGCCCTAAAG GTGAGACAGG GCCAGCTGG 1200
 CCTGCAGGAT ACCCTGGGGC TAAGGGTGA AGGGGTTCCT CTGGTTCAGA TGGAAACCA 1260
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 CCAAAATAT TGAAATTCAT CTGAAATGCA AGGTGCTTTC ATCAATGAAC CTTTCAAAA 2820
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 GACCTATTCT TATTAGTTA ACACAAGTGT GATTAATTG ATTCTTTAA TTCCTTATG 2940
 AATCTTATGT GATATGATT TCTGGATTTA CAGAACATTA GCACATGTAC CTTGTGCTC 3000
 CCATTCAAGT GAAGTTATAA TTTACACTGA GGGTTTCAA ATTGAGTAG AAGTGGAGAT 3060
 ATATTATTTA TTTATGCACT GTACTGTATT TTTATATTGC TGTATAAAC TTTAAGCTG 3120
 TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTTACGAC ACAATAAAT 3180
 AACATCAATA GATTTTAGG CTGAATTAAT TTGAAAGCAG CAATTGCTG TTCTCAACCA 3240
 TCTTTCAAG GCTTTTCATT CGACACAATA AAATAACATC AATAG

Seq ID NO: 110 Protein sequence
 Protein Accession #: NP_000484.2

1 11 21 31 41 51
 MLPQIPFLLL VSLNLVHGVP YAERYQMPTG IKGPLPNTKT QFFIPYTIKS KGIIVRGEQG 60
 TPGPPGPAGP RGHPPGSGPP GKPGYGSFGL QGEPGLPGPP GPSAVKPGPV PGLPGKPGER 120
 GPYQPKGDVG PAGLPGRGP PGPPGIPGPA GISVPGKPGQ QGPTGAPGR GPFGKEGAPG 180
 VPGMNGQKGE MGYGAPGRPG ERGLPGPQGP TGPSGPPGVG KRGENGVPGQ PGIKGDRGFP 240
 GEMGPIGPPG PQGPPGERGP EGIGKPGAAG APGQPIGPT KGLPGAPGIA GPPPPPGPK 300
 PGLPGLKGER GPAGLPGGPG AKGEQGPAGL PGKPLGTGPP GNMPPQGPKG IPGSHGLPGP 360
 KGETGPAGPA GYPGAKGERG SPGSDGKPGY PGKPLDGPFG GNPGLPGPKG DPGVGGPPGL 420
 PGFVGPAGAK GMPGNGEAG PRGAPGIPGT RGPFGPPIF GPPGSKGDPG SPGPPGPAIG 480
 ATKGLNGPTG PPGPPGPRGH SGEPGLPGPP GPPPPGQAV MPBGPPIKAG RPSLSGTLV 540
 SANQGVTPMP VSAFTVLSK AYPATGTPP FDKILYNRQQ HYDPRGTGFT CQIPGIYFYS 600
 YHVHVKGTHV WVGLYKNGTP VMYTYDEYTK GYLDQASGSA IIDLTNDQV WLQLPNAESN 660
 GLYSSEVYHS SPFGFLVAPM

Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_000949
Coding sequence: 285..2153

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ATGTCTCTGT	GCAGGAAGTA	CTCATCGACT	GATGTGGCAG	ACTTTGCTCC	CTGACAAAAAC	180
TAAAGAACTC	TGCTATTATC	GGAGGCGAAC	ACTGAGGATG	CTTTCCACAT	GAACCTTGAA	240
GTGAACCTTC	GATACATTTC	CTGCAGCAAG	AGAAGGCAGC	CAACATGAAG	GAAAAATGTGG	300
CATCTGCAAC	CGTTTTCAGT	CTGCTACTTT	TTCTCAACAC	CTGCCTTCTG	AATGGACAGT	360
TACCTCTCTG	AAAACTGAG	ATCTTTAAAT	GTGCTTCTCC	CAATAAGGAA	ACATTACCTT	420
GCTGGTGGAG	GCTGGGGACA	GATGGAGGAC	TTCTTACCAA	TTATTCACCT	ACTTACCACA	480
GGGAAGGAGA	GACACTCATG	CATGAATGTC	CAGACTACAT	AACCGGTGGC	CCCAACTCCT	540
GCCACTTTGG	CAAGCAGTAC	ACCTCCATGT	GGAGGACATA	CATCATGATG	GTCAATGCCA	600
CTAACCAGAT	GGGAAGCAGT	TTCTCGSATG	AACCTTATGT	GGACGTGACT	TACATAGTTC	660
AGCCAGACCC	TCCTTTGGAG	CTGGCTGTGG	AAGTAAACAA	GCCAGAAGAC	AGAAAAACCTT	720
ACCTGTGGAT	TAAATGGTCT	CCACCTACCC	TGATTGACCT	AAAAACTGGT	TGGTTCAGCG	780
TCCTGTATGA	AATTCGATTA	AAACCCGAGA	AAGCAGCTGA	GTGGGAGATC	CATTTTGCTG	840
GGCAGCAAAC	AGAGTTTAA	ATTCTCAGCC	TACATCCAGG	ACAGAAATAC	CTTGTCCAGG	900
TTGCTGCAA	ACCAGACCAT	GGATACTGGA	GTGCATGGAG	TCCAGCGACC	TTCAATCAGA	960
TACCTAGTGA	CTTCACCATG	AATGATACAA	CCGTGTGGAT	CTCTGTGGCT	GTCTTTCTCT	1020
CTGTCTCTCT	TTTGATTATT	GTCTGGGCAG	TGGCTTTGAA	GGGCTATAGC	ATGGTGACCT	1080
GCATCTTTCC	TGCTATCTCT	GGGCCAAAAA	TAAAAGGATT	TGATGCTCAT	CTGTGGAGAA	1140
AGGGCAGTCT	TGAAGAACTA	CTGAGTGCCT	TGGGATGCCA	AGACTTTCCT	CCCACTTCTG	1200
ACTATGAGGA	CTTGCTGGTG	GAGTATTTAG	AAGTAGATGA	TAGTGAGGAC	CAGCATCTAA	1260
TGTCAGTCCA	TTCAAAAGAA	CACCCAAAGT	AAGGTATGAA	ACCCACATAC	CTGGATCCTG	1320
ACACTGACTC	AGGCCGGGGG	AGCTGTGACA	GCCCTTCCCT	TTTGTCTGAA	AAGTGTGAGG	1380
AACCCCAAGC	CAATCCCTCC	ACATTCTATG	ATCCTGAGGT	CATTGAGAAG	CCAGAGAATC	1440
CTGAACAAC	CCACACCTGG	GACCCCCAGT	GCATAAGCAT	GGAGGCGAAA	ATCCCTTAAT	1500
TTCATGTCTG	TGGATCCAAA	TGTTCAACAT	GGCCCTTACC	ACAGCCGAGC	CAGCACAAAC	1560
CCAGATCTCT	TTACCACAAT	ATTACTGATG	TGTTGTAGCT	GGCTGTGGGC	CCTGCAGGTG	1620
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AGTCTAGAGA	AGAGGGAAG	GCAACCCAGC	AGAGGGAGGT	AGAAAGCTTC	CATTCTGAGA	1740
CTGACCAGGA	TAGCCCTGG	CTGCTGCCCC	AGGAGAAAC	CCCCTTTGGC	TCCGCTAAAC	1800
CCTTGGATTA	TGTGGAGATT	CACAAGGTCA	ACAAAGATGG	TGCATTATCA	TTGCTACCAA	1860
AACAGAGAGA	GAACAGCGGC	AAGCCCAAGA	AGCCCGGAC	TCCTGAGAAC	AATAAGGAGT	1920
ATGCCAAGGT	GTCCGGGGTC	ATGGATAACA	ACATCCTGGT	GTGGTGCCCA	GATCCACATG	1980
CTAAAAAGCT	GGCTTGCTTT	GAAGAATCAG	CCAAAGAGGC	CCCACCATCA	CTTGAACAGA	2040
ATCAAGCTGA	GAAAGCCCTG	GCCAACTTCA	CTGCAACATC	AAGCAAGTGC	AGGCTCCAGC	2100
TGGGTGGTTT	GGATTACCTG	GATCCCGCAT	GTTTACACAC	CTCCCTTTCAC	TGATAGCTTG	2160
ACTAATGGAA	TGATTGGTTA	AAATGTGATT	TTTCTTCAGG	TAACTACTAC	GAGTACGTGA	2220
AATGCTCAAG	AATGTAGTCA	GACTGACACT	ACTAAAGCTC	CCAGCTCCTT	TCATGCTCCA	2280
TTTTTAACCA	CTTGCCCTCT	TCTCCAGCAG	CTGATTCCAG	AACAAATCAT	TATGTTTCCT	2340
AACGTGTGAT	TGTAGATTTA	CTTTTGTCTG	TTAGTTATAA	AACATATGTT	TCAATGAAAT	2400
AAAAGCACAC	TGCTTAGTAT	TCTTGAGGGA	CAATGCCAAT	AGGTATATCC	TCTGGAAAAG	2460
GCCTTTCATG	TTTGGCATGG	GACAGACGGA	AATGAAATTG	TCAAAATTGT	TTACCATAGA	2520
AAGATGACAA	AAGAAAATTT	TCCACATAGG	AAAAATGCCAT	GAAAAATGCT	TTTGAAAAAC	2580
AACGTGACAA	CTTTACACTC	CCTGTCCAT	TTTATTAGGA	TTACCCAAAT	ATAACCATTT	2640
AAAGAAAGAA	TGCATTCCAG	AACAAATGTT	TTACATAAGT	TCCTATACCT	TACTGACACA	2700
TTGCTGATAT	GCAAGTAAGA	AAT				

Seq ID NO: 112 Protein sequence
Protein Accession #: NP_000940

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SLTYHREGET	LMHECPDYIT	GGPNSCHFGK	QYTSMWRTYI	MMVNATNQMG	SSFSDELYVD	120
VYTIQVDPDP	LELAVEVKQP	EDRKPYLNIK	WSPFTLIDLK	TGWFTLLYEI	RLKPEKAAEW	180
BIHPAGQQT	FKILSLHPGQ	KYLIVQVRCKP	DHGYNSAWSP	ATFIQIPSDF	TMDTITVWIS	240
VAVLSAVICL	IIVVAVALKG	YSMTVCIFPP	VPGPKIKGFD	AHLLEKKGSE	ELLSALGQD	300
FPPTSDYEDL	LVEYLEVDD	EDQHLMSVHS	KEHPSQGMKP	TYLDPDTS	RGSCDSPSL	360
SEKCEPQAN	PSTFYDPEVI	EKPENPETTH	TWDPQCISME	GKIPYFHAGG	SKCSTWPLPQ	420
PSQHNPRSSY	HNITDVCELA	VGPAGAPATL	LNEAGKDALK	SSQTIKSREE	GKATQOREVE	480
SFHSSTDDQT	PNLLPQEKTP	FGSAKPLDYV	ELHKVNKQGA	LSLLPKQREN	SGKPKKPGTP	540
ENNKEYAKVS	GVMDDNNILVL	VDPHAKNVA	CFEESAKEAP	PSLEQNQAEK	ALANFTATSS	600
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Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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TGGCTGGACG	CGCAGGGCGT	CTGCGCGATC	GGCTTCCAGT	GTCCCGAGCG	CTTGCAGCGC	180
GGCGAGCGCA	CCATCTGCTG	CGCGAGCTGC	CGTGTGCGCT	ACTGCTGCTC	CAGCGCGGAG	240
GCGCGCTTGG	ACCAGGGGCG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCCTGGC	300
CGGGCGGACA	AAGACGGCCC	CGACGGCTCG	GCAGTGCCCA	TCTACGTGCC	GTTCTCTCAT	360
GTTGGCTCCG	TGTTTGTGCG	CTTTATCATC	TTGGGGTCCD	TGGTGGCAGC	CTGTTGCTGC	420

5
 AGATGTCTCC GGCCTAAGCA GGATCCCCAG CAGAGCCGAG CCCCAGGGGG TAACCGCTTG 480
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 CCCACGAAT TCTCTGTGCT GAACTGTCTG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
 CAGTATCTGC ATCCCCCATA CGTGGGGTAC ACGGTGCAGC ACGACTCTGT GCCCATGACA 780
 GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CCTGGCTACA GGCAGATTCA GTCCCCCTTC 840
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 Seq ID NO: 114 Protein sequence
 Protein Accession #: XP_062811

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 VGSVFVAFII LGSIVAACCC RCLRPKQDPQ QSRAPGGRNL METIPMIPSA STSRGSSSRQ 180
 SSTAASSSSS ANSGARAPPT RSQTNCCLPB GTMNNVYVM PTNPSVLNCQ QATQIVPHQG 240
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 TTTGATAAAC TTTATAACAC TTTAAAAAAA CAGTTTCCTG CTATGGCCCT GAAGATTCTT 240
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 AGAGCATTC TCAAAATGGA CAGTCCAAAA CACCAGTCAG ATCCATCTGA AGATGAGGAT 420
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 Seq ID NO: 116 Protein sequence
 Protein Accession #: NP_037389

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 1 11 21 31 41 51
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 YAVKVLQKKI VLNRKEQKHI MAERNVLLKN VKHPLVLGLH YSPQTTEKLY FVLDPVNGGE 180
 LFFHLQERS PFEHRARFYA AEIASALGYL HSIKIVYRDL KPNILLDSV GHVVLTDPL 240
 CKEGIAISDT TTTFCGTPEY LAPEVIRKQP YDNTVDWVCL GAVLYEMLY LPPFYCRDVA 300
 EMYDNLHKE LSLRPGVSLT AWSILEELLE KDRQNLGAK EDFLEIQNHP PFESLSWADL 360
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 Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: NM_004004.1

Coding sequence: 1..681

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AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTGTCTGCA ACACCTCGCA GCCAGGCTGC 180
AAGAACGTGT GCTACGATCA CTACTTCCCC ATCTCCACA TCGGCTATG GGCCCTGCAG 240
CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
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ATCAAAACCC AGAAGGTCGG CATCGAAGGC TCCTGTGGT GGACCTACAC AAGCAGCATC 420
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TTCTCCATCG AGCGCTGGT GAAGTCCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
15 | | | | |
TTTGTGTCCC GGCCCAAGGA GAAGACTGTC TTCACAGTGT TCATGATTGC AGTGTCTGGA 600
ATTTGCATCC TGCTGAATGT CACTGAATGT TGTATTTCG TAATTAGATA TTGTTCTGGG 660
AAGTCAAAA AGCCAGTTTA A

Seq ID NO: 118 Protein sequence
Protein Accession #: NP_003995.1

20 | | | | |
MDWNTLQTL GGVNKHSTSI GKWLTVLFI FRIMILVVAA KEVMGDEQAD PNCNTLQPGC 60
KNVCYDHYFP ISHRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEFKDIEE 120
25 | | | | |
IKTKVRIEG SLWMTYTTSSI FPRVIFEAFF MYVYVMDG PSMQRLVKCN AMPCPNTVDC 180
FVSRPTEKTV FTFVMIASVG ICILLNVTEL CYLLIRYCSG KSKRPV

Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

1 11 21 31 41 51
35 | | | | |
ATGCCAAATA CTTACGGAAC AACCAGGATT GAAATTGGC TTCTCCAAGA GCCGCCCGGG 60
CACCGAGCGC TGGTCGCGCG TCTCCTTCOG GTGAGTCCCA GCCCCGAGTT GGCTCTGGOG 120
CCCGGTATCC CGCCAGTGCC GGCTGCGGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
CAGATGCATG GTGAGAAGGT AGATCTCTCG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
40 | | | | |
GTTGGGAAGC CTCCTTTTGA GGCAAAAGAA GTCCATGTAA GCAAGAAAC CATCGGAAG 300
ATTTACAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCCTGTA 360
GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
GTCTGTGAGC GTCTGGACAT CAGCCCCGAG AGGGTCAGAG TGGGAGCATT CCAGTTCAGT 480
TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCAACAGGA AGTGAAGGCA 540
45 | | | | |
AGAAATCAAGA GGAATGGTTT CAAAGGAGGG CGCAGGAGA CGGAACCTGC TCTGAAATAC 600
CTTCTGCACA GAGGGTTGCC TGGAGGAGGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACTGCCAT CCAAGCAGCT GAAGGAAAGG 720
GGTGTCACTG TGTTTGCTGT GGGGTCAGG TTTCCAGGT GGGAGGAGCT GCATGCATG 780
GCCAGCGAGC CTAGAGGGCA GCACGTGCTG TTGGCTGAGC AGGTGGAGGA TGCCACCAAC 840
GGCTCTCTCA GCACCTCTAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
50 | | | | |
CCCGAGCTTG TCTTCATGGA GCGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
CAGCCCTGCG AGAATGGAGG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAATGCTTC 1020
TGCCCGCTCG CCTTTGAGG GAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
GTGACCTCC TCTTCTGCT GGACAGCTCT GGGGGCACA CTCTGAGCG CTTCCTGCGG 1140
55 | | | | |
GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG GCGGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
GTGGGTGTGG CCACATACAG CAGGAGAGCTG CTGGTGGCGG TGCCCTGTGGG GGAATACCG 1260
GATGTGTGAG ACCTGTGCTG GAGCCTCGAT GGCATTCCCT TCGGTGGTGG CCCCACCTG 1320
ACGGGCACTG CCTTGGCGCA GCGGCGAGG CGTGGCTTGG GAGGCGCCAC CAGGACAGGC 1380
CAGGACCGGC CAGGTAGAGT GGTGGTTTGG CTCACTGAGT CACACTCGGA GGATGAGGTT 1440
60 | | | | |
GCGGGCCCGA CGCGTCAAGC AAGGGCGGGA GAGCTGCTCC TGCTGGGTGT AGGCAGTGAG 1500
GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGGCCAA AGCATGTGAT GGTCTACTCG 1560
GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGGCAG 1620
CGGCCAGGGT GCGGACACA AGCCCTGGAC CTGCTCTTCA TGTGACAC CTCTGCCTCA 1680
GTAGGGCCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CTTCAGTTT 1740
65 | | | | |
GAGGTGAACC CTGACGTGAC ACAGGTCCGC CTGGTGGTGT ATGGCAGCCA GGTGCAGACT 1800
GCCTTCGGGC TGGACACCAA ACCCACCCTG GCTGCGATGC TGGGGCCAT TAGCCAGGCC 1860
CCCTACCTAG GTGGGGTGGG CTCAGCCGGC ACGGCCCTGC TGCACATCTA TGACAAAGTG 1920
ATGACCGTCC AGAGGGGTGC CCGGCTGGT GTCCCAAG CTGTGTGTGT GCTCAGAGC 1980
GGGAGAGGGC CAGAGGATGC AGCGGTTCTT GCCCAGAAGC TGAGGAACAA TGGCATCTCT 2040
70 | | | | |
GTCTTGTGTC TGGGGTGGG GCCTGTCTTA AGTGAGGGTC TGGGAGGCT TGCAGGTCCC 2100
CGGGATTCCC TGATCCAGCT GGCAGCTTAC GCGACCTGC GGTACCAACA GGCAGTGTCT 2160
ATTGAGTGGC TGTGTGAGA AGCCAAGCAG CCAATCAACC TCTGCAAAAC CAGCCGTGTC 2220
ATGAATGAGG GCAGTGGCT CTGCGAAT GGGAGCTACC GCTGCAAGTG TCGGATGTC 2280
TGGGAGGGCC CCCACTGCGA GAACCGTGA TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
75 | | | | |
GGATGGATTG TTGAGACGCC CCGAGGCAC ATGGCTCCCG TGCAGGAGG CAGCAGCCGT 2400
ACCCCTCCCA GCACTACAG AGAAGCCCTG GGCAGTAAA TGTGCTTAC CTCTGGAAT 2460
GTCTGTGCC CAGGCTCTTA G

Seq ID NO: 120 Protein sequence
Protein Accession #: XP_061091.1

80 | | | | |
MPNTSGTTRI EIWLLQEPPE HRALVAALLP VSPSPALALA PGYPPVPAAD DRFTLPMIGG 60
QMHGEKVDLW SLGLVCEYFL VGRPPPEANE VHSVETIGK ISAASKMMWC SAAVDIMPLL 120

DGSNSVGKGS PERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEPPLD SFSTQQEVKA 180
 RIKRMVFKGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTTFVAVGR PPRNEELHAL ASEPRGQHLV LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVPMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAPGGGAN CALKLSLECR 360
 5 VDLLPLDSS AGTTLDGFLR AKVPVKRFVR AVLSEDSRAR VGVATYSREL LVAVPVGEBYQ 420
 DVPDLVMSLD GIPPRGGPTL TGSALRQAAE RGFSGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEIEIT GSPKHMVMS DPQDLFNQIP ELQGLKCSRQ 540
 RFGCRTQALD LVFMLDTSAS VGPENFAQMQ SPVRSALQF EVNPDVTQVQ LVVYGSQVQT 600
 10 APGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
 GRGAEDAAVP AQKLRRNNGIS VLVVGVGPVL SEGLRRLAGP RDSLIHVAAY ADLRYHQDVL 720
 IEWLCEGAQK PVNLCKPSPC MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVSQ 780
 GWILETFLRH MAPVQEGSSR TTPSNYREGL GTEMVPTFWN VCAPGP

Seq ID NO: 121 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2424

1 11 21 31 41 51
 20 ATGCCCCCTT TCTCTGTGCT GGAGGCCGTC TGTGTTTCC TGTITTTCCAG AGTCCCCCA 60
 TCTCTCCTC TCACGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
 AGCAAAATGA TGTGTGTCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180
 AGCGTCGGGA AAGGAGCTT TGAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
 25 CTGGACATCA GCCCGAGAG GGTGAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT 300
 CTGGAATTC CTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
 ATGTTTTC AAGGAGGGCG CACGAGACG GAACCTTGCT TGAATACCT TCTGCACAGA 420
 GGGTGTGCTG GAGGCAGAAA TGCTTCTGTG CCCCAGATCC TCATCATGCT CACTGATGGG 480
 AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
 TTTGCTGTGG GGGTCAGGTT TCCCAGGTGG GAGGAGCTGC ATGCACTGGC CAGCGAGCCT 600
 30 AGAGGGCAGC AGTGTCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT GAGGGCTCAC 720
 CCCTGTGAGC ACAGGACGCT GGAGATGGTC CGGAGTTGCT CTGGCAATGC CCCATGCTGG 780
 AGAGGATGCG GGGGAGCCCT TGGGGTGTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
 AGAGTGTGTC TAACCCAGCT TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC 900
 35 TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAAGTGC 960
 CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CTTGGAATGC 1020
 AGGGTCGACC TCCTCTTCCT GCTGCACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCTG 1080
 CGGGCCAAAG TCTTCGTGAA CGGCTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
 40 CGAGTGGGTG TGGCCACATA CAGCAGGAG CTGCTGTGTG CGGTGCCTGT GGGGGAGTAC 1200
 CAGGATGTGC CTGACCTGCT CTGGAGCCTC GATGGCATTG CCTTCGGTGG TGGCCCCACC 1260
 CTGACGGGCA GTCCCTTGGG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA 1320
 GGCCAGGACC GGCACGTAAG AGTGGTGGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
 GTTGGGGGCC CAGCGGTGCA CGCAAGGGCG CGAGAGCTGC TCCTGCTGGG TGTAGGCAAT 1440
 GAGGCGGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
 45 TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
 CAGCGCCGAC GTGCGCGGAC ACAAGCCCTG GACCTGTGCT TCATGTTGGA CACCTCTGCC 1620
 TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
 TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGTTGG TGTATGGCAG CCAGGTGACG 1740
 50 ACTGCTCTGG TGGCTGACAC CAAACCCACC CGGCTGCGGA TGCTGCGGGC CATTAGCCAG 1800
 GCCCCTCACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
 GTGATGACG TCCAGAGGGG TGCCCGGCTT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA 1920
 GCGCGGAGAG GCGCAGAGGA TGCACCGGTT CCTGCCCAGA AGCTGAGGAA CAATGGCATC 1980
 TCTGTCTTGG TCGTGGGGCT GGGGCTGTCT CTAAGTAGAG GTCTGCGGAG GCTTGCAGGT 2040
 CCGCGGGATT CCCTGATCCA CTTGGCAGCT TACGCGGACC TGCGGTACCA CCAGGACGTT 2100
 55 CTGATGAGT GGTGTGTGG AGAAGCCAA GAGCCAGTCA ACCTCTGCAA ACCAGGCCGG 2160
 TGCAATGAAT AGGCGAGCTG CTTCTGTCAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
 GGTGAGGAG GCCCCACTG CAGAAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280
 CAGGGATGGA TTCTGTAGAC GCCCTGAGG CACATGGCTC CCGTGACGGA GGGCAGCAGC 2340
 60 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGTTGCC TACCTTCTGG 2400
 AATGTCGTG CCCCAGGTCC TTAG

Seq ID NO: 122 Protein sequence
 Protein Accession #: Eos sequence

65 1 11 21 31 41 51
 MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
 SVGKGSFERS KHPAITVCDG LDISPERVRV GAFQPSSTPH LBPPLDSFST QSEVKARIKR 120
 70 MVFKGRTET ELALKYLLHR GLFGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
 FAVGVPRFRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMW REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCGPGCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLPLDLS SAGTTLDGFL 360
 RAKVPVKRFV RAVLSERSRA RVGVATYSRE LLVAVPVGEY QDVPDLVMSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT QDRPRRVVVL LTESHSEDE VAGPARHARA RELLLGVGS 480
 75 EAVRAELEIEI TGSPKHMVMS SDQDLFNQI PELQGLKCSR QRPGRCTQAL DLVFMMLDTS 540
 SVGPENFAQM QSFVRSALQ FEVNPDTQV GLVVYGSQVQ TARGLODKPT RAAMLRAISQ 600
 APYLGGVGS A TALLHIYDK VMTVQRGARV GVPKAVVVL GORGAEDAAV PAQKLRRNNGI 660
 SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCEGAQ PVNLCKPSP 720
 80 MNEGSCVLQ NGSYRCKCRD WEGPHCENR EWSSCSVCVS QGWILETFLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAPGP

Seq ID NO: 123 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 89..2356

	1	11	21	31	41	51	
5	1	11	21	31	41	51	60
	60	120	180	240	300	360	420
10	420	480	540	600	660	720	780
15	780	840	900	960	1020	1080	1140
20	1140	1200	1260	1320	1380	1440	1500
25	1500	1560	1620	1680	1740	1800	1860
30	1860	1920	1980	2040	2100	2160	2220
35	2220	2280	2340	2400	2460	2520	2580
40	2580	2640	2700	2760			

Seq ID NO: 124 Protein sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
55	1	11	21	31	41	51	60
	60	120	180	240	300	360	420
60	420	480	540	600	660	720	780
65	780	840	900	960	1020	1080	1140
70	1140	1200	1260	1320	1380	1440	1500

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

	1	11	21	31	41	51	
75	1	11	21	31	41	51	60
	60	120	180	240	300	360	420
80	420	480	540	600	660	720	780

5	AATTTTTTGG	AGAAAAGGGC	TTTAAATATA	AAGCAAAACA	AAGCAATGCT	TGCAAACTC	540
	ATGTCGAAT	TAGAAAGCTT	CCCTGGCTCG	TTCCGTGGAA	GACATCCCTC	CCCAGGCTCC	600
	GACTCACAAT	CAAGGAGACC	GCGAAGGCGT	ACATTCCTCG	GTGTTGCTTC	CAGGAGAAAC	660
	CCTGAACGGA	GAGCTCGTCC	TCTTACCAGG	TCAAGGTCCC	GGATCCTCGG	GTCCCTTGAC	720
	GCTCTACCCA	TGGAGGAGGA	GGAGGAAGAG	GATAAGTACA	TGTTGGTGGAG	AAAGAGGAAG	780
	ACCGTGGATG	GCTACATGAA	TGAAGATGAC	CTGCCAGGAA	GCCGTGCTC	CAGATCATCC	840
	GTGACCTTC	CGCATATAAT	TGCCCCAGTG	GAAGAAATTA	CAGAGGAGGA	GTGGAGAAAC	900
	GTCTGCAGCA	ATTCTCGAGA	GAAGATATAT	AACCGTTCAC	TGGGCTCTAC	TTGTCACTAA	960
10	TGCCGTGAGA	AGACTATTGA	TACCAAAACA	AATGTCAGAA	ACCCAGACTG	CTGGGGCGTT	1020
	CGAGGCCAGT	TCTGTGGCCC	CTGCCCTCGA	AACCGTTATG	GTGAAGAGGT	CAGGGATGCT	1080
	CTGCTGGATC	CGAACTGGCA	TTGCCCGCCT	TGTCGAGGAA	TCTGCAACTG	CAGTTTCTGC	1140
	CGGCAGCGAG	ATGGACGGTG	TGCGACTGGG	GTCCCTTGTT	ATTTAGCCAA	ATATCATGGC	1200
	TTTGGGAATG	TGCAATGCCTA	CTTGAAGAGC	CTGAAACAGG	AATTTGAAAT	GCAAGCATAA	1260
15	TATCTGGAAG	ATTGTCTGCC	TGCCCTCTAC	TTCTCAAATC	TTTCTTGTA	AAGTTTCCAA	1320
	TTTTTTCACT	GAAACCTGAG	TTAAAAATCT	TGATGATCAG	CCTGTTTCAT	AAGAACTCC	1380
	AATCAAGTTA	ATCTTAGCAG	ACATGTGTTT	CTGGAGCATC	ACAGAAGSTA	TATTGCTAGT	1440
	TACACTTTGC	CCTCCTGCAG	TTTCTTCTCT	GCTCCCAACC	CCCATCTCAT	AGCATCCCCC	1500
	TCTATTTCGA	ATGCTCCTCT	CCAACCGCTT	AGTTTCTGAA	TTTCTTTTAA	ATTACAGTTT	1560
20	TATGAAAGCA	TATTTTATTT	ACTTGGTGTT	GAAATAGCCC	TCATAAAACC	TAAGCACTTG	1620
	GAAACACAAT	AATAGTATTA	ACTAACTAGA	TCTATTGAAT	TTGAGAGAG	AGCCTTCTAA	1680
	CTTGTTTTACA	CAAAAACGAG	TATGATTTAG	CACCTCATCT	AGTTGAAAT	TTTAATAGAA	1740
	TCAAGGCACA	AAAGTCTTAA	AACCATGTGG	AAAAATTAGG	TAATTATGTC	AGATTGATGT	1800
	CTCTCAATCC	CATGTATTGC	GCTTATGTTA	CAAGTTGTTG	TCACAGTTGA	GACTTAATTT	1860
25	CTCCTAATTT	CTTCTGCCCG	AAGGGTAAGT	GGTGCGTCCA	GCTTACACGA	TCATAATTCA	1920
	AAGGTTGGTG	GGCAATGTAA	TACTTAATTA	AAATAATGAT	GGAAGAGCTA	TCTGGAGATT	1980
	ATGAGTAAGC	TGATTTGAAT	TTTCAGTATA	AAACTTTAGT	ATAATTGTAG	TTTGCAAGT	2040
	TTATTTCACT	TCACATGTAA	GGTATTGCAA	ATAAATCTT	GGACAATTTT	GTATGGAAC	2100
	TTGATATTAA	AAACTAGTCT	GTGGTTCTTT	GCAGTTTCTT	GTAAATTTAT	AAACCAAGCA	2160
30	CAAGGTTCAA	GTTTAGATTT	TAAGCACTTT	TATAACAATG	ATAAGTGCTT	TTTTGGAGAT	2220
	GTAACTTTTA	GCAGTTTGT	AACCTGACAT	CTCTGCCAGT	CTAGTTTCTG	GGCAGGTTTC	2280
	CTGTGTCAGT	ATTCCCCCTC	CTCTTGTCAT	TAATCAAGGT	ATTGGTAGA	GGTGAATCT	2340
	AAGTGTTTGT	ATGTCCAAAT	TACTTGACATA	TGTAAACCAT	TGCTGTGCCA	TTCAATGTTT	2400
35	GATGCATAAT	TGGACCTTGA	ATCGATAAGT	GTAATACAG	CTTTTGATCT	GTAATGCTTT	2460
	TATACAAAG	TTTATTTTAA	TAATAAAATG	TTTGTCTTAA	AAAAAATAA		

Seq ID NO: 126 Protein sequence
Protein Accession #: NP_114148.1

40	1	11	21	31	41	51	
	MDARRVPQKD	LRVKLNKKF	RYVKLISMET	SSSSDDSCDS	PASDNFANTR	LQSVREGCRT	60
	RSQCRHSGLP	RVAMKPPARS	TRGATNKKAE	SRQPSSENSVT	DSNSDSEDES	GMNPLEKRAL	120
	NIQKNKAMLA	KLMSELESFP	GSFGRHPLP	GSDSQSRRPR	RRTFPGVASR	RNPERRARPL	180
45	TRSRSRILGS	LDALPMEEEE	EEDKYMLVRK	RKTVDGYMWE	DDLPRSRRSR	SSVTLPHIIR	240
	FVEEITEEEL	ENVCNSNREK	IYNRSIGSTC	HQCRQKIDT	KTNCRNPDOW	GVRGQFCGPC	300
	LRNRYGEEVR	DALLDPNWHC	PPCRGICNCS	FCRQRDGRCA	TGVLVYLAKY	HGFNGVHAYL	360
	KSLKQEFEMQ	A					

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: AF305616.1
Coding sequence: 1..863

55	1	11	21	31	41	51	
	ATGCACCGCT	TGATGGGGGT	CAACAGCACC	GCCGCCGCG	CCGCCGGGCA	GCCCAATGTC	60
	TCCTGCACGT	GCAACTGCAG	ACGCTCTTTG	TTCCAGAGCA	TGGAGATCAC	GGAGCTGGAG	120
	TTTGTTCAGA	TCATCATCAT	CGTGGTGGTG	ATGATGGTGA	TGGTGGTGGT	GATCACTGTC	180
	CTGCTGAGCC	ACTACAAGCT	GCTGCACCG	TCCCTCATCA	GCCGCCACAG	CCAGGGGGCG	240
60	AGGAGAGAAG	ATGCCCTGTC	CTCAGAAGGA	TGCCTGTGGC	CCTCGGAGAG	CACAGTGTCA	300
	GGCAACGGAA	TCCAGAGGCC	GCAGGTCTAC	GCCCCGCCCT	GGCCCAACGA	CCGCTGCGCC	360
	GTGCCGCCCT	TGCCCCAGCG	GGAGCGCTTC	CACCGCTTCC	AGCCCACTTA	TCCGTACCTG	420
	CAGCAGGAGA	TGCACCTGCC	ACCCACCATC	TGCTGTCTAG	ACGGGAGGGA	GCCCCACCCC	480
	TACCAGGGCC	CCTGCACCTC	CCAGCTTCGG	GACCCCGAGC	AGCAGCTGGA	ACTGAACCGG	540
65	GAGTCCGTGC	GCGCACCCCC	AAACAGAAC	ATCTTCGACA	GTGACCTGAT	GGATAGTGCC	600
	AGGCTGGGGG	GCCCCGTGCC	CCCCAGCAGT	AACTCGGGCA	TCAGCGCCAC	GTGCTACGGC	660
	AGCGGGGGG	GCATGGAGGG	GCGCGGCCCC	ACCTACAGCG	AGGTATCTCG	CCACTACCCG	720
	GGGTCTCTCT	TCCAGCACA	GCAGAGCAGT	GGCGCGCCCT	CCTGTCTGGA	GGGAGCCCGG	780
70	CTCCACCACA	CACACATCGC	GCCCCTAGAG	AGCGCAGCCA	TCTGGAGCAA	AGAGAAGGAT	840
	AAACAGAAAG	GACACCTCT	CTAG				

Seq ID NO: 128 Protein sequence
Protein Accession #: AAL09357.1

75	1	11	21	31	41	51	
	MHRLMGVNST	AAAAAGQPNV	SCTCNCKRSL	FQSMETILE	FVQIIIVVV	MMVMVVVITC	60
	LLSHYKLSAR	SFISRHSGQR	RREDALSSSE	CLWPSESTVS	GNIGIREPOVY	APPRPTDRLA	120
	VPPPAQRERF	HRQPTYPYFL	QHEIDLPPPT	SLSDGEBPPP	YQGPCTLQLR	DPEQQLNLNR	180
80	ESVRAPFNRT	IFOSDLMDSA	RLGGPCPPSS	NSGISATCYG	SGGRMEGPPP	TYSEVIGHYP	240
	GSSPQHQSS	GPPSLLEGTR	LHETHIAPLE	SAAIWSKEKD	RQKGHPL		

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_004952.1

Coding sequence: 1..718

5
10
15

1	11	21	31	41	51	
ATGGCGGCGG	CTCGCTGCT	GCTGCTGCTG	CTGCTGCTGC	CGTGCGCGCT	GCTGCGCGTG	60
CTGGCCCAAG	GGCCCGGAGG	GGCGCTGGGA	AACCGGCATG	CGGTGTACTG	GAACAGCTCC	120
AACCAGCACC	TGCGGCGAGA	GGGCTACACC	GTGCAGGTGA	ACGTGAACGA	CTATCTGGAT	180
ATTTACTGCC	CGCACTACAA	CAGCTCGGGG	GTGGGCCCCG	GGGCGGGAAC	GGGGCCCGGA	240
GGCGGGGCGA	AGCAGTACGT	GCTGTACATG	GTGAGCCGCA	ACGGCTACCG	CACCTGCAAC	300
GCCAGCCAGG	GCTTCAAGCG	CTGGGAGTGC	AACCGGCGCG	ACGCCCCGCA	CAGCCCCATC	360
AAGTTCTCGG	AGAAGTTCCA	CGGCTACAGC	GCCTTCTCTC	TGGGCTACGA	GTTCACGCGC	420
GGCCACGAGT	ACTACTACAT	CTCCACGCCC	ACTCACAACC	TGCACTGGAA	GTGTCTGAGG	480
ATGAAGGTGT	TGCTCTGCTG	CGCCTCCACA	TCGCACTCCG	GGGAGAAGCC	GGTCCCCACT	540
CTCCCCAGT	TCACCATGGG	CCCCAATGTG	AAGATCAACG	TGCTGGAAGA	CTTTGAGGGA	600
GAGAACCCTC	AGSTGCCCAA	GCTTGAGAAG	AGCATCAGCG	GGACCAGCCC	CAACCGGGA	660
CACCTGCCCC	TGGCCGTGGG	CATCGCCTTC	TTCTCATGA	CGTTCTTGGC	CTCTCTAG	

Seq ID NO: 130 Protein sequence
Protein Accession #: NP_004943.1

20
25

1	11	21	31	41	51	
MAAAPLLLLL	LLVPVPLPL	LAQGGPGALG	NRHAVYWNSS	NQHLRREGYT	VQVNVNDYLD	60
IYCPHYNSSG	VGPGAGPGPG	GGAEQYVLYM	VSRNGYRTCN	ASQGFKRWEC	NRPHAPHSPI	120
FPSEKQRTYS	APSLGYEPHA	GHEVYVISTP	TENLHWKCLR	MKVVFVCCAST	SHSKEKPVPT	180
LPQPTMGPNV	KINVLDPFEG	ENPQVPKLEK	SISGTSKPRE	HLPLAVGIAP	FLMTFLAS	

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

30
35
40
45
50
55
60
65

1	11	21	31	41	51	
GCAOGAGGGA	AGAGGGTGAT	CGACCCCGGG	GAAGGTGCGT	GGGCAGGGCG	AGTTGGGAAA	60
GCGGCAGCCC	CCGCGCGCCC	CGCAGCCCTT	TCTCCTCCTT	TCTCCACGCT	CCTATCTGCC	120
TCTCGCTGGA	GGCCAGGCGG	TGCAGCATCG	AAGACAGGAG	GAACCTGGAGC	CTCATTTGCC	180
GGCCCGGGGG	GC CGGCTCG	GGCTTAAATA	GGAGCTCCGG	GCTCTGGCTG	GGACCCGACC	240
GCTGCCGGCC	GGCGTCCCGC	TGCTCCTGCC	GGGTGATGGA	AAACCCGAGC	CGGCGCGCCG	300
CCCTGGGCAA	GGCCCTCTGC	GCTCTCCTCC	TGGCCACTCT	CGGCGCCGCC	GGCCAGCCTC	360
TTGGGGGAGA	GTCCATCTGT	TCCGCCAGAG	CCCCGGCCAA	ATACAGCATC	ACCTTTCAGG	420
GCAAGTGGAG	CCAGACGGCC	TTCCCAAGC	AGTACCCCTT	GTTCGCGCCC	CCTGCGCAGT	480
GGTCTTCGCT	GCTGGGGGCC	GGCAGTACGT	CCGACTACAG	CATGTGGAGG	AAGAACCACT	540
ACGTCACTAA	CGGCTCGCGC	GACTTTGCGG	AGCGCGGCGA	GGCCTGGGCG	CTGATGAAGG	600
AGATCGAGGC	GGCGGGGAGG	GGGCTGCAGA	GGGTGCAAGC	GGTGTTTTCG	GGCGCCCGCG	660
TCCCGAGCGG	CACCGGGCAG	ACGTCCGGCG	AGCTGGAGGT	GCAGCGCAGG	CACCTGCTGG	720
TCTGTTTGT	GGTGGCATC	GTGCCAGGCC	CCGACTGGTT	CGTGGGCGTG	GACAGCCTGG	780
ACCTGTGCGA	CGGGGACCGT	TGGGGGAAC	AGGCGGGGCT	GGACCTGTAC	CCCTACGACG	840
CGGGGACGGA	CAGCGGCTTC	ACCTTCTCCT	CCCCCAACTT	CGCCACCATC	CGCCAGGACA	900
CGGTGACCGA	GATAACGTCC	TCCTCTCCCA	GCCACCGGCG	CAACTCTCTT	TACTACCCGC	960
GGCTGAAGGC	CCTGCCCTCC	ATCGCCAGGG	TGACACTGGT	GGGCTCGCGA	CAGAGCCCCA	1020
GGGCCTTCAT	CCCTCCCGCC	CCAGTCTTGC	CCAGCAGGGA	CAATGAGATT	GTAGACAGCG	1080
CCTCAGTTCC	AGAAACGCGG	CTGGAAGTGC	AGGTCTCCCT	GTGGTCTGTC	TGGGAGCTGT	1140
GGGAGGCGCA	CTGTGGGAGG	CTCGGGACCA	AGAGCAGGAC	TCGCTACGTC	CGGTTCCAGC	1200
CGCCACACAA	CGGGAGCCCC	TGCCCCGAGC	TGSAAGAAGA	GGCTGAGTGC	GTCCCTGATA	1260
ACTGCGTCTA	AGACAGAGAG	CCCGCAGCCC	CTGGGGCCCC	CGAGGCCATG	GGGTGTGCGG	1320
GGCTCTCTTG	CAGGCTCATG	CTGCAGGCGG	CCGAGGCACA	GGGGGTTTCG	CGCTGCTCCT	1380
GACCGCGGTG	AGGCGCGGCC	GACCATCTCT	GCACTGAAGG	GGCCTCTGCT	GGCGGCGACG	1440
GGCATTGGGA	AACAGCCTCC	TCCTTTCCCA	ACCTTGCTTC	TTAGGGGCCC	CGGTGTCCCG	1500
TCTGCTCTCA	GCCTCCTCCT	CCTGCAGGAT	AAAGTCATCC	CCAAGGCTCC	AGCTACTCTA	1560
AATTATGGTC	TCCTTATAAG	TTATTGCTGC	TCCAGGAGAT	TGTCTCTCAT	CGTCCAGGGG	1620
CCTGCTCTCC	ACGTGGTTCG	AGATACCTCA	GACCTGGTGC	TCTAGGCTGT	GCTGAGCCCC	1680
CTCTCCCGAG	GGCGCATCCA	AGCGGGGGCC	ACTTGAGAAG	TGAATAAATG	GGGCGGTTTC	1740
GGAAGCGTCA	GTGTTTCCAT	GTTATGATGC	TCTCTGGGTT	TGAATAAAGA	CTATCTCTGT	1800
TGCTCAC						

Seq ID NO: 132 Protein sequence
Protein Accession #: NP_016577.1

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1	11	21	31	41	51	
MENFSPAAL	GKALCALLLA	TLGAAGQPLG	GESICSARAP	AKYSITFTGK	WSQTAPPKQY	60
PLFRPPAQWS	SLIGAARHSSD	YSMRKNQYV	SNGLRDPFAER	GEAWALMKEI	EAAGEALQSV	120
HAVFSAPAVP	SGTGQTSABL	EVQRRLSLVS	FVVRIVSPDP	WFGVDSLDEL	CDGDRWREQA	180
ALDLYPYDAG	TDSGFTFSSP	NPATIPQDVT	TBITSSSPSH	PANGFYYPRL	KALPPIARVT	240
LVRRLQSPRA	FIPFAPVLP	RDNEIVDSAB	VPETPLDCEV	SLWSSWGLCG	GHCGRGLGTS	300
RTRVRVQPA	NNGSPCPDNC	V				

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

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1	11	21	31	41	51	
ATGTTACAGG	ATCCTGACAG	TGATCAACCT	CTGAACAGCC	TGATGTCAA	ACCCCTGCGC	60

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AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCCATCAT CATAGCACTA 120
CTGAGCCCTGG CGAGTATCAT CATTGTGGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTCT CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC GGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
GGGAACCTGTT TCTGTGCTGT TTTGACAAAC TTCACAGAAG CTCTGCTGTA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAACCCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTTGTGAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACCAGAAAAC GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCAGCGGAG CCCACTGTCT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAAGATGCT 1020
GACATACTGG TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
GGTACAGGCG GGGAAATGAC CGAGAAGATG ATGTGTGCGG GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
TTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260
AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
  
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Seq ID NO: 134 Protein sequence
 Protein Accession #: NP_063947.1

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1 11 21 31 41 51
MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIV VLIKVILDKY 60
YFLOGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPPEGP AVAVRLSKDR STLIQVLDAT 120
GNWPSACPN FTEALARTAC RQMGSYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNRS 180
GPCLSGSLVS LHLCLAGKSL KTRPVVGGEE ASVDSWPNQV SIQYDKQHC GGSILDPHWV 240
LTAHACFRKH TDVFNWKVRA GSKLGSFSPS LAVAKIIIE FNPMPKQND IALMKLQFPL 300
TFSGTVRPI C LFFDDELTP ATPLWIIWGW PTKQNGKMS DILLQASVOV IDSTRNADD 360
AYQGEVTERK MCAGIPEGGV DTCQGDGGP LMYQSDQNHV VGIVSWGYGC GGPSTPGVYT 420
  
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Seq ID NO: 135 DNA sequence
 Nucleic Acid Accession #: NM_003045
 Coding sequence: 148..2037

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1 11 21 31 41 51
CGATCCTGCC GGAGCCCCGC CGCGSCCGGC TTGGATTCTG AAACCTTCCT TGTATCCCTC 60
CTGAGACATC TTTGCTGCAA GATCGAGGCT GTCTCTGGT GAGAGAGTGG TGAGGCTTCC 120
CGTCATATTC CAGCTCTGAA CAGCAACATG GGGTGCAAG TCCTGCTCAA CATTGGGCG 180
CAGATGCTGC GCGGGAAGGT GGTGGACTGT AGCCGGGAGG AGACGCGGCT GTCTGCTGCG 240
CTGAACACTT TTGATCTGGT GGCCCTCGGG GTGGGCAGCA CACTGGGTGC TGGTGTCTAC 300
GTCTTGCTGC GAGCTGTGGC CGGTGAGAAT GCAGGCCCTG CCATTGTCTC CTCCTTCCCTG 360
ATGCTGCGC TGGCCTCAGT CTGTGCTATG GCGAGTTTGG TGCTCGGGTC 420
CCCAAGACGG GCTCAGCTTA CCTCTACAGC TATGTCAACG TTGAGAGCTC CTGGGCTTCC 480
ATCACCGGCT GGAACCTTAA CTCTCTCTAC ATCATCGGTA CTTCAAGCGT AGCGAGGGCC 540
TGGAGCGCCA CCTTCGACGA GCTGATAGGC AGACCCATCG GGGAGTTCTC ACGGACACAC 600
ATGACTCTGA ACGCCCCCGG CGTCTGGCT GAAAACCCCG ACATATTGCG AGTGATCATA 660
ATTCTCATCT TGACAGGACT TTAACTCTT GGTGTGAAG AGTCGGCCAT GGTCAACAAA 720
ATATTCACTT GTATTAAAGT CCTGGTCTGT GGCTTCATAA TGGTGTCAAG ATTTGTGAAA 780
GGATCGGTTA AAAACTGGCA GCTCACGGAG GAGGATTTTG GGAACACATC AGGCGCTCTC 840
TGTITGAACA ATGACACAAA AGAAGGGAAG CCGGTGTITG GTGATTTCAT GCCCTTCGGG 900
TTCTCTGGTG TCTGTGCGG GGCAGCGACT TGCTTCTATG CCTTGTGGG CTTTGACTGC 960
ATCGCCACCA CAGGTGAAGA GGTGAAGAAC CCACAGAAGG CCATCCCGT GGGGATCGTG 1020
GGTCCCTCT TGATCTGCTT CATCGCTTAC TTGGGGTGT OGGCTGCCCT CACGCTCATG 1080
ATGCCCTACT TCTGCTGCTT CAATAACAGC CCGCTGGCCG AGCCCTTTAA GCACGTGGGC 1140
TGGGAAGGTG CCAAGTAGCG AGTGGCCGTG GGCTCCCTCT GCGCTCTTTC CGCCAGTCTT 1200
CTAGGTTCCA TGTTTCCCAT GCCTGCGGTT ATCTATGCCA TGGCTGAGGA TGAAGTGTCTA 1260
TTTAAATTCT TAGCCAAAGT CAATGATAGG ACCAAAACAC CAATAATGCG CACATTAGCC 1320
TCGGGTGCGG TTGCTGTCTT GATGGCTTTC CTCTTTGACC TGAAGGACTT GGTGGACCTC 1380
ATGTCCATTG GCACTCTCTT GGCTTACTCG TTGGTGGCTG CCTGTGTGTT GGTCTTAACG 1440
TACCAGCCAG AGCAGCTTAA CTTGTATATC CAGATGGCCA GTACTTCCGA CGAGTTAGAT 1500
CCAGCAGACC AAAATGAATT GGCAAGCACC AATGATTCCC AGCTGGGGTT TTTACCAGAG 1560
GCAGAGATGT TCTCTTTGAA AACCATACTC TCACCCAAA ACATGGAGCC TTCCAAAATC 1620
TCTGGGCTAA TTGTGAACAT TTCAACAGC CTATAGCTG TTCTCATCAT CACCTTCTGC 1680
ATTGTGACCG TGCTTGAAG GAGGCTCTC ACCAAGGGG CGCTGTGGGC AGTCTTCTG 1740
CTGCGAGGCT CTGCCCTCTT CTGTGCCGTG GTCACGGGCG TCATCTGGAG GCAGCCCGAG 1800
AGCAAGACCA AGCTCTCAT TAAAGTTCCC TTCTGCCAG TGCTCCCATC CCTGAGCATC 1860
TTGTTGAAGC TCTATCTCAT GATGAGCTG GAACAGGCA CCTGGGTCCG GTTGTCTGTG 1920
TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCATATGCC TGTGGCAGAG CAGGAGGCGG 1980
TCCCTGGAAT CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAAGT CAAGTGAACG 2040
ACAGCCCGCG CCCCCGAGG TGGCAGCAGC CCGAGGGGAC GCGCCACAGG GACCGGAGG 2100
CACCCCAACC TCCCCACAG TGAACACAG ACCACCTGGG TCCACACCTC CACTGCA
  
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Seq ID NO: 136 Protein sequence
 Protein Accession #: NM_003045

1 11 21 31 41 51

5 MGCKVLLNIG QQMLRRKVV D CSREETRLSR CLNTFDLVAL GVGSTLIGAGV YVLGAVARE 60
 NAGPAIVISF LIAALASVLA GLCYGEFGAR VPKTGSAYLY SYVTVGELMA FITGWNILIS 120
 YIIGTSSVAR AWSATFDELI GRPIGEFSRT HMTLNAPGVL AENPDIFAVI IILILTGLLT 180
 LGVKESAMVN KIPTCINVLV LGFIMVSGFV KGSVKWQLT BEDPGNTSGR LCLANDTKEG 240
 KPGVGGFMPF GFSGLVSGAA TCFYAFVGF D CIATTGSEVK NPKAKIPVGI VASLLICPIA 300
 YFGVSAALTL MMYPCLDNN SPLPDAFKHV GWEGAKYAVA VGSICALSAS LIGSMFPMR 360
 VIYAMAE DGL LFKPLANVND RTKTPIIATL ASGAVAAVMA FLFDLKDLDV LMSIGTLAY 420
 SLVAACVLVL RYQPEQPNLV YQMASTSEDL DPADQNELAS TNDSQLGLFLP EAEMPSLKI 480
 10 LSPKMEPSK ISGLIVNI ST LIAVLIITF CIVTVLGRE A LTKGALWAVP LLAGSALLCA 540
 VVTGVINRQP ESKTKLSFKV PFLFVLPILS IFVNVYLMQ LDQGTWVRFA VMMLIGPIIY 600
 FGYGLWHSEE ASLDADQART PDGNLDQCK

Seq ID NO: 137 DNA sequence

Nucleic Acid Accession #: NM_032044.1

Coding sequence: 182..658

1 11 21 31 41 51
 20 AAGATATAAA AGCTCCAGAA ACGTTGACTG GGACCACTGG AGACACTGAA GAAGGCAGGG 60
 GCCCTTAGAG TCTTGGTTGC CAAACAGATT TGCAGATCAA GGAGAACCCA GGAGTTTCAA 120
 AGAAGCGCTA GTAAGTCTC TGAGATCCTT GCACTAGCTA CATCCTCAGG GTAGGAGGAA 180
 GATGGCTTCC AGAAGCATGC GGCTGCTCCT ATTGCTGAGC TGCCTGGCCA AAACAGGAGT 240
 CCTGGGTGAT ATCATCATGA GACCCAGCTG TGCTCCTGGA TGGTTTACC ACAAGTCCAA 300
 25 TTGCTATGGT TACTTCAGGA AGCTGAGGAA CTGGTCTGAT GCGAGGCTCG AGTGTCTAGT 360
 TTACGGAAC GGAGCCACC TGGCATCTAT CCTGAGTTTA AAGGAAGCCA GCACCATAGC 420
 AGAGTACATA AGTGGCTATC AGAGAAGCCA GCGGATATGG ATTGGCCTGC ACGACCCACA 480
 GAAGAGGCGAG CAGTGGCAGT GGATTGATGG GGCCATGTAT CTGTACAGAT CCTGGTCTGG 540
 CAAGTCCATG GTTGGGAACA AGCACTGTGC TGAGATGAGC TCCAATAACA ACTTTTAAAC 600
 30 TTGGAGCAGC AACGAATGCA ACAAGCGCCA ACACCTCTCTG TGCAAGTACC GACCATAGAG 660
 CAAGAATCAA GATTCTGCTA ACTCCTGCAC AGCCCCGTCC TCTTCTCTTC TGCTAGCCTG 720
 GCTAAATCTG CTCATTATTT CAGAGGGGAA ACCTAGCAAA CTAAGAGTGA TAAGGGCCCT 780
 ACTACACTGG CTTTTTAGG CTTAGAGACA GAAACTTTAG CATTTGGCCA GTAGTGGCTT 840
 CTAGCTCTAA ATGTTTGGCC CGCCATCCCT TTCCACAGTA TCCTTCTTCC CTCTCCCTCT 900
 35 GTCTCTGGCT GTCTCGAGCA GTCTAGAAGA GTGCATCTCC AGCCTATGAA ACAGCTGGGT 960
 CTTTGGCCAT AAGAAGTAAA GATTGAAGA CAGAAGGAAG AAATCTCAGGA GTAAGCTTCT 1020
 AGACCCCTTC AGCTCTTACA CCTTCTGCC CTCTCTCCAT TGCCCTGCACC CCACCCGAGC 1080
 CACTCACTC TGCTTGTGTT TTCTTTGGC CATAGGAAGG TTTACCACTA GAATCCTTGC 1140
 TAGGTTGATG TGGGCCATAC ATTCTTTTAA TAAACCATTG TGTACATAAG AAAAAAAAAA

Seq ID NO: 138 Protein sequence

Protein Accession #: NP_114433.1

1 11 21 31 41 51
 45 MASRSMRLLL LLSCLAKTGV LGDIIMRPSK APGWFYHKS N CYGYFRKL RN WSDAELECCS 60
 YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHD PQ KRQQWQWIDG AMYLRYRWSG 120
 KSMGNGKHCA EMSNNFLT WSSNECNKRO HFLCKYRP

Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM_051860.2

Coding sequence: 52..3042

1 11 21 31 41 51
 55 GCTCACCCAG GAAAAATATG CAATGCTGCC ATTGATATAC AGGCCACTAC AATGGATGGA 60
 GTTAACCTCA GCACCGAGGT TGTCTACAAA AAAGGCCAGG ATTATAGGTT TGCTTGCTAC 120
 GACCGGGGCA GAGCCTGCCG GAGCTACCGT GTACGGTTCC TCTGTGGGAA GCCTGTGAGG 180
 CCCAACTCA CAGTCACCAT TGACACCAAT GTGAACAGCA CCATTCTGAA CTTGGAGGAT 240
 60 AATGTACAGT CATGGAAACC TGGAGATACC CTGGTCATTG CCACTACTGA TTAATCTCAT 300
 TACCAGGCGA AAGAGTTCCA GGTGCTTCCC TGCAGATCCT GCGCCCCCAA CCAGGTCAAA 360
 GTGGCAGGGA AACCAATGTA CCTGCACATC GGGGAGGAGA TAGACGGCGT GGACATGCGG 420
 GCGGAGGTTG GGTCTCTGAG CCGGAACATC ATAGTGATGG GGGAGATGGA GGACAAATGC 480
 TACCCCTACA GAAACCACAT CTGCAATTTT TTTGACTTGG ATACCTTTGG GGGCCACATC 540
 65 AAGTTTGTCT TGGGATTTAA GGCAGCACAC TTGAGGGGCA CGGAGCTGAA GCATATGGGA 600
 CAGCAGCTGG TGGGTCTAGT CCGATTCTAC TTCCACCTGG CCGGTGATGT AGACGAAAGG 660
 GGAGGTTATG ACCCAACCCAC ATACATCAGG GACCTCTCCA TCCATCATAC ATTCTCTGGC 720
 TGGCTCACAG TCCATGGGCTC CAATGGCTTG TTGATCAAGG ACGTTGTGGG CTATAACTCT 780
 TTGGGCCACT GCTTCTTAC GGAAGATGGG CCGGAGGAAC GCAACACTTT TGACCACTGT 840
 70 CTTGGCCTCC TTGCAAGTC TGGAAACCTC CTCCCCTCGG ACCGTGACAG CAAGATGTGC 900
 AAGATGATCA CAGGAGACTC CTACCCAGGG TACATCCCA AGCCGAGGCA AGACTGCAAT 960
 GCTGTGTCCA CTTCTTGAT GGCCAATCCC AACAAACAAC TCATCAACTG TGCCGCTGCA 1020
 GGATCTGAGG AAATGGGATT TTGGTTTATT TTTCACCAAG TACCAACGGG CCCCTCGGTG 1080
 75 GGAATGTACT CCCAGGTTA TTCAGAGCAC ATTCCACTGG GAAATTTCTA TAACCAACGA 1140
 GCACATTCCA ACTACCGGGC TGGCATGATC ATAGACAAGG GAGTCAAAC CACCGAGGCC 1200
 TCTGCCAAGG ACAAGCGGCC GTTCTCTCA ATCATCTCTG CCAGATACAG CCCTCACAGG 1260
 GACGCGACC CGCTGAAGCC CCGGAGCGCG GCATCATCA GACACTTCTA TGCCCTACAAG 1320
 AACCAAGGACC ACGGGGCGCT GCTGCGCGCG GGGGATGTGT GGTCTGACAG CTGCGGTTT 1380
 GCTGACATG GCAATGGGCT GACCTGGGCC AGTGCTGGAA CCTTCCCGTA TGACGACGCG 1440
 80 TCCAAGCAAG AGATAAAGAA CAGCTTGTCT GTTGGCGAGA GTGGCAACGT GGGGACGAGG 1500
 ATGATGGACA ATAGGATCTG GGGCCCTGGC GGTCTGGAGC ATAGCGGAAG GACCTCTCTC 1560
 ATAGGCCAGA ATTTCTCAAT TAGAGGAATT CAGTTTATAT ATGGCCCAAT CAACATCCAA 1620
 AACTGCATCT TCGAAGATT TGTGGCCCTG GAGGGCCGCG ACACCGAGCG CCTGGCCTTC 1680
 CGCCTGAATA ATGCTCTGCA GAGCTGCCCC CATAACAAG TGACCGGCAT TGCTTTTGA 1740
 GACGTTCCGA TTAATCTCCAG AGTGTCTCTC GGAGAGCCTG GGCCCTGGTT CAACGAGCTG 1800

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GACATGGATG GGGATAAGAC ATCTGTGTTT CATGACGTGG ACGGCTCCGT GTCCGAGTAC 1860
 CCTGGCTTCCT ACCTCAGCAA GAATGACAAC TGGCTGGTCC GGCACCCAGA CTGCATCAAT 1920
 GTTCCCGACT GGAGAGGGGC CATTTGCAGT GGGTGCTATG CACAGATGTA CATTCAAGCC 1980
 TACAGACCA GTAACCTGCG AATGAAGATC ATCAAGAATG ACTTCCCAG CCACCTCTTT 2040
 TAOCCTGGAG GGGGCTCTAC CAGGAGCACC CATTACCAGC AATACCAACC GGTGTCAACC 2100
 CTGCAGAAGG GCTACACCAT CCACTGGGAC CAGACGGCCC CGCCGAACT CGCCATCTGG 2160
 CTATCAACT TCAACAAGGG CCACTGGATC CGAGTGGGGC TCTGCTACCC GCGAGGCACC 2220
 ACATTCTCCA TCTCTCGGA TGTTCACAA CTGCTGCTGA AGCAAAAGTC CAAGACGGGC 2280
 GTCTTCGTGA GGACCTTGCA GATGACAAA GTGGAGCAGA GCTACCTCG CAGGAGCCAC 2340
 TACTACTTGG ACGAGGACTC AGGGCTGTGG TTCTGAAAGC TGAAGAGTCA GAACGAGAGA 2400
 GAGAAGTTGG CTTTCTGCTC CATGAAAGGC TGTGAGAGGA TAAAGATTAA AGCTCTGATT 2460
 CCAAAGAACG CAGGCGTCAG TGAATGCACA GCCACAGCTT ACCCAAGTT CACCGAGAGG 2520
 GCTGTGCTAG ACGTGGCGAT GCCCAAGAAG CTCTTTGGTT CTCAGCTGAA AACAAAGGAC 2580
 CATTTCTTGG AGGTGAAGAT GGAGAGTTCC AAGCAGACT TCTTCCACT CTGGAACGAC 2640
 TTGCTTACA TTGAAGTGA TGGGAAGAAG TACCCAGTT OGGAGGATGG CATCCAGGTT 2700
 GTGGTGATTG ACGGGAACCA AGGGCGCGTG GTGAGCCACA CGAGCTTCAG GAACCTCCAT 2760
 CTGCAGGCCA TACCATGGCA GCTTTTCAAC TATGTGGCGA CCATCCCTGA CAATTCCATA 2820
 GTGCTTATGG CATCAAAGGG AAGATACGTC TCCAGAGGCC CATGGAACCA AGTGCTGGAA 2880
 AAGCTTCTGG CAGACAGGGG TCTCAAGTTG AAAGAGCAAA TGGCATTCGT TGGCTTCAA 2940
 GGCAGCTTCC GGCCCATCTG GGTGACACTG GACACTGAGG ATCACAAGC CAAAATCTTC 3000
 CAAGTGTTCG CATCCCTGT GGTGAAGAAG AAGAAGTTGT GAGGACAGCT GCGCCCGGT 3060
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 GGGAAAGGCT CTTGGAGACC TGGTGTGCTC ACCTGCCCTT ACTCAAGTGT CTACCTGGAG 3240
 CCCCCTGGGG GGTGCTGGCC AATGCTGGAA ACATTCACTT TCCTGCAGCC TCTTGGGTGC 3300
 TTCTCTCTCA TCTGTGCTCT TFCAGTGGGG GTTGGGGAC CATATCAGGA GACCTGGGTT 3360
 GTGCTGACAG CAAAGATCCA CTTTGGCAGG AGCCCTGACC CAGCTAGGAG GTAGTCTGGA 3420
 GGCTGTGTCA TTCAAGATCA CCATGTGCTC TCAGCAGACA AGTGAGGGTG GTAAATGTAG 3480
 GAGAAAGGCT CTTGGCTTTA AGGAAATCTT TACTCCTGTA AGCAAGAGCC AACCTCAGAG 3540
 GATTAGGAGG TGGGTAGAAA CTGCTATACC TTGGGGAAGA GGCAGGCCCT GCCTCTGGCC 3600
 GTGTCCACTT TFCAGGAGAC TTTAGTGGC AGGTTTGAC TTGAGTGA TGAATCTCAA 3660
 AGGCCCTTTT AGTTCGAGA TTCCAGAAAT CTGCTGCATT TCACATGGTA CCTGGAACCC 3720
 AACAGTTTAT GGATATCCAC TGATATCCAT GATGCTGGGT GCCCAGCGC ACACGGGATG 3780
 GAGAGGTGAG AACTAATGCC TAGCTTGAGG GGTCTGAGT CCACTAGGGC AGGCAGTCAG 3840
 GTCCATGTGC ACTGCAATGC CAGGTGAGGA AATCAGAGAG AGGTAAATG GAGGCCAGTG 3900
 CCAATTGAGA GGGGAGGCTC AGGAAGGCTT CTTGCTTACA GGAATGAAGG CTGGGGGATG 3960
 TTTGCTGGGG GGAGATGAGG CAGCCTCTGG AATGGCTCAG GGATTCAGCC CTCCTGCGG 4020
 CTGCTCTGCT AAGCTGTGTA CTACGGGGTC GGCCTTTGCT CAGCTCTCTC TGGCCCACTC 4080
 ATGATGGAGA TGGTGTGTC GAGGGGAGCA ATGGGCTTTG CTGCTTATGA GCACAGAGGA 4140
 ATTCACTCCC CAGGCAGGCC TGCTCTGAG TCCAAGAGGG TGAAGTCCAC AGAAGTGAGC 4200
 TOCTGCTTIA GGGCTCTATT TGCTCTTCA CTCCCTGCGC CTGGGATTTT AGAGCTGGAA ATATAGAAAA 4320
 AGACCTTAGA TGTGCTCGTA CTCCCTGCGC CTGGGATTTT AGAGCTGGAA ATATAGAAAA 4380
 TATCTAGCCC AAAGCTTCA TTTTAAACA TGGGAAAGT GAGCCCCAA GATGGGAAAG 4440
 AACCAACAAA CTAATCTCTT GCTCTGAGG GCTGAGGAG CCCCACCTTA GGCCTTGTG CACACACACA 4500
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 GACAAGTCCC CTCGAAGGAA AGGAATGAC TAGAGTAGAA TGACAGCTAG CAGATCTCTT 4620
 CCTCTCTGCT CCAAGGCGAC ACAAACCCGC CCTCCCTTGT GTGTGGGGG TCCCTGTGGC 4680
 CTTCACTTTG TTCACTACCT GTCAGCCAG CCTGGGTGCA CAGTAGCTGC AACTCCCCAT 4740
 TGGTGTACCT TGGCTCTCTT GTCTCTGAG CTCTACAGG GAGGCCAGC AGAGGGAGTA 4800
 GGGCTGCGCA TGTTCCTGGT GAGCCAATTT GGCTGATCTT GGGTGTCTGA ACAGCTATTG 4860
 GGTCCACCCC AGTCCCTTTC AGCTGCTGCT TAATGCCCTG CTCTCTCTCT GGGCCACCTT 4920
 ATAGAGAGCC CAAAGAGCTC CTGTAAGAGG GAGAACTCTA TCTGTGTTT ATAATCTTGC 4980
 ACGAGGCACC AGAGCTCTCC TGGGTCTTGT GATGAATAC ATTTATCCCC TTTCTGCCCC 5040
 CAACCAACAA CTAATCTCTT CAAAGAGGCG CTGCTGAGG CCTCCACCC AACTGCACCC 5100
 ATGAGACTCG GTCCAGAGT CCAATCCCCA GGTGGGAGCC AACTGTGAGG GAGGTCTTTC 5160
 CCACCAACAA TCTTTCAGCT GCTGGGAGGT GACCATAGGG CTCTGCTTTT AAAGATATGG 5220
 CTGCTTCAAA GGCCAGAGTC ACAGGAAGGA CTTCTTCCAG GGAGATTAGT GGTGATGGAG 5280
 AGGAGAGTTA AAATGACCTC ATGTCTTCTT TGTCCACGGT TTTGTTGAGT TTTCACTCTT 5340
 CTAATGCAAG GGTCTCACAC TGTGAACCA TTAGGATGTG ATCACTTTCA GGTGGCCAGG 5400
 AATGTTGAAT GTCTTTGGCT CAGTTCATT AAAAAAGATA TCTATTGAA AGTTCCTAGA 5460
 GTTGTACATA TGTTCACAG TACAGGATCT GTACATAAAA GTTCTTTTCC TAAACCATTC 5520
 ACCAAGAGCC AATATCTAGG CATTTCTTG GTAGCACAAA TTTCTTATT GCTTAGAAAA 5580
 TGTCTCTCT TGTATTCTCT GTTTGTAAGA CTTAAGTGAG TTAGGTCTTT AAGGAAAGCA 5640
 ACGCTCTCT GAAATGCTTG TCTTTTCTCT GTTGCAGAAA TAGCTGTGTC TTTTTCGGGA 5700
 GTTAGATGTA TAGAGTGTTC GTATGTAAAC ATTTCTTGTG GGCATCACA TGAACAAAGA 5760
 TATATTTTCT ATTTATTTAT TATATGTGCA CTTCAAGAAG TCACTGTGAG AGAAATAAAG
 AATTGTCTTA AATGTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

70 Seq ID NO: 140 Protein sequence
 Protein Accession #: KP_051860.2

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Seq ID NO: 146 Protein sequence
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Seq ID NO: 148 Protein sequence
Protein Accession #: AAH12089.1

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Seq ID NO: 149 DNA sequence
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Protein Accession #: NP_149038.1

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Seq ID NO: 152 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 DRGRFKVVVS VLSAVTTCLA FVKPAINNIS LMTLGVPTCA LLIAELKRCR NMRVFKLQLP 180
 SGLWTLALF CWISDRAPCE LLSFPNPPYL HCMWHILICL AAYLGCVCPA YFDAASEIPE 240
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Seq ID NO: 153 DNA sequence
 Nucleic Acid Accession #: NM_001432.1
 Coding sequence: 167..676

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Seq ID NO: 154 Protein sequence
 Protein Accession #: NP_001423.1

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Seq ID NO: 155 DNA sequence
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 Coding sequence: 85..2466

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Seq ID NO: 156 Protein sequence
Protein Accession #: NP_037414.2

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PADEMDHDET ELGLYKVNEY VDARDTNMGA WFEAQVVRVT RKAPSRDEPC SSTSRPALEE 180
DVIYHVKYDD YFENGVVQMN SRDVRARART IIKWQDLEVG QVVMNLNYPD NPKERGFWDY 240
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SCXHKDDVN RLRCVACHL CGGRQDPDKQ LMCDECDMAF HIYCLDPPLS SVPSDEWNYC 360
PECRNDASEV VLAGERLRSE KKKAKMASAT SSSQRDWGKG MACVGRTKEC TIIPSNHYGP 420
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SGGRDLGSMK RTABQSCDQK LNTNTRALAL NCFAPINDQB GAEAKDWRSG KPVVRVVRNVK 540
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SPRRTSKTKK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP PQLFLSKVEE 720
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Seq ID NO: 157 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

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Seq ID NO: 158 Protein sequence
Protein Accession #: NP_000747.1

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Seq ID NO: 159 DNA sequence
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Coding sequence: 325..1514

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Seq ID NO: 160 Protein sequence
Protein Accession #: NP_001191.1

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Seq ID NO: 162 Protein sequence
Protein Accession #: NP_001990.1

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	GQVCRNGRCF NEIGSPKCLC NEGYELTFDG KNCIDTNECV ALPGSCSPGT CQNLGSGFRC 2040
	ICPPGYEVKS ENCIDINECD EDPNICLFSG CTNTPGGFQC LCPGFLVLD NGRRCFDTRQ 2100
30	SPCPTNFENG KCSYPIKAFNT TKAKCCSKM PGEWGWDPC LCPKDEEAP QDLCPYGHGT 2160
	VPSLHDTREV VNECLSPGI CSNGQCINTD GSFRCECPMG YNLDYTGVR VDTDECISGN 2220
	PCNGTCTNV IGSFECNCE GFEPGPMNC EDINECAQNP LLCALRCMT FGSYECTCI 2280
	GYALREDQXM CKDLDECABG LHDCEBGRMM CKNLIGTMC ICPPGMARRP DGEQCVDENE 2340
	CRKPGICEN GRCVNIIGSY RCECEGFPQS SSSGTECLDN RQGLCFEVL QTIQMASS 2400
35	RNLVTKSECC CDGGRNGHQ CELCPLPGTA QYKICPHGP GTTDTGRDID ECKVMPNLCT 2460
	NGQCINTMGS FRFCRVGYT TDISGTSCID LDECSQSPKP CNYICKNTG SYQCSCPRGY 2520
	VLQEDGKTK DLDECQTKH NCQFLCVNTL GGFCTCKEPG FTQHTACID NNECGSQPLL 2580
	CGGKICQNT PGSFCECQR GFSLDATGLN CEDVDECDGN HRCQHGQNI LGGYRCGCPQ 2640
	QYIHYQMNQ CVDENECSNP NACGSASCYN TLGSYKCACP SGFSFDQFSS ACHDVNECSS 2700
40	SKNFCNYGCS NDEGGLYLCG PPGYRVGQG HCVSGMGFNK GQYLSLDTE DEBNALSPEA 2760
	CYECKINGYP KDSRQKRSI HEPDPTAVEQ ISLESVDMDS FVMKFNLSH LGSKEHILEL 2820
	RPAIQPLNHN IRYVLSQDND DSVFRIHQRN GLSYLHTAKK KLMPGTYTE ITSIPLYKKK 2880
	ELKLEBSNE DDYLLGELGE ALRMRLQIQL Y

45 Seq ID NO: 163 DNA sequence
Nucleic Acid Accession #: NM_013372.1
Coding sequence: 63..617

50	1 11 21 31 41 51	GCAGGCCGAC TCAGCGCCAC GCGTCGAAAG CGCAGGCCCC GAGGACCCGC GCACTGACA 60
		GTATGAGCCG CACAGCCTAC ACGGTGGGAG CCTGCTTCT CCTCTTGGG ACCTGCTGC 120
		CGGCTGCTGA AGGAAAAAG AAAGGTCCC AAGGTGCCAT CCCCCGCCA GACAAGGCC 180
		AGCAATGAG CTCAGAGCAG ACTCAGTGC CCCAGCAGC TGGCTCCAG AACCGGGGG 240
55		GGGGCCAGG GCGGGCACT GCCATGCCCG GGGAGGAGT GCTGGAGTC AGCCAAGAG 300
		CCCTGCATGT GACGGAGCGC AAATACCTGA AGCAGAGCTG GTGCAAAAC CAGCCGCTTA 360
		AGCAGACCAT CACAGAGGAA GGCTGCAACA GTGCAACCAT CATCAACGC TTCTGTTAG 420
		GCCAGTGCAA CTCTTTCTAC ATCCCCAGGC ACATCCGAA GGAGGAAGT TCCTTTCTAGT 480
		CCTGCTCCT CTGCAAGCCC AAGAAATTA CTACCATGAT GGTCAACCT AACCTGCCCTG 540
60		AACTACAGCC ACCTACCAAG AAGAGAGAG TCACACGTGT GAAGCAGTGT CGTTGCATAT 600
		CCATCGATT GGAATTAAGC AAATCCAGGT GCACCCAGCA TGTCTTAGGA ATGCAGCCCC 660
		AGGAAGTCCC AGACCTAAAA CAACAGATT CTACTTGGC TTAACCTAG AGGCCAGAAG 720
		AACCCCCAGC TGCCCTCTGG CAGGAGCCTG CTTGTGCGTA GTTCTGTGTC ATGATGTGTG 780
		ATGGGTGCT GTGGGTGTT TTAGACACCA GAGAAACAC AGTCTCTGT AGAGAGCACT 840
65		CCCTATTTG TAAACATATC TGCTTTAATG GGAATGTACC AGAAACCCAC CTACCCCGG 900
		CTCACATCTA AAGGGGCGGG GCGGTGGTCT GGTCTGACT TTGTGTTTT GTGCCCTCCT 960
		GGGGACGAGA ATCTCCTTTC GGAATGAATG TTCAATGAA AGGCTCTCT GAGGGCAAGA 1020
		GACCTGTTTT AGTGCTGCAT TGCACATGGA AAAGTCCCTT TAACCTGTGC TTGCATCTCT 1080
		CTTCTCTCT CTCTCTCACA ATCCATCTCT TCTTAAGTTG ATAGTGACTA TGTGAGTCTA 1140
70		ATCTCTGTT TGCCAAAGTT CCTAAATTAA TTCACTTAAC CATGATGCAA ATGTTTTTCA 1200
		TTTGTGAAG ACCCTCCAGA CTCTGGGAGA GGCTGGTGTG GGCAGGACA AGCAGGATAG 1260
		TGGAGTGAGA AAGGGAGGGT GGAGGGTGAG GCCAATCAG GTCCAGCAA AGTCAGTAGG 1320
		GACATTGCAG AAGCTTGAAG GGCCAATACC AGAACACAGG CTGATGCTTC TGAGAAAGTC 1380
		TTTTCTTAGT ATTTAAACGA ACCCAAGTGA ACAGAGGAGA AATGAGATTG CCAGAAAGTG 1440
75		ATTAACCTTG GCGGTGCAA TCTGCTCAAA CCTAACCA CAAGTGAAGT ATAAATACTG 1500
		ACCACCTCTA TGTTCGAGCC CAAGCAAGTT AGCTAAACCA AACCACTCC TCTGCTTGT 1560
		CCCTCAGTGT GAAAGAGAGG GTAGTTTGA ACTCTCTGCA TAGGGGTGGG AATTAATCAA 1620
		AAACCKCAGA GGCTGAATTT CCTAATACCT TTCCTTTATC GTGGTTATAG TCAGCTCATT 1680
		TCCATTCCAC TATTTCCCAT AATGCTTCTG AGAGCCACTA ACTTGATTGA TAAAGATCCT 1740
80		GCTCTGCTG AGTGTACCTG ACAGTAAGTC TAAAGATGAR AGAGTTTAGG GACTACTCTG 1800
		TTTTAGCAAG ARATATTCTG GGGTCTTTT TGTTTAACT ATTTGTCAGGA GATTGGGCTA 1860
		RAGAGAAGAC GACGAGAGTA AGGAAATAAA GGGRATTGCC TCTGGCTAGA GAGTAAGTTA 1920
		GGTGTTAATA CTGGTAGAA ATGTAAGGGA TAGGACCTCC CTTTCTTTAT GTGCTCACTG 1980
		AGGATCTGAG GGGACCTGT TAGGAGAGCA TAGCATCATG ATGTATTAGC TGTTCATCTG 2040
		CTACTGTTG GATGACATA ACTATTGTAA CTATTGAGTA TTTACTGGA GGCATGCTCC 2100

5 TCTGATTAAA CTGGCCTAC TGGCAATGGC TACTTAGGAT TGATCTAAGG GCCAAAGTGC 2160
 AGGGTGGGTG AACTTTATTG TACTTTGGAT TTGGTTAAAC TGTTTTCTTC AAGCCTGAGG 2220
 TTTTATATAC AAACCTCCCTG AATACTCTTT TTGCCTTGTA TCTTCTCAGC CTCCTAGCCA 2280
 AGTCCATATG AATATGGAAA ACAAACACTG CAGACTTGAG ATTCAAGTGC CGATCAAGGC 2340
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 TCCAGTGCTC TCCATCTAA CAACTAAACA GGAGCCATTT CAAGGCGGGA GATATTTTAA 2460
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 CCAATCTTT GTATTGTCCA CATTCTCCAA CAATAAAGCA CAGAGTGGAT TTAATTAAAGC 2640
 10 ACACAAATGC TAAGGACGAA TTTTGAGGCT GGGAGAGAAG AAAAGGGAAA GAAGCTGAAA 2700
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 AGCAGTAAT TTCTTTTAGG AGCTTGTACC ACAGTCTTGC ACATAAGTGC AGATTTGGCT 2880
 CAAGTAAGA GAATTTCTC AACACTAACT TCACTGGGAT AATCAGCAGC GTAACTACCC 2940
 15 TAAAGATCTA CTAATGACCA AAGAGGGAAT TATCTGTTCT TCTTACTGTG CCTATATTAA 3000
 GACTAGTACA AATGTGGTGT GTCTTCCAAC TTTCATTGAA AATGCCATAT CTATACCATA 3060
 TTTTATTCGA GTCACTGATG ATGTAAATGAT ATATTTTTC ATTATTATAG TAGAATATT 3120
 TTATGGCAAG ATATTGTGG TCTTGATCAT ACCTATTAAA ATAATGCCAA ACACCAATA 3180
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 20 GTCTGTAAAT TGTTTTTTGT TACTGTAGT CTTCAAAGTT AAGAGTGTAA GTGAAAAATC 3300
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 ATTTAATGTA ATTATTACTT CAAATCCTTT GTTCACTGTG ATTTCAAGCA TGTTTTCTTT 3420
 TTCTCTTTA TATGACTTTC TCTGAGTTGG GCAAAGAAGA AGCTGACACA CGTATGTTG 3480
 25 TTAGAGTCTT TTATCTGGTC AGGGGAAACA AAATCTTGAC CCAGCTGAAC ATGTCTTCT 3540
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 AAGCAATATT AAGAAGACT TTAATGTTA TTTTGAAGA CTTACGATGC ATGTATACAA 3660
 ACGAATAGCA GATAATGATG ACTAGTTTAC ACATAAAGTC CTTTAAAGGA GAAAATCTAA 3720
 AATGAAAAGT GGATAAACAG AACATTATA AGTGATCAGT TAATGCCTAA GAGTGAAAGT 3780
 30 AGTTCTATTG ACATTCTTCA AGATATTAA TATCAACTGC ATTATGTATT ATGTCTGCTT 3840
 AAATCATTTA AAAACGGCAA AGAATTATAT AGACTATGAG GTACCTTGTCT GTGTAGGAGG 3900
 ATGAAAGGGG AGTTGATAGT CTCATAAAAC TAATTTGGCT TCAAGTTTCA TGAATCTGTA 3960
 ACTAGAAATT AATTTTCAAC CCAATAATGT TCTATATAGC CTTTGCTAAA GAGCAACTAA 4020
 TAAATTAAAC CTATTCTTTC AAAAAAAAA

35 Seq ID NO: 164 Protein sequence
 Protein Accession #: NP_037504.1

40 1 11 21 31 41 51
 MSRTAYTVGA LLLLLGLTLP AAEKKKKSQ GAIPPPDKAQ HNDSEQTQSP QPGRSRNRGR 60
 GQGRGTAMPG BEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIEEGCNS RTIINRFYCG 120
 QCNSEYIPRH IRKEGFSQS CSFCKPKKFT TMMVTLCNPS LQPFKKGRV TRVQCRCIS 180
 IDLD

45 Seq ID NO: 165 DNA sequence
 Nucleic Acid Accession #: CAT cluster

50 1 11 21 31 41 51
 GAATTGCATC GGACAGAGCT TCGCCATGGC CGAGTTGGCG GTGGTTGTGG CACTAACACT 60
 GCTACGTTTC CGCCTGAGCG TGGACCGAAC GCGCAAGGTG CGGCGGAAGC CGGAGCTCAT 120
 ACTGCGCACG GAGAACGGGC TCTGGCTCAA G

55 Seq ID NO: 166 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1650

60 1 11 21 31 41 51
 ATGCCACCTC TGCCATCCAG AATGTCTCGG GGGCCCTCCT TGGTGACAGG CAGGATGCTG 60
 CCCATCAGAG ACGCCTGCT GCACCTCCCTG GGGCTGGAGA AGACGGCGTT CCGCATATAC 120
 GCGGTGTCCA CCCTTCTCCT CTCTCTGCTC TTCTTCTGT TCCGCTGCT GCTGCGGTTT 180
 65 CTGAGGCTCT GCAGGAGCTT CTACATCACC TGCCGCGGCG TGCGCTGCTT CCCCAGCCT 240
 CCGCGGCGCA ACTGCTGCT GGGCCACCTG GGCATGTACC TTCCAAATGA GCGCGGCTT 300
 CAAGATGAGA AGAAGGTACT GGACACATG CACCATGTAC TCTTGGTATG GATGGGACCT 360
 GTCTGCGCGC TGTGTGTTCT GGTGCACCTT GATTACATCA AACCCCTTTT GGGAGCTTCA 420
 GCTGCCATCG CCCCAGGA TGACCTCTTC TATGGCTTCC TAAAACTTGT GCTAGGGGAT 480
 70 GGGCTGCTGC TCAGCAAGG TGACAAAGTG AGCCGCGCAC GTGCGCTGCT GACACCGGCC 540
 TTCCACTTGT ACATCTGTAA GCCTTACATG AAGATCTTCA ACCAGAGCGC TGACATTATG 600
 CATGCTAAAT GCGGCACTCT GGCAGAGGGC TCAGCGGTCT CCCTTGATAT GTTTGAGCAT 660
 ATCAGCCTCA TGACCTGTGA CAGTCTTCAG AAATGTGTCT TCAGCTACAA CAGCAACTGC 720
 CAAGAGAAGA TGAGTGATTA TATCTCCGCT ATCATTTAAG TGAGCGCTCT GTCTGTCCGG 780
 75 CGCCAGTATC GCTTGACCCA CTACCTCGAC TTCACTTACT ACGCTCGGC GGATGGGCGG 840
 AGGTTCCGCG AGGCTGTGA CATGGTGCAC CACTTCACCA CTGAAGTCAT CCAGGAACGG 900
 CCGCGGCGAC TGGCTCAGCA GGGGCGGAG GCTTGGCTTA AGGCCAAGCA GGGGAAGACC 960
 TTGACTTTA TTGATGTGCT GCTCCTGGCC AGGAGTGAAG ATGGAAGGA ACTGTGAGAC 1020
 GAGGATATCC GAGCCGAAGC AGACACCTTC ATGTTTGAAG GTCACGACAC AACATCCAGT 1080
 80 GGGATCTCTT GGATGCTGTT CAATTGGCA AAGTATCCGG AATACCAGGA GAAATGCGGA 1140
 GAAGAGATTG AGGAAGTCA GAAAGGCCGG GAGCTGGAGG AGCTGGAGTG GGAOGATCTG 1200
 ACTCAGCTGC CCTTTACAC TATGTGCATT AAGGAGAGCC TGCGCCAGTA CCCACCTGTC 1260
 ACTCTTGTCT CTGCGCAATG CACGGAGGAC ATCAAGCTCC CAGATGGGCG CATCATCCCC 1320
 AAAGGAATCA TCTGCTTGGT CAGCATCTAT GGAACCCACC ACAACCCACC AGTGTGGCCT 1380
 GACTCCAAGG TGTACAACCC CTACCGCTTT GACCCGACCA ACCCAGACGA GCGCTCTCCA 1440

CTGGCCTATG TGCCCTTCTC TGCAGGACCC AGGAATTGCA TCGGACAGAG CTTCGCCATG 1500
 GCGAGTTTC GCGTGGTTGT GGCCTAACA CTGCTACGTT TCCGCCTGAG CGTGGACCGA 1560
 ACGCGCAAGG TGCCGCGGAA GCGGAGCTC ATACTGCGCA CGGAGAACGG GCTCTGGCTC 1620
 AAGGTGAGGC CGCTGCCTCC GCGGGCCTGA

Seq ID NO: 167 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 MPPLPSRMSR GPSLVTGRML PITDRLLHLL GLEKTAFRY AVSTLLLPFL FPLFRLLLRP 60
 LRLCRSFYIT CRRLRCPQP PRRNWLLGHL GMYLPNEAGL QDEKKVLDNM HHVLLVWMGP 120
 VLPDLLLVHP DYIKPLLAGS AAIAPKDDLF YGFLKPWLG DGLLSKGDW SRHRLRLTPA 180
 PHFDILKPYM KIFNQSADIM HAKWRHLAEG SAVSLDMFEH ISLMTLDSLQ KCVFSYNSNC 240
 QEKMSDYISA IELSALSVR RQYRLHHYLD FIYYSADGR RFRQACDMVH HPTTEVIQER 300
 RRALRQQGA AWLKAQGGKT LDFIDVLLLA RDEDGKELSD EDIRAEADTF MPEGHDTTSS 360
 GISWMLFNLA KYPBYQSKCR EEIQEVMKGR ELEELEWDDL TQLPFTTMC I KESLRQYPPV 420
 TLVSRQCTED IKLPDGR IIP KGIICLVSIY GTHNPTVWP DSKVYNPYRF DFDNPPQRRSP 480
 LAYVPSAGP RNCIGQSFAM AELRVVVALT LLRFRLSVDR TRKVRKRP EL ILRTENGLWL 540
 KVEFLPFRA

Seq ID NO: 168 DNA sequence

Nucleic Acid Accession #: AK058088.1

Coding sequence: 252..1772

1 11 21 31 41 51
 AGGAAACCAA GGCAAGCTCC CCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60
 GCCCCAGATG TGTAGAGGCG TTCCAGGCTT CAGGCTCAGA AGGCCGCCCC AGCTCTCTCTG 120
 TAACTCAGAG CGGAGTGTGA TGGGAGTTCC TCCACTCAGC ACACCTCCCC TGTAAACACG 180
 CCTGTGGTGG GCAAAAGGGC TTTGGAACGG TTGCTTGTCT TTTCTCTCCT CGGTAATTTC 240
 CACTTTCATT CATGATAATG TCGAACACGC ACAAGGCTCG GCTGGAAACG CGGGTCACTG 300
 GCTCAACCAA CCGGTGGGCT TTGCCCAAAC AGCCTTTCTC TGGGGACCTG CTCTCACTTT 360
 CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420
 TATGCTATTC ACAAAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAAG GACATCCAAA 480
 GTGGGGAAGC AGATGTGATT CTCGAGTGCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540
 GGCTTTTTCG GTCTGAGACC TTGGCCAAAG TCTACCTGAA AGCCCTGGCG CAGGGCACC 600
 CACACCCCTT GAGGAGCTG GAGGAGCTTC TCGAGCTCA ATCACTAAG AAGACCAAG 660
 AAAAAATCCC TGCAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720
 AAGTCGCTCT GAGCAAGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACCTGG 780
 AAGACCTACT GGGAGTGCTG GCTCCGCCCC ACATCCTCCA GTTCAGTGGC CTGTTTCAAA 840
 GGTGCGTGGA TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900
 CGGCTGCATA GGTCAAGGAA GAGCAGCTCA CCACCGGCTG CGAAGAGTGG CTGGAATGA 960
 ACTTGTGTTC TCTAGGGGGG ACAGAGATCC ACCTCCACAA AATCCACAG GACCTGCTCC 1020
 ACAAGTGTCT GAGTCCCTCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080
 TGCTTTTGTG GGTCTTCTTG CAACTGAACT ACAAGATTCA GGCAATTCCG ACTTATGAAA 1140
 CCGTGATGAC ATTTTAAAG AGCTTTCCTG AGAACTGTGT CTCTCTGAGC CGGGACATAG 1200
 GAGGAGCTT GAGGCGCTCT TTCTCTGCT TGCCTCTGCA CGGCATCACC AAAGGCAAGG 1260
 ATCTGAGAGT GCTCGGCGAC CTTAACTTCT TCCAGAGTCC ATGGCTCGAG CAGGTTACAG 1320
 TCAACCATTA CCAAGCACTG GAGAATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380
 CCCAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAACCTAT TCGAAAACGA 1440
 TTGCTCTATA TGGATTCTTC TTTAAGATAA AGGGACTCAA ACATGATACT ACCTCTTATA 1500
 GTTTTACAT GCAGAGATAA AAGCACACAG ACCTGGAATC TCCCTCTGCG GTCTACGAGC 1560
 ACAACCAAGT CAGCTCGCA GCGGCAAGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620
 TGGTTGACCG CAAGTGGCAG GAGTTCAGGA CAAACAGAT CAAGCAGAAG TTTGGGTGTA 1680
 CCACGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAAC TGTGGGCATC CCAATCTATG 1740
 TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGAAATC ATGGGATTTT 1800
 CCCCCACTG GTCTGCATAA AAGAAATAA AATGACATAA AAGGGAGC

Seq ID NO: 169 Protein sequence

Protein Accession #: BAB71658.1

1 11 21 31 41 51
 MIMSNTHKAR LERRVTGSTN RWRLPKPPPS GDLLSLQSMC KALSIDPEEA LRNPDRLCIS 60
 QIQKFFPFENF KNKDIOGSEA DVILECLGPK WELHQPRLFQ SETLAKLYLK ALAQGTTHPL 120
 RELEELLRAQ SPKKTKEKSP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180
 GVLASAHILQ FSGLFQRCDV VMIA RLKPST IKKPYEAGCK YKEEQLTTCG EKWLEMLNVP 240
 LGGTQIHLHK IPQDLLHLKVL KSPRLFTFSE FHLKTMLLW VFLQLNYKIQ AIPTYETVMT 300
 FFKSFPENCCL FLORDIGRSL RPLFLCLRLH GITKGDLEV LRHLNFPFES WLDQVTVNHV 360
 HALENGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFFKIKGLK HDTTSYSFYM 420
 QRIKHTDLES PSAYYEHNV SLRAARLVKY EIRAEALVDG KWQEPRTNQI KQKFLGTTSS 480
 KSETLKIQT VGIPYVSPA PIPPAS

Seq ID NO: 170 DNA sequence

Nucleic Acid Accession #: NM_007000.1

Coding sequence: 1...777

1 11 21 31 41 51
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 GTTGTGGGCA ATATCATTAT TCTGCTGTCA GGCCTGTCCC TGTTTGCTGA GACCATATGG 120
 GTGACAGCCG ACCAGTACCG TGTATACCCA CTGATGGGAG TCTCAGGCAA GGATGACGTC 180
 TTGCTGGTGG CCTGGATTGC CATCTTCTGC GGCTTCTCCT TCTTCATGGT AGCCAGTTT 240

5
10
GGTGTGGGTG COGCACTCTG COGCGCGCGG TCCATGGTCC TCACGTACCT GGTGCTCATG 300
CTCATGTCTT ACATCTTGA GTGCGCTTCC TGCATCAGT CCTACACCCA CCGTGACTAC 360
ATGGTGTCCA ACCCATCCCT GATCACCAG CAGATGCTGA CCTTCTACAG CGGGACACC 420
GACCAGGGCC AGGAGCTGAC COGCTCTGG GACCGGTCA TGATTGAGCA AGAATGCTGT 480
GGCACATCTG GTCCCATGGA CTGGGTGAAC TTCAGTCACT CCTTCGGGC GGCACTCCG 540
GAGGTGGTGT TCCCTGGCC CCACTGTGC TGTGCGCGA CGGAAACTT CATCCCCCTC 600
AACGAGGAGG GCTGCGCTT GGGGCACATG GACTACCTGT TCACCAAGGG CTGCTTCGAA 660
CACATCGGCC ACGCCATCGA CAGCTACAG TGGGTATCT CGTGGTTTGG GTTTGCCATC 720
CTGATGTGGA CGCTCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGA

Seq ID NO: 171 Protein sequence
Protein Accession #: NP_008931.1

15
20
1 11 21 31 41 51
MASAAAAEAE KGSFVVVGLL VVGNIIILLS GLSLPASTIW VTADQYRVYP LMGVSGKDDV 60
PAGAWIAIPC GFSFPMVASP GVGAALCRRR SMLVTLVLM LIVYIFECAS CITSYTHRDY 120
MVSNPSLITK QMLTFYSADT DQGQELTRLW DRVMIEQECG GTSGPMDWVN PTFSAFRAATP 180
EVVFPWPPLC CRRTGNPIPL NEEGCRLGHH DYLPKGCPE HIGHAIDSYT WGISWFGFAI 240
LMTLPLVMLL AMFYPTML

Seq ID NO: 172 DNA sequence
Nucleic Acid Accession #: NM_006760.1
Coding sequence: 39..593

25
30
35
40
1 11 21 31 41 51
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ACATCTCAAG CCTCTCTGGT CTGCTGTCCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCT 180
TGCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGGAGA GCCAATGACA 240
GCAAGTGGT GACGTCCAGC TTTGTGGTGC CTCGTGCGG TGGGCGCAGG GAACTGGTGA 300
GTGTGGTGA CAGTGGTGT GGCCTTCACAG TCACTCGGT CAGTGCATAC CAGGTGACAA 360
ACCTCGTGCC AGGAACCAAA TTCTACATTT CCTACCTAGT GAAGAAGGGG ACAGCCACTG 420
AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGAA TCCATTGGGC 480
TGGGTATGCC CCGCACAGGG GGCATGGTGG TCATCAGGT GCTGCTCTCT GTGCCCATGT 540
TCTGCTGGT GCTGGGCTTC ATCATTGCCC TGGCACTGGG CTCGCGCAAG TAAGGAGGTC 600
TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGGCACA TCCAGCTCCC CAGCCCACT 660
GCTCCAGGC CCCAGGCTG TGGCTCCCTT GGTGCCCTCG CCTCTCTCT CTGCCCTCT 720
CTCCCTAGA GCCCTCTCCT CCTCTGTTC CTCTCCTTGC CCCAGTGCC TCACCTTCCA 780
ACACTCCATT ATTCTCTCA CCCCACTCCT GTCAGAGTTG ACTTTCCTCC CATTTTACCA 840
CTTTAAACAC CCCCATACA ATTCGCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900
GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

45
Seq ID NO: 173 Protein sequence
Protein Accession #: NP_006751.1

50
1 11 21 31 41 51
MAPLLPIRTL PLILILLALL SPGAADPNIS SLSGLLSPAL TESLLVALPP CHLTGGNATL 60
MVRRANDSKV VTSFVVPPC RRRRELVSUV DSGAGFTVTR LSAYQVNLV PGTKFYISYL 120
VKKGTAESS REIPMSTLPR RNMESIGLGM ARTGMVVIT VLLSVAMPLL VLGFILALAL 180
GSRK

55
Seq ID NO: 174 DNA sequence
Nucleic Acid Accession #: Bos sequence
Coding sequence: 1..2733

60
65
70
75
80
1 11 21 31 41 51
ATGAAAGTTG GAGTCTGTG GCTCATTCTT TTCTTCACT TCACTGACGG CCACGGTGGC 60
TTCCTGGGGA AAAATGATGG CATCAAAACA AAAAAAGAAC TCATTGTGAA TAAGAAAAAA 120
CATCTAGGCC CAGTCGAAGA ATATCAGCTG CTGCTTCAGG TGACCTATAG AGATTCCAAG 180
GAGAAAGAG ATTTGAGAAA TTTTCTGAAG CTCTGAAGC CTCCATTATT ATGGTCACAT 240
GGGCTAATTA GAATTATCAG AGCAAGGCT ACCACAGACT GCAACAGCCT GAATGGAGTC 300
CTGCAGTGA CCTGTGAAGA CAGCTACACC TGGTTTCCTC CCTCATGCCT TGATCCCCAG 360
AACTGTCTACC TTCACAGGC TGGAGCACTC CCAAGCTGTG AATGTCACTT CAACAACCTC 420
AGCCAGAGTG TCAATTTCTG TGAGAGAACA AAGATTGGG GCACTTTCAA AATTAATGAA 480
AGGTTTACAA ATGACCTTTT GAATTCTCT TCTGCTATAT ACTCCAAATA TGCAAATGGA 540
ATTGAAATTC AACTTAAAA AGCATATGAA AGAATTCAG GTTTTGAGTC GGTTCAGGTC 600
ACCCAATTC GAAATGGAAG CATCGTTGCT GGGTATGAAG TTGTTGGCTC CAGCAGTGCA 660
TCTGAACTGC TGTGAGCCAT TGAACATGTT GCGAGAAGG CTAAGACAGC CCTTCACAAG 720
CTGTTTCCAT TAGAAGACGG CTCCTTCAGA GTGTTCCGAA AAGCCAGTG TAATGACATT 780
GTCTTTGGAT TTGGGTCCAA GGAATGATGA TATACCTTGC CCGTCAGCAG TGGCTACAGG 840
GGAAACATCA CAGCCAAGTG TGAGTCTCTT GGGTGGCAGG TCATCAGGGA GACTTGTGTG 900
CTCTCTCTGC TTGAAGAACT GAACAAGAAT TTCAGTATGA TTGTAGGCAA TGCCACTGAG 960
CGAGCTGTGT CATCTTGTG GCAAAATCTT TCTGTCTCA TCGGCAAAA CCATCAACCC 1020
ACAGTGGGGA ATCTGGCTTC GGTGGTGTG ATTCTGAGCA ATATTTCATC TCTGTCACTG 1080
GCCAGCCATT TCAGGGTGT CAAATCAACA ATGGAGGATG TCATCAGTAT AGCTGACAA 1140
ATCCTTAATT CAGCCTCAGT AACCACTGG ACAGTCTTAC TGCGGGAAGA AAAGTATGCC 1200
AGCTCAGGCT TACTAGAGAC ATTAGAAAAC ATCAGCACTC TGGTGCCTCC GACAGCTCTT 1260
CCTCTGAATT TTTCTCGGAA ATTCATTGAC TGGAAAGGGA TTCCAGTGAA CAAAGGCCAA 1320
CTCAAAAGGG GTTACAGCTA TCAGATTAAA ATGTGTCCCC AAAATACATC TATTCCCATC 1380
AGAGGCCGTG TGTTAATTGG GTCAGACCAA TTCCAGAGAT CCCTCCAGA AACTATTATC 1440

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Seq ID NO: 175 Protein sequence
Protein Accession #: Eos sequence

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Nucleic Acid Accession #: AB035089.1
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 TCAATGGAT TTGCTGGCA GGCACCTGAA GATATTAGTC TAAATCTCAG AAACAGATAA 11280
 TGATCTAAG CTTAAATTT GTGATATTCA ATATAAATAC TTTAGAGTCA TTGGGATAAA 11340
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 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTTACTCC CATAGATTCT 11520
 TCCC

Seq ID NO: 177 Protein sequence
 Protein Accession #: BAB21525.1

1 11 21 31 41 51
 | | | | |
 MNSLSEANTK FMPDLFQQFR KSKENNIFYS PISITSALGM VLLGAKONTA QQISKVLHFD 60
 QVTENTTEKA ATYHVDNRSG VHHQFQKLLT EPNKSTDAYE LKIANKLFG ERTYQFLQEYL 120

5
DAIKFYQTS VESTDFANAP EESRKKINSH VESQTNEKIK NLFPGDTIGN DTTLVLVNAI 180
YFKQWENIF KKEKTEKEEF WPNKNTYKSV QMRQYNSFN FALLEDVQAK VLEIPYKSKD 240
LSMIVLLPNE IDGLQKLEEK LTAEKLMEMT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
TMGMVNIFNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VAAAAATAVV VVELSSPSTN 360
EFPCCNHPFL PPIRQNKINS ILFYGRFSSP

Seq ID NO: 178 DNA sequence

Nucleic Acid Accession #: NM_001910.1

Coding sequence: 50..1240

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15 GCCCTCAGG AGGCATCOGT CCCTCAAGAA GAAGCTCGGG GCA CGGAGCC AGCTCTCTGA 180
GTTCTGGAAA TCCATAAAT TGGACATGAT CCAGTTCCACC GAGTCTGCT CAATGGACCA 240
GAGTGGCAAG GAACCCCTCA TCACTACTT GGATATGGAA TACTTCGGCA CTATCTCCAT 300
TGGCTCCCCA CCACAGAACT TCACTGTCA CTTCGACACT GGCTCCTCCA ACCTCTGGGT 360
20 CCCCTCTGTG TACTGCACTA GCCAGCCTG CAAGAGCCAC AGCAGTTTC AGCTTCCCA 420
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GTCCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGGA CTAACCGTGG TTGGCCAGCA 540
GTTTGGAGAA AGTGTACAG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT 600
TCTGGGCGTG GGATACCCCT CCTTGGCTGT GGGAGGAGTG ACTCCAGTAT TTGACAACAT 660
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25 AGGTGGTGGG GGGAGCGAGC TGATTTTGG AGGCTACGAC CACTCCCAT TCTCTGGGAG 780
CCTGAATTGG GTCCAGTCA CCAAGCAAGC TTA CTGGCAG ATTGCACTGG ATAACATCCA 840
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TTCCCTCATC ACTGGCCCTT CCGACAAGAT TAAGCAGCTG CAAAACGCCA TTGGGGCAGC 960
30 CCCCGTGGAT TGAGCAATAT CTGTGGAGTG TGCCAAACCTT AACGTCATGC CGGATGTAC 1020
CTTCACCAAT AACGGAGTCC CCTATACCTT CAGCCCAACT GCCTACACCC TACTGGACTT 1080
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45 TTGAAATGCC GAGGTGTCTT TTGACATGTT TCTCTGAACT TATCTTCTCT ATAAAATGTT 1920
TGAAATCCC GAGGTGTCTT TTGACATGTT TCTCTGAACT TATCTTCTCT ATAAAATGTT 1980
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CTTGTTCATC CCTGTACGGA GGCAGATAAT GCTGGTGCCT CTCTATTGTT AATGTTAAGA 2100
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Seq ID NO: 179 Protein sequence

Protein Accession #: NP_001901.1

55 1 11 21 31 41 51
MKTLLLLLLV LLELGEAQGS LHRVPLRRHP SLKKKLRRAS QLSEFWKSHN LDMIQFTESC 60
SMDQSAKEPL INYLDMEYFG TISIGSPPON FTVIFDTGSS NLWVPSVYCT SPACKTHSRF 120
QPSQSSTYSQ PQQSFSIQYG TGSLSGIIGA DQVSVEGLTV VQQQFGESVT EPGQTTPVDAE 180
FDGLLGLGYP SLAVGVGTFV FDMNMAQNLV DLFMFSVYMS SNPEGGAGSE LIFGGYDHSR 240
60 PSSLNMPVP TRQAYNQIAL DNIQVGGTVM FCSEGCQAIV DTGSLITGP SDKIKQLQNA 300
IGAAFPVDGEY AVECANLNMV FVTFPTINGV PYTLSTPATY LLDFVDGMQF CSSGFQGLDI 360
HPPAGPLWIL GDVPRIQFYS VFDRGNRNVG LAPAVP

Seq ID NO: 180 DNA sequence

Nucleic Acid Accession #: NM_018058.1

Coding sequence: 319..1575

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70 TACACCGACA AGTTGTTCAA GTTCCGCAAT AACCGGTGGG AAGACATCCT GAGCGATGAG 180
GTCAACGTGG CCCGTGGTGT GGCCAGCCTC TTTGCGGGAC GCTCTGTGGC CTGTGTGGAC 240
AGAAAGGGCT CTGAGCGCTA CTCTATCTAC ATTGCCAATT ACGCCCTACG TAATGTGGGC 300
75 CCTGATGCCC TCATTGAAAT GGACCCCTGAG GGCAGTGACC TCTCCCGGGG CATCTGGCG 360
CTCAGAGATG TGCTGTCTGA GGCTGGGGTC AGCAATATA CAGGGGGCCG AGGCCTCAGC 420
GTGGGCCCCA TCCCTCAGAG CAGTGCCTCG GATATCTTCT GCGACATGA GAATGGCCCT 480
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GTGGACGACC CCCACCGACA TGGGCGAGGT GTGCGCTTGG CTGACTTCAA COGTGATGTC 600
80 AAGTGGACA TCGTCTATGG CAACGTGAAT GGCOCOCACC GCCTCTATCT GCAATGAGC 660
ACCCATGGGA AGGTCCGCTT CCGGGACATC GCCTCACCCA AGTCTCCAT GCCTCCCTCT 720
TCCGACAGG TCATCACCGC GACCTTTGAC AATGACGAG AGCTGGAGAT CTCTCTCAAC 780
AACATTGCTT ACCGAGCTC CTCAGCCAAC CGCCTCTTCC GGTTCATCG TAGAGAGCAC 840
GGAGACCCCT TCATCGAGGA GCTCAATCCC GCGCAAGCCT TGGAGCTGA GGGCCGGGGC 900
ACAGGGGGTG TGTGACCGCA CTTGACCGGA GACGGGATGC TGGACCTCAT CTGTGCCAT 960

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GGAGAGTCCA TGGCTCAGCC GCTGTCCGTC TTCCGGGGCA ATCAGGGGCTT CAACAACAAC 1020
TGGCTCGCAG TGGTGCCACG CACCCGSGTT GGGGCTTTTG CCAGGGGAGC TAAGGTCTGTG 1080
CTCTACACCA AGAAGAGTGG GGGCCACCTG AGGATCATCG ACGGGGGCTC AGGCTACCTG 1140
TGTGAGATGG AGCCCGTGGC ACACCTTGGC CTGGGGAAAG ATGAAGCCAG CAGTGTGGAG 1200
GTGACGTGGC CAGATGGCAA GATGGTGAGC CGGAACGTGG CCAGCGGGGA GATGAACCTA 1260
GTGCTGGAGA TCCTCTACCC CCGGGATGAG GACACACTTC AGGACCCAGC CCACTGGAG 1320
ACACCAATGA ATGCATCCAG TTCCCAITCG TGTGCCCTCG AGACAAGCCC GTATGTGTCA 1380
ACACCTATGG AAGCTACAGG TGCCGGACCA ACAAGAAGTG CAGTCGGGGC TAGGAGCCCA 1440
ACGAGGATGG CACAGCCTGC GTGGGGACTC TCGGCCAGTC ACCGGGCCCC CGCCCCACCA 1500
CCCCACCGC TGCTGTGCCC ACTGCGCGTG CTGTGCGCGC TGCTGGAGCT GCCACTGTCTG 1560
CACCGGCTCT CGTAGATGGA GATCTCAATC TGGGGTCGGT GGTAAAGGAG AGCTGCGAGC 1620
CCAGCTGCTG AGCAGGGGGT GGACATGAAC CAGCGGATGG AGTCCAGCAG GGGAGTGGGA 1680
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CTGTGCTGGG CACATAGCTG TGATCAGCAG AGACAGGGTC GTCGCCCTGA TGGCGCTTAC 1860
ATTCCAGTGG GTCTAATGAC CATATCTTAG GACACAGATG TGCCAGGGA GGTGGTGTCA 1920
CTGCACAGGA AGTATGAGCA CTTTAGTGTG CTGAGTTCAA ATCTGTGATC AGGAACTCAC 1980
AAAGCTATGT GACCTTACAC CAGTCACTTA ACTTGTAGC CATCCATTAT CGCATCTGCA 2040
AAATGGGGAT TAAGAAATAGA ATCTTGGGGT TAGTGTGGAG ATTAGATTAA ATGTATGTAA 2100
GACACTTGGC ACAAAACCTG GCACATAGTA AAGGCTCAAT AAAACAAGT GCCTCTCACT 2160
GGGCTTTGTC AACACGTG

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Seq ID NO: 181 Protein sequence
Protein Accession #: NP_060528.1

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1 11 21 31 41 51
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RGDGTFFVDA ASAGVDDPHQ HGRGVALADF NRDGKVDIVY GNWNGPHERLY LQMSTHGKVR 120
FRDIASPKFS MSPSVRTVIT ADFDNDQBLE IFPMNIAYRS SSANRLFRVI RREHGDPLIE 180
ELNPGDALEP EGRGTGGVVT DFDGDGMLDL ILSHGESMAQ PLSVFRGNQG FNNNWLRVVP 240
RTRVGAFARG AKVVLTKKS GAHLRIIDGG SGYLCMEFV AHFLGKDER SSVVETWPDG 300
KMSVRNVASG EWSVLEILY PRDETLQDP APLETPMNAS SSHSCALET S PYVSTPMEAT 360
GAGPTRSAVG ATSPTRMAQP AWGLSASHRA PAPPPPLLLL PLPLLLPLLE LPLLHRS

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Seq ID NO: 182 DNA sequence
Nucleic Acid Accession #: AJ279016
Coding sequence: 1..1962

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1 11 21 31 41 51
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TTTGAGATCG TCGTGGCGGG GTACAATGGA CCCAACCTGG TTCTGAAGTA TGACCGGGCC 240
CAGAAGCGCG TGGTGAACAT CGCGGTGGAT GAGCGCAGCT CACCCTACTA CGCGCTGGCG 300
GACCGGCAAG GGAACGCCAT CGGGGTACA GCCTCGGACA TOGACGGGA CGGCCGGGAG 360
GAGATCTACT TCCTCAACAC CAATAATGCC TTCTCGGGGG TGGCCAAGTA CACCGACAAG 420
TTGTTCAGGT TCCGCAATAA CCGGTGGGAA GACATCCTGA GCGATGAGGT CAACGTGGCC 480
CGTGGTGTGG CCAGCCTCTT TGCCGGACGC TCTGTGGCCT GTGTGGACAG AAAGGGCTCT 540
GGACGCTACT CTATCTACAT TGCCAATTAC GCCTACGGTA ATGTGGGCCC TGATGCCCTC 600
ATTGAATGG ACCCTGAGGC CAGTGAOCTC TCCCGGGGCA TTCTGGCGCT CAGAGATGTG 660
GCTGCTGAGG CTGGGGTCAG CAAATATACA GGGGGCCGAG GCGTCAGCGT GGGCCCCATC 720
CTCAGCAGCA GTGCTCTGGA TATCTCTGTC GACAATGAGA ATGGGCCTAA CTTCCTTTTC 780
CACAAACCGG GCGATGGCAC CTTTGTGGAC GCTGCGGCCA GTGCTGTGTG GGAAGACCCC 840
CACCAGCATG GCGGAGGTGT CGCCCTGGCT GACTTCAACC GTGATGGCAA AGTGGACATC 900
GTCTATGGCA ATCGGAATGG CCCCCACGTC CTCTATCTGC AAATGAGCAC CCAATGGGAG 960
GTCCGCTTCC GGGACATGCG CTCACCAAG TTCTCCATGC CCTCCCTGT CCGCACGCTC 1020
ATCACGCGCG ACTTTGACAA TGACCCAGGAG CTGGAGATCT TCTTCAACAA CATTGCTTAC 1080
CGCAGCTCCT CAGCCAACCG CCTCTTCCGC GTCATCGTA GAGAGCACGG AGACCCCTC 1140
ATCGAGGAGC TCAATCCCGG CGAGCGCTTG GAGCCTGAGG GCGCGGGCAC AGGGGGTGTG 1200
GTGACCGACT TCGACGGAGA CCGGATGCTG GACCTCATCT TGTCCCATGG AGAGTCCATG 1260
GCTCAGCGCG TGTCCGTCTT CCGGGGCAAT CAGGGCTTCA ACAACAACCT GCTGCGAGTG 1320
GTGCCACGCA CCGGTTTGGG GGCTTTGGCC AGGGGAGCTA AGGTGCTGCT CTACACCAAG 1380
AAGAGTGGGG CCCACCTGAG GATCATCGAC GGGGGCTCAG GCTACCTGTG TGAGATGGAG 1440
CCCGTGGCAC ACTTTGGCCT GGGGAAGGAT GAAGCCAGCA GTGTGGAGGT GACGTGGCCA 1500
GATGGCAAGA TGGTGAGCGG GAACTGGGCC AGCGGGGAGA TGAATCAGT GCTGGAGATC 1560
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TTCTCCAGC AGGAATAATGG CCAITGCATG GACACCAATG AATGCATCCA GTTCCCATTC 1680
GTGTGCCCTC GAGACAAGCC CGTATGTGTC AACACCTATG GAAGCTACAG GTGCCGGACC 1740
AACAGAAGT GCAGTCGGGG CTACGAGCCC AACGAGGATG GCACAGCCTG CGTGGGGACT 1800
CTCGGCAAGT CACCGGGGCC ACCGCCACCC ACTGCTGCTG CACTGCGCTG 1860
GCTGCTGCCG CTGCTGGAGC TGCCACTGCT GCACCGGCTC TCGTAGATGG AGATCTCAAT 1920
CTGGGGTCGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
CCAGCGGATG GAGTCCAGCA GGGAGTGGG AAAGTGGGCT TGTGCTGCTG CCTAGACAGT 2040
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CAGACAGGGT CGCTGCCCTG ATGGCGCTTA CATTCCAGTG GGTCTAATGA CCAATCTTCA 2220
GGACACAGAT GTGCCCAGGG AGGTGGTGTG ACTGCACAGG AAGTATGAGG ACTTTAGTGT 2280
CCTGAGTTCA AATCCTGATT CAGGAACCTA CAAAGCTATG TGACCTTACA CCACTCACTT 2340
AACTTGTTAG CCATCCATTA TCGCATCTGC AAAATGGGGA TTAAGAATAG AATCTTGGGG 2400
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Seq ID NO: 183 Protein sequence
Protein Accession #: CAC08451

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5      1      11      21      31      41      51
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EIIYFLATNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180
GRYSIIYIANY AYGVNGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
10     LSSASDIIFC DNENGNFLP HNRGDGTFPD AAASAGVDDP HQHGRGVALA DFNRDGKVDI 300
VYGNWNGPHR LYLQMSHGHK VRFRDIASPK FMPSPVRTV ITADFDNDQE LEIFFNNIAY 360
RSSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDFDGDGML DLILSHGESM 420
AQPLSVFRGN QGFNNNWLVR VPRTRFGAFA RGAKVVLYTK KSGAHLRIID GSGGYLCEME 480
PVAHFGLGKD EASSVEVWTP DGMVSRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
15     FSQQENGHCN DTNECICFPF VCPDRKPVCV NTYGSYRCRT NKKCSRGEYEP NEDGTACVGT 600
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Seq ID NO: 184 DNA sequence
Nucleic Acid Accession #: FGENESH1
Coding sequence: 1..4794

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GTCTGAAGT ATGACCGGGC CCAGAAGCGG CTGGTGAACA TCGCGTGA TGAGCGCAGC 180
TCACCTACT ACGCCGTGCG GGACCGGCAG GGAACGCCA TCGGGTCA AGCCTGCGAC 240
ATCGACGGG AGCGCGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTTCGGGGC 300
CACAGCAGT AGGTCAAGT CCCTCTGGG CTCACAGAA ACAGGCTGT GCTGAAGCT 360
30     CCACCTACAA CCCCTGCAAG CCTCTGGGT CTGCTCCAC TCAGCGGAAG GGACTTTTC 420
TCTCTCTGG GTCAAGCTTC TCGGACAGC AGGCAGGAG AGAGGTGCC GGTTCCTGC 480
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CTGAGCGAT AGGTCAAGT GGCCCGTGG GTGCCAGCC TCTTTCGGG ACGCTCTGT 660
35     GCGCTGTGG ACAGAAAGG CTCTGGAAG TACTCTATC ACATTGCCA TTAAGCCTAC 720
GGTAATGTG GCCTGTATG CCTCATTGA ATGGACCTG AGGCCAGTA CCTCTCCGG 780
GGCATTCTG CGCTCAGAGA TGTGGCTGT GAGGCTGGG TCAGCAATA TACAGAAGC 840
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GGCGCTTCT CAGCCACCC TTTCCCTGCC CGCAAGCCC CCAACACTA CCTGTAGCC 1200
45     CCGCTTGTCA CCGCATTAAT GACACATGGA CGTCTGGCT GAAACTAGC CCGGAGTGT 1260
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60     TTCCACAA CCGGCGATG CACCTTGTG GACGCTGCG CCACTGTGA ACGTGTGTA 2160
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GTCCAATCAC TACCACAGAA AGGGGCTACG GGCTCCAATC ACTACCAGGA AAAGGGGCTA 3720
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GCTATGGGGT CCAATCACTA CCAGGAAAAG GGGCTACGGG CTCCAATCAC TACCAGGAAA 3840
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Seq ID NO: 185 Protein sequence
Protein Accession #: PGENESHH

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1 11 21 31 41 51
MACPGGLPAR CSGWMGLGGP SGSSPASPPH SSSRYNGPNL VLKYDRAQKR LVNIAVDERS 60
SPYYALRDRQ GNAIGVTACD IDGDGREBIY FLNTNNAFSG HSSSAQVPSG LHRNRPVLKP 120
PPTTFAGLLG LPPLSQDRFS SSLGQASPDF RQGERVPVPC CRGGLRPTHE PRPFLLRPKS 180
GVATYTDKLF KFRNNRWEDI LSDEVNVARG VASLFAGRSV ACVDRKSGSR YSIYIANYAS 240
GNVGFDALIE MDPEASDLSR GILALRDVAA EAGVSKYTEG FSHTASPSIG EISGRTEERE 300
GGDPFEEADEE HSGDGSSTQL CRLGWKDGQF KEEAALVEE QREAGAAGVP RGRVRTALQT 360
SKSHLADKNR PGPPCYYSV APSPAHPFPA RQAPQHYFVA PLVTQLMTHG RLAKGLARSV 420
PHPRAPGMDP KCKGRHAEPG LMAEALGAWP ALSTTVVPGG LRSWEESRQK GQAMSRCLAR 480
ELGGFWQAT QHLPARELYD LGEPPILQRT DGDPRRRRDS PKVTQECHLV ATMPALGGLE 540
GPGRVAIGREI GRETGAVGRP LSHPLVNFPP SCLRLPEAGT VPGAALPGNP GNVVLDMAKA 600
LAWNQMEKEE GKIHGDHEPR FRLRKAREAE FPPGSSEEP LQFPSSGLRGS FVLQVGLGLA 660
SATHCGSMSP LGGRGVSVGP ILSSASDIP CDNENGPNFL FENRGDGTFF DAAASAERRL 720
AFIVHLKYHL CRDPFHSLLCH LABTGSSSSC CPWHARLLQA PHCHGLSMS PTRTGSRFYS 780
FLTQGLASSA HRRLLSLQGS QGAPPCLLAR APCVLGSLIP TAYYIVLWSA IPESLMTHSY 840
LSSSRVNVGV DDPHQHGRGV ALADPNRDGK VDIVYGNWNG PHRLYLQMTS HGKVRFRDIA 900
SPKFSMPSPV RTVITADFDN DQLEIFFN N IAYRSSANR LFRCSILARG SSSLTAGGRN 960
GQGEGLIRIR LGFPQPGGQA KVTGPLMKK QKGRKDEDWA RCGNAGQSL AKSPASAIAG 1020
KKGKNAQSV PRTOAPQDTK PHYHKKGLQG PITTTRKRGY VQSLPGKGAT GSNHYQEKGL 1080
RGPITTRKRG YGVQSLPGKG ATGSNHYQEK GLQGPIITRK RGYGLQSLPG KGATGSNHYH 1140
RKGLRAPITT RKRGYGVQSL PGKATGSNH YQEKGLRGP I TTRKRGYGLQ SLPGKGATGS 1200
NHYQEKGLQG PITTTRKRGY VQSLPGKGAT GSNHYQEKGL RGPITTRKRG YGLQSLPGKE 1260
AMGSNHYQEK GLRAPITTRK RGYGVQSLPG KGATGSNVIR REHGDPLIEB LNPGDALPE 1320
GRGTGGVVD FQDGMGLDI LSHGESMAQP LSVFRGNQGF NNNWLRVVR TRFGAFARGA 1380
KVVLYTKKSA HRLRLIDGGS GYLCEMEPVA HFGLGKDEAS SVEVTWPDGK MVRNVASGE 1440
MNSVLEILYP RDEDTLQDPA PLECGQGPSQ QENGHCMQTN ECIQFPFVCP RDKPVCVNTY 1500
GYSYRCRNKK CSRGYEPNED GTACVGTGLG SRHTMTWKPR PKKELQLSQG ICTPVWSFFL 1560
PQCLLLKRA QLQAAPSTLL QKAPGIPEAQ VYBQDQE

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Seq ID NO: 186 DNA sequence
Nucleic Acid Accession #: NM_000584.1
Coding sequence: 75..374

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65
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75
80

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1 11 21 31 41 51
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CTGCAGCTCT GTGTGAAGGT GCAGTTTTCG CAAGGAGTGC TAAAGAACTT AGATGTCACT 180
GCATAAAGAC ATACTCCAAA CCTTCCACCC CCAAAATTAT CAAAGAACTG AGAGTGATTG 240
AGATGGGACC ACACCTGCGC AACACAGAAA TTATTGTAAA GCTTCTGAT GGAAGAGAGC 300
TCTGTCTGGA CCCCAGGAA AACTGGGTGC AGAGGGTGTG GGAGAAGTTT TTGAAGAGGG 360
CTGAGAAATC ATAAAAATAT TCATTCTCTG TGGTATCCAA GAATCAGTGA AGATGCCAGT 420
GAAACTTCAA GCAAAATCTAC TTCAACACTI CATGTATTGT GTGGGTCTGT TGTAGGGTTG 480
CCAGATGCAA TACAAGATTG CTGGTTAAAT TTGAATTICA GTAAACAATG AATAGTTTIT 540
CATTTGACCA TGAAATATCC AGAACATACT TATATGTAAA GTATTATTTA TTTGAATCTA 600
CAAAAAACAA CAAATAATTT TTAATATATA GGATTTCTCT AGATATTGCA CGGAGAGAATA 660
TACAATATAGC AAAATTTAGC CAAGGGCCAA GAGAATATCC GAACTTTAA TFCAGGAATT 720
GAATGGGTCT GCTAGAAATG GATATTGAA GCATCACATA AAAATGATG GACAATAAAT 780
TTTGCCATAA AGTCAAATTT AGCTGGAATC CCTGGATTTT TTTCTGTATA ATCTGGCAAC 840
CCTAGTCTGC TAGCCAGGAT CCACAAGTCC TTGTTCCACT GTGCGCTGGT TTTCTCTTTA 900
TTTCTAAGTG GAAAAAGTAT TAGCCACCAT CTTACCTCAC AGTGATGTTG TGAGGACATG 960
TGGAGACACT TTAAGTTTIT TCATCATAAC ATAAATTATT TTCAAGTGA ACTTATTAAC 1020
CTATTATTAT TTTATGTATT TATTAAAGCA TCAAAATATT GTGCAAGAA TTTGAAAAAT 1080
AGAAGATGAA TCATTGATTG AATAGTTATA AAGATGTTAT AGTAAATTTA TTTTATTTTA 1140
GATATTAAAT GATGTTTTAT TAGATAAATT TCAATCAGGG TTTTATGATT AAACAAAGAA 1200
ACAAATGGGT ACCAGTTTAA ATTTTCATTT CAGATAAACA ACAAATAATT TTTTAGTATA 1260
AGTACATTAT TGTATTCTCT AAAGTTTATA TTGAATAAC AATCTAGTT TGATACTCCC 1320
AGTCTTGTCA TTGCGAGCTG TGTGGTAGT GCTGTGTTGA ATTAGCGAAT AATGAGTTAG 1380
AACTATTAAA ACAGCCAAAA CTCACAGTCT AATATTAGTA ATTTCTGTCT GGTGAAACT 1440
TGTTTATTAT GTACAAATAG ATTTCTATAA TATTATTATA ATGACTGACT TTTTAAATAC 1500

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AAGCGTTTAT ATTTTAACT TTAAGATGTT TTTATGTGCT CTCAAAATT TTTTACTGT 1560
 TTCTGATTGT ATGGAAATAT AAAAGTAAAT ATGAACATT TAAATATAA TTTGTGTCA 1620
 AAGTAAAAAA AAAAAAAA

5 Seq ID NO: 187 Protein sequence
 Protein Accession #: NP_000575.1

1 11 21 31 41 51
 10 MTSKLAVALL AAFLLISAALC EGAVLPRSAK ELRCQCIKTY SKPFHPKFIK ELRVIESGPH 60
 CANTBIIVKL SDGRELLCLDP KENWVQRVVE KFLKRAENS

15 Seq ID NO: 188 DNA sequence
 Nucleic Acid Accession #: NM_003661.1
 Coding sequence: 1..1152

1 11 21 31 41 51
 20 ATGAGTGCAC TTTTCTTGG TGTGGGAGTG AGGCGAGAGG AAGCTGGAGC GAGGGTGCAA 60
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 GCTGCTGGCA CCATGGACCC AGAGAGCAGT ATCTTTATTG AGGATGCCAT TAAGTATTTC 180
 AAGGAAAAAG TGAGCACACA GAATCTGCTA CTCTGCTGA CTGATAATGA GGCCTGGAAC 240
 GGATTGCTGG CTGCTGCTGA ACTGCCCAGG AATGAGGCAG ATGAGCTCCG TAAAGCTCTG 300
 25 GACRAACCTTG CAGACAAAT GATCATGAAA GACAAAACT GGCACGATAA AGGCCAGCAG 360
 TACAGAACT GGTTCCTGAA AGAGTTTCTT CGGTGAAAA GTGAGCTTGA GGATAACATA 420
 AGAAGGCTCC GTGCCCTTGC AGATGGGGTT CAGAAGGTCC ACAAGGCAC CACCATCGCC 480
 AATGTGGTGT CTGGCTCTCT CAGCATTTCC TCTGGCATCC TGACCCCTGT CGGCATGGGT 540
 CTGGCACCTT TCACAGAGGG AGGCAGCCTT GTACTCTTGG AACCTGGGAT GGAGTTGGGA 600
 30 ATCAGAGCGG CTTTGACCGG GATTACCAGC AGTACCATGG ACTACGAAA GAGTGGTGG 660
 ACACAAGCCC AAGCCCACGA CCGTGTCTATC AAAAGCCTTG ACAATTGAA GGAGGTGAGG 720
 GAGTTTTTGG GTGAGAACAT ATCCAACCTT CTTCCTTAG CTGGCAATAC TTACCAACTC 780
 ACACGAGGCA TTGGGAAGGA CATCCGTGCC CTCAGACGAG CCAGAGCCAA TCTTCAGTCA 840
 GTACCGCATG CCTCAGCCTC ACGCCCCCGG GTCACTGAGC CAATCTCAGC TGAAAGCGGT 900
 35 GAACAGGTGG AGAGGGTTAA TGAACCCAGC ATCCTGGAAA TGAGCAGAGG AGTCAAGCTC 960
 ACGGATGTGG CCCCTGTAAG CTCTTTCTT GTGCTGGATG TAGTCTACCT CGTGTACGAA 1020
 TCAAAGCACT TACATGAGGG GGCAAAGTCA GAGACAGCTG AGGAGCTGAA GAAGGTGGCT 1080
 CAGGAGCTGG AGGAGAAGCT AAACATTTCT AACATAAATT ATAAGATTCT GCAGGCGGAC 1140
 CAGAACTGT GA

40 Seq ID NO: 189 Protein sequence
 Protein Accession #: NP_003652.1

1 11 21 31 41 51
 45 MSALFLGVGV RAEAGARVQ QNVPSGTDTG DPQSKPLGDW AAGTMDPESS IFIEDAIKYP 60
 KERVSQNLIL LLLTDNEAMN GFVAAAELEPR NEADELRKAL DNLRQMIMK DFNWHDKGQQ 120
 YRNWFLKEFP RLKSELEDNI RRLRALADGV QKVHKGTTIA NVVSGSLIS SGILTLVGMG 180
 LAPFTEGGSL VLLSPGMELG ITAALTGITS STMDYGGKMW TQAQADLVI KSLDLKLEVR 240
 EFLGENISNF LSLAGNTYQL TRGIGKDIRA LRRARANLQS VPHASASRPR VTEPIAESG 300
 50 EQVERVNEPS ILEMSRGVKL TDVAPVSFPL VLDVVYLVEY SKHLHEGAKS ETAEBLKRVA 360
 QLEELKLNIL NNNYKILQAD QEL

55 Seq ID NO: 190 DNA sequence
 Nucleic Acid Accession #: NM_014452.1
 Coding sequence: 1..1968

1 11 21 31 41 51
 60 ATGGGGACCT CTCGAGCAG CAGCACCGCC CTGCGCTCCT GCAGCGCAT CGCCCGCGA 60
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 GCTCAGCCAG AACAGAAGGC CTCGAACTCT ATTGGCATAT ACGGCCATGT TGACCGTGCC 180
 ACCGGCKEFP TGCTAACTCT TGACAAAGTG CCAGCAGGAA CCTATGCTC TGAGCATTGT 240
 ACCAACACAA GCCTGCGCGT CTGAGCAGT TGCCCTGTGG GGACCTTTAC CAGGCATGAG 300
 65 AATGGCATAG AGAAATGCCA TGACTGTAGT CAGCCATGCC CATGGCCAAT GATTGAGAAA 360
 TTACCTTGTG TGCCCTTGAC TGACCGAGAA TGCACTTGCC CACCTGSCAT GTTCCAGTCT 420
 AACGCTACCT GTGCCCCCCA TACGGTGTGT CTTGTGGGTT GGGGTGTGCG GAAGAAAGGG 480
 ACAGAGACTG AGGATGTGGT GTGTAAGCAG TGTGCTCGGG GTACCTTCTC AGATGTGCCT 540
 TCTAGTGTGA TGAATGCAA AGCATAACA GACTGTCTGA GTCAGAACCT GGTGTGTATC 600
 70 AAGCCGGGGA CCAAGGAGAC AGACAAOGTC TGTGGCACAC TCCCGTCCCT CTCAGCTCC 660
 ACCTCACCTT CCCCTGGCAC AGCCATCTTT CCAOGCCCTG AGCACATGGA AACCCATGAA 720
 GTCCCTTCTT CCACCTTATG TCCCAAAGGC ATGAATCAAA CAGAAATCAA CTCTTCTGCC 780
 TCTGTAGAC CAAAGGTACT GAGTAGCATC CAGGAAGGGA CAGTCCCTGA CAACACAAGC 840
 TCAGCAAGGG GGAAGGAAGA CGTGAACAAG ACCCTCCCAA ACCTTCAGGT AGTCAACCAAC 900
 75 CAGCAAGGCC CCCACCACAG ACACATCCTG AAGCTGTGTC CGTCCATGGA GGCCACTGGG 960
 GCGAGAAAGT CCAGCACGCC CATCAAGGGC CCCAAGAGGG GACATCCTAG ACAGAACCTA 1020
 CACAAGCATT TTGACATCAA TGAGCAATTG CCTGTGATGA TTGTGCTTTT CCGTCTGCTG 1080
 GTGCTTGTGG TGATTGTGGT GTGCAGTATC CGGAAAAGCT CGAGACTCT GAAAAAGGGG 1140
 CCCCAGCAGG ATCCAGTGC CATTTGTGAA AAGGCAGGGC TGAAGAAATC CATGACTCCA 1200
 80 ACCCAGAACC GGGAGAAATG GATCTACTAC TGCAATGGCC ATGGTATCGA TATCTGTAAG 1260
 CTGTGTAGCAG CCCAAGTGGG AAGCCAGTGG AAAGATATCT ATCAGTTTCT TTGCAATGCC 1320
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 GCAGCTCTGC AGCACTTGAC CATCCGGGGC CCGAGGCGCA GCTTCGCCCA GCTAATFAGC 1440
 GCGCTGCGCC AGCACCGGAG AAACGATGTT GTGGAGAAGA TTGTTGGGCT GATGGAAGAC 1500
 ACCACCCAGC TGGAACTGAA CAACTAGCT CTCCGATGA GCCCGAGCCC GCTTAGCCCG 1560

5 AGCCCCATCC CCAGCCCCAA CGCGAAACTT GAGAATTCOG CTCTCCTGAC GGTGGAGCCT 1620
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 GACTCTACAT CCAGCGGCTC CTCCGCGCTG AGCAGGAACG GTTCTTTTAT TACCAAGAA 1740
 AAGAAGGACA CAGTGTTCOG GCAGGTACGC CTGGAACCCCT GTGACTTGCA GCCTATCTTT 1800
 GATGACATGC TCCACTTTCT AAATCCTGAG GAGCTGCGGG TGATTGAAGA GATTCCCCAG 1860
 GCTGAGGACA AACTAGACOG GCTATTGAA ATTATTGGAG TCAAGAGCA GGAAGCCAGC 1920
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10 Seq ID NO: 191 Protein sequence
 Protein Accession #: NP_055267.1

15 1 11 21 31 41 51
 MGTSPSSSTA LASCRIARR ATATMIAGSL LLLGFLSTTT AQPEQKASNL IGTYRHVDRA 60
 TGOVLTCDKC PAGTYVSEHC TMTSLRVCSS CPVGTPTREH NGIEKCHDCS QPCPWPMEIK 120
 LPCAALTRE CTCPGPMFQS NATCAPHTVC PVGNGVRKKG TETEDVRCKQ CARGTFSDVP 180
 SSVMKCKAYT DCLSNLNVVI KPGTKETDNV CGTLPSFSSS TSPSPGTAIF PRPERMETHE 240
 VPSSTYVFKG MNTSESSSA SVRPKVLSSI QEGTVPDNTS SARGKEDVNK TLPNLQVNVH 300
 QQGFHHRHIL KLLPSMEATG GEKSTPIKG PKRGHPQNL HKHFDINEHL PMMIVLFLLL 360
 20 VLVVIVVCSI RKSRTLLKKG PRQDPSAIVE KAGLKKSMTP TONREKWIYY CNHGIDILK 420
 LVAAQVGSQW KDIIYQLCNA SEREVAAPSN GYTADHERAY AALQHWITRG PEASLAQLIS 480
 ALRQHRRNDV VEKIRGLMED TTQLETDKLA LPMSPSPISP SPIPSFNKL ENSALLTVEP 540
 SPQDKKGFPP VDESEPLLRC DSTSGSSSL SRNGSPITKE KMDTVLRQVR LDPCDLQPIF 600
 25 DDMLEHLEIFE ELRVIEEIPQ AEDKLDRLFE IIGVKSQEAS QTLLEDSVYSH LFDLL

Seq ID NO: 192 DNA sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

30 1 11 21 31 41 51
 GCTCTGCCCA AGCCGAGGCT GCGGGGCGGG CGCCGCGGGG AGGACTGCGG TGCCCGCGGG 60
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 GGAGGGGGGG GCGCCCGGGG CGACTCGGGG GCGGACCGCG GGGCGGAGCT GCGCCCGGTG 180
 35 AGTCCGCGCG AGCCACCTGA GCCCGAGCGG CGGACACCGG TCGCTCTGCG TCTCCGAATG 240
 CTGCGCAGCG CGATGGGCTT GAGGAGCTGG CTCGCGCGCC CATGGGGCGC GCTGCGCGCT 300
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 40 TTGAAAGCTG AACACATCTC CAACACACA GCCCTTCTGC TGAGCAGGGA TGGCAGGACC 480
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 AGCGGAGCTG ACCTGTTCCCT CTGTGGCACA GCAGCCTTCA GCCCATATGT TACCTACATC 720
 45 AACATGGAGA ACTTCACCTT GGCAAGGGAC GAGAAGGGGA ATGTCTCTCT GGAAGATGGC 780
 AAGGGCGGTT GTCCCTTCGA CCCGAATTTC AAGTCCACTG CCCTGGTGGT TGATGGCGAG 840
 CTCTACACTG GAACAGTCAG CAGCTTCCAA GGAATGACC CGGCCATCTC GCGGAGCCAA 900
 AGCCTTCGCG GCTTCAAGAG CGAGAGCTCC CTCAACTGGC TGCAAGAGCC AGCTTTTGTG 960
 GCCTCAGCTT ACATTCCTGA GAGCCTGGGC AGCTTGCAAG GCGATGATGA CAAGATCTAC 1020
 50 TTTTCTCTCT GCGAGACTGG CCAGGAATTT GAGTCTCTTG AGAACACCAT TGTGTCCCGC 1080
 ATTGCCCGCA TCTGCAAGGG CGATGAGGGT GGAGAGCGGG TGCTACAGCA GCGCTGGACC 1140
 TCTTCTCTCA AGGCCAGCT GCTGTGCTCA CGGCCGAGG ATGGCTTCCC CTTCACGCTG 1200
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 GGGGTCTTCA CTTCCAGATG GCACAGGGGA ACTACAGAA GCTCTGCCGT CTGTGTCTTC 1320
 55 ACAATGAAGT ATGTGACAGG AGTCTTCAGC GGCTCTACA AGGAGGTGAA CGGTGAGACA 1380
 CAGCAGTGGT ACACCGTGAC CCACCCCGTG CCCACACCCC GGCTGGAGC GTGCATCAC 1440
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 CCCCAGGCTG GCTACAGCGG GTTGGCTGTA CACCGGTGCC CTGGCTGCA CCAACCTTAC 1620
 60 GATGTCTCTT TCTTGGGCAC TGGTGACGGC CGCTCCACA AGGCAGTGA GGTGGGCCCC 1680
 CCGGTGCACA TCATTGAGGA GCTGCAGATC TTCTCATCGG GACAGCCCGT GCAGAATCTG 1740
 CTCCTGGACA CCCACAGGGG GCTGTGTATG GCGGCTCAG ACTCGGCGT AGTCCAGGTG 1800
 CCCATGGCCA ACTGCAGCCT GTACAGGAGC TGTGGGACT GCCTCTCGC CCGGACCCCC 1860
 TACTTGCTCT GGAGCGGCTC CAGCTGCAAG CAGCTCAGCC TCTACAGCC TCAGCTGGCC 1920
 65 ACCAGGCGGT GGATCCAGGA CATCGAGGGA GCCAGGCCA AGGACCTTTG CAGCGGTCT 1980
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 TGGCTACGCA ACGGGGCCCC GGTCAATGCC TGGGCTCTCT GCCACGTGCT ACCCACTGGG 2160
 GACCTGTGCG TGGTGGGCAC CCAACAGCTG GGGGAGTTC AGTGTGCTC ACTAGAGGAG 2220
 70 GGCTTCCAGC AGCTGGTAGC CAGCTACTGC CCAGAGGTGG TGAGGAGCG GGTGGCAGAC 2280
 CAAACAGATG AAGGTGGCAG TGTACCCGTC ATTATCAGCA CATCGGTGT GAGTGCACCA 2340
 GCTGTGTCGA AGGCCAGCTG GGGTGCAGAC AGGTCTTACT GGAAGGAGTT CCTGGTGTAT 2400
 TGCACTGCTT TGTGCTGCGC CGTGTGCTG CCACTTTTAT TCTTGTCTTA CCGGACCCGG 2460
 AACAGCATGA AAGTCTTCTT GAAGCAGGGG GAATGTGCCA GCGTGCAACC CAAGACCTGC 2520
 75 CCTGTGTGTC TGCCCCCTGA GACCGGCCA CTCACGGGCC TAGGGCCCCC TAGCACCCCG 2580
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 80 TCCCTCCGCG TCTGCTCTTC GTGGAACACG ACCGTGTGTC CCGGCCCTTG GAGGCTTTGG 2880
 GGCAGAGTGG CCTGCTGCTC TCCAGTCAAG TAGCGAAGCT CCTACCAACC AGACACCCAA 2940
 ACAGCCGTGG CCCCAGAGGT CCTGGCCAAA TATGGGGGCC TGCTTAGGTT GGTGGAACAG 3000
 TGCTCCCTAT GTAAACTGAG CCCTTTGTTT AAAAAACAAT TCCAAATGTG AAACCTAGAAT 3060
 GAGAGGGAAG AGATAGCATG GCATGCAGCA CACACGGCTG CTCCAGTTCA TGGCCTCCCA 3120
 GGGGTGCTGG GGATGCATCC AAAGTGTGTT TCTGAGACAG AGTTGGAACC CCTCACCAAC 3180

5 TGGCCTCTTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCCTGTCTC ACTGCAGATT 3240
 CAGGACCAGC TTGGGCTGCG TGGCTTCTGC CTTGCCAGTC AGCCGAGGAT GTAGTTGTGTG 3300
 CTGCGGTGCT CCCACCCTT CAGGACCAG AGGGCTAGGT TGGCACTGCG GCCCTCACC 3360
 GGTCTCGGGC TCGGACCCAA CTCTCGGACC TTTCCAGCCT GTATCAGGCT GTGGCCACAC 3420
 GAGAGGACAG CGCGAGCTCA GGAGAGATT CTGTGACAATG TACGCTCTTC CCTCAGAAT 3480
 CAGGGGAAGAG ACTGTGCGCT GCCTTCTCTC GTTGTGCGT GAGAACCGT GTGCCCCCTC 3540
 CCACCATATC CACCTCGCT CCATCTTGA ACTCAACAC GAGGAACATA CTGCACCTG 3600
 GTCTCTCTCC CAGTCCCGAG TTCACTCTCC ATCCTCACC TTCCTCCACT CTAAGGGATA 3660
 10 TCAACACTGC CCAGCACAGG GGCCTGAAT TTATGTGTT TTTATACATT TTTTAATAAG 3720
 ATGCACTTTA TGTCAATTTT TAATAAAGTC TGAAGAATTA CTGTTT

Seq ID NO: 193 Protein sequence
 Protein Accession #: XP_044533.3

15 1 11 21 31 41 51
 MLRTAMGLRS WLAAPWGALP PRPPLLLLLL LLLLLQPPPP TWALSPRISL PLGSEERPPL 60
 RFBAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLSPL PGSEYQELLW QADAEKQQC 120
 20 SPKGDQPDQ CQNYIKILLP LSGSHLPTCG TAAPSPMCTY INMENFTLAR DEKGNVLLED 180
 GKGRCPPDFN PKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLNWLQDPAF 240
 VASAYIPESL GSLQDDDDKI YPPFSETQGE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKAQLLC SRPDDGPPFN VLQDVPTLSP SPQDWRDTLF YGVPTSQWHR GTTEGSAVCV 360
 FTKMDVQRFV SGLYKEVNRE TQWYTVTHP VTPRPGACI TNSAREKIN SSIQLPDRVL 420
 NFKDHPQMD GQVRSRMLLL QPQARYQRYA VHRVPLHHT YDVLFLGTGD GRLHKAVSVG 480
 25 PRVHIEELQ IFSSGQPVQN LLLDTHRGLL YAAHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCANSSSC KHSLSYQPOL ATRFWIQDIE GASAKDLCSA SSVVSPSFVP TGEKPCBQVQ 600
 FQNTVNTLIA CPLLSNLATR LMLRNGAPVN ASASCHVLT GDLLLVGTQQ LGEPQCSLE 660
 EGPQQLVASV CPEVVEDGVA DQTEGGSSVP VIISTSRVSA PAGGKASWGA DRSYNKEFLV 720
 30 MCTLFVLAVL LPVLFLLYRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNLGLPPST 780
 PLDHRGYQSL SDSPFGSRVF TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSVV

Seq ID NO: 194 DNA sequence
 Nucleic Acid Accession #: NM_022819.1
 Coding sequence: 1..635

35 1 11 21 31 41 51
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 40 AGCTCGGGTA TGAAGAAATT CTTCAACCTG GCATCCTCTG CTGGCAGCGT TCTGTCCACA 180
 GTCACGGCA GCCTGCTCAA CCTGAAGGCC ATGGTGGAGG CCGTCACAGG GAGGAGCGCC 240
 ATCTCTGTCT TGTGTGGCTA CGGTGTCTAC TGTGGGCTGG GGGGCCGTGG CCAGCCCAAG 300
 GATGAGGTGG ACTGGTGTG CCACGCCAC GACTGCTGCT ACCAGGAAT CTTTGACCAA 360
 45 GGCTGTCAAC CCTATGTGGA CCACTATGAT CACACCATCG AGAACCAAC TGAGATAGTC 420
 TGCACTGACC TCAACAAGAC AGAGTGTGAC AAGCAGACAT GCATGTGTGA CAAGAACATG 480
 GTCTGTGGCC TCATGAACCA GACGTACCGA GAGGAGTACC GTGGCTTCTT CAATGTCTAC 540
 TGCCAGGGCC CCACGCCCAA CTGCAGCATC TATGAACCGC CCCCTGAGGA GGTCACTGTC 600
 AGTACCAAT CCCAGCGGCC CCCC GCCCT CCCTAG

Seq ID NO: 195 Protein sequence
 Protein Accession #: NP_073730

55 1 11 21 31 41 51
 MADGAKANPK GPKKKVLDRC FSGWRGPRFG ASCPSTSRSS SLGKKQPTTV AILAGSVLST 60
 AEGSLLMLKA MYBAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDWCCIAH DCCYQELFDQ 120
 GCHPYVDHYD HTIENNTBIV CSDLNKTECD KQTCMCDKNM VLCLMNQTYR ERYRGFLANVY 180
 CQGTPTNCBI YEPPPREVTC SHQSPAPPAP P

Seq ID NO: 196 DNA sequence
 Nucleic Acid Accession #: XM_028196.1
 Coding sequence: 1315..1791

65 1 11 21 31 41 51
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 AGACTGGGGG GCTGTGAGAG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
 70 ATGGCCTGGG CTGGGCCCCC GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCAGG 240
 CTCTTGTGGG CAAAGCAGGG GAGGCCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300
 CTGCTCTCTG GAGCGGTGCG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CTTGGGCTG 360
 GGGTCACCTT AGGCCCATG TAGCACCTG GTTCCCCTGC CTGTAGGTGA CAGGAGCCAG 420
 CCGAGCCAGG TGTGTCTCCT CCCCAGGCCC TAGGCAGGGG GGTACAGGGG CCAGCAGCTG 480
 75 CGCCCGCCCC ACCTTCTCTC CCACCCACAT GCGGAAGGGT GGCAGGCGAG GCAGGTGGAC 540
 GAGTCCAGGC AGCGGCTGAG TCAGTGTGTG TGAATGTTC TGGCGCTCC CAGCTGCACC 600
 CTGCCCCTAC CTGCCAGCAG CTCACCTTCA TCCTCAGGCG CTGGGCGCCT GAGCCCTGCG 660
 CAGGAATGCA CCTTTAGCCC AGGCCTGCTC AGTGAGCTCC GCCACAGCC AGCCCTGCTC 720
 CTCCCGCCAT GACCTGTGAG ACCCTCTGCG GCTTCAAGT TCCTGGGGGG TGCAGTGAAC 780
 80 ATGCTCCACC TGTCTGCTG GCAAACCATG GTGGGCCCCA GCTGTGTGTC GTGCTGGGGT 840
 AGAGGCAAGG AGATGATGGG ACCGACAGA TGAGACCCCG AGGAGTGAAG TGGGACCCCG 900
 AGGACGGGCC CAGGGTCCAG GGCACAGGAG AGAGAAGCAG GAGGAGGAG AGCTTCTG 960
 TGGAGGACGC ATCTACAGT GGGGGCAAG GTGCTCTGAG GTCCGCTGAA GGCAGGAGCT 1020
 AGGCTGCCCA GGCCTGCTC GCTTGGCTGG GCTGGGGGGT TGTGGGAGG TGGCTGGGAG 1080
 GCTGGGCTG GGCAGCTAAG CTGGAGCTTT GGCACGGGTC CAGAGCTCC CTCCCTTCAG 1140

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CTTCTGCTGT CACAGAACCC TCGCCCTG GACCCCGTG CTGCTCCTT GCCCTGGCAG 1200
ACCCAGCACT GGTCTGCTGT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC 1260
TCCAGCTGA CACAGCTCC TGGGCGCTT CTTCCAAACC AGCAGGGTAG AAAGATGGGG 1320
CACCCACCAG TCTCTCCAG TGGCCCGGCC CAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380
ATTCCAGACC TTGTGCGCGG GACCCCTGT GAGTTGTGGG ATTCACAGA GGGGTGTGGG 1440
GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500
CAGGGGCCCC GTGGGGCTCT CATTGCGGGC GCCCTTGCGG CGGGGCTCCT CCGCTCTCC 1560
TGCTCTCTCT GTGCTGCTGT CTGCTGCTGC CGCGCCACA GGAAGAAGCC CAGGGACAAG 1620
GAGTCCGTGG GTCTGGGCGG TGGCCCGGGC ACCACCACCA CCCACCTGGT GAGGAGCGGC 1680
TCCTTGCTCA CTCAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740
GGCGAGTTCA GCGCCAGGGA TGGTTTAAAC CCAACAGAGG CAGGGCGTTG AGGACCTTCC 1800
TGGCAGGGA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCCAT 1860
GGGCGGAGG GAGCCACAGC GGGTTCTGA GGAAGGCAGG GGGTACCCCA GATGCCACGT 1920
TTTGGGTGGG TTTGGCGCGT CTCACAGAGC GAAGCCGAGC ATTTGTGCTT GTTGGGTGGC 1980
CTGGCTTGA GCGGGGGGT CTTGACCCAT GTCATGCAAG GGTGCCCCG GAGCCAGGG 2040
CTCTGATGCA GCAAGTGTG AGCACCACT GCCCCTTGTG CCAACTCACT CCAGGTGCAA 2100
CTGATGTGG ATGCCCTGGA GTCCAGCCCG GGGATGCTC AGCAATGGGG GTGCTGCAG 2160
CTCTCCCTGG AGTTGACTT TGGAAAGCCAG GAGGTGAAGG GCCCGCTGC GCAGACCAG 2220
CGTTCTGCG AGTTTCCGGA AAGGGTGAGC GGGGAAGGGC AGACCCCATG CCGTGGGTGG 2280
TGGGAGCTG ACAGGCGAGG GGCCTTGGC TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340
TGCGGAGTCA GGCAGGCGAG CAGCTGAGG CCGTGGGGCA CCGTGGACCC CTATGCCCGG 2400
TGACGCTCT CACCCAGGC CGGACACAGA CATGAGACAA AAGTGACCG AGGCAAGCTC 2460
TGCCCGTGT TTGACGAGAC CTGCTGCTTC CAGTGAAGT AGGATGGTC GGTGGGTGG 2520
GCTTGACCG CTGAGTGGG CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580
GCTGGGTGG CCGTGGCTAG GGCAGCAGGG CCGTGGCTCAG GCGCTGCTC CAGATCCCGC 2640
AGGCGGAGG GCGAGGGGCC ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700
GGCATGAGCC CCGGTGTGAG CTGCTGCTGC CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760
TGGAGCACTG GTACCTGCTG GGCCTGCTGC CTGCCACTCA GGTGAGGTGC TGGTCAACAG 2820
GCCACAGCCC AAGCAGAGG TGGCAGGGAC CCGTGGCTAT GGGCCATCGG AAAGACAGGC 2880
CTGATGGGCA GCAATTTTGG GGTCTGAGC CCAACTCGG CCAGAACTAC CCGTCCGGGC 2940
TGAAGCCCTT CTGCTGCGC ACAGCCGAG CAGGTGCGGG AGCTGTGCTT CTCTCTCGG 3000
TAAGTGCCCA GCTCAGGCCG GCTGACCGTG GTGGTGTCTG AGGCTCAGG CCGTGGTCCA 3060
GACTTGGCAG AGCCCTACGT GAAGGTCCAG CTCATGTCTG ACCAGAGGAA GTGGAAGAA 3120
AGAAAGACAA CACCAAAAAG GGGCAGCGGC GCCCCTACT TCAATGAGGC CTTACCTTC 3180
CTGGTGCCCT TCAGCCAGGT CCAGAAATGT GACCTGTGTC TGGCTGTCTG GGAACCGAGC 3240
CTGCGCTCC GAACTGAGCC GGTAGGCAAG GTGACCTGG GTGCCCGGGC CTCGGGGCAG 3300
CCCCTGCAGC ACTGGGAGAG CATGCTGGCC CACGCCCCGC GGCCTATGCG CCAGCGGCAC 3360
CCCCTGCGGC CAGCCAGGGA GGTGGACCGC ATGCTGGGCC TGCAGCCCCG CCTTCCCGCTG 3420
CGCTGCGCTT TGCCCACTC CTGAATGCAC CACATGCCCT TGTCTCCCGC CTGAGCCAG 3480
GCATTCGCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

Seq ID NO: 197 Protein sequence
Protein Accession #: XP_028196.1

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1 11 21 31 41 51
MGHPVPVPSA PAPAGTTAIP GLIPDLVAGT PCELWDSQEG CGDNPAKWGL QLSTDALSLA 60
STPFPWRALI AGALAAGVLL VSLCLCAACC CRRHRKKPR DKESVGLGSA RGTTHLVR 120
SGSLLTQSRG GLKSLRLQSPG QRGEFSPRDG LTPTEAGR

Seq ID NO: 198 DNA sequence
Nucleic Acid Accession #: NM_000612.2
Coding sequence: 553..1095

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1 11 21 31 41 51
TTCTCCCGCA ACCTTCCCTT CGTCCCTCC CGTCCCCCCC AGTCTCTAGC CTCGACTCC 60
CTCCCCCCTT CAOGCCCGCC CTCTGCGCTT CGCGGAACCA AAGTGGATTA ATTACACGCT 120
TTCTGTTTCT CTCGCTGCTG TTCTCTCCCG CTGTGCGCCT GCGCGCTCT CGCTGTCTCT 180
TCTCCCCCTC GCGCTCTCTT GGGCCCCCCC CTTCACGTTT CACTCTGTCT CTCCACTAT 240
CTCTGCCCTC CTCTATCCTT GATACAACAG CTGACCTCAT TTCCGATAC CTTTTCCCCC 300
CGGAAAGATA CAACATCTGG CCGCCCCAG CCGAAGACA GCGCGTCTC CCGGACAT 360
CAGACGAATT CTCGCCCTCC CCGCAAAAA AAAAGCCATC CCGCGCTCT GCGCGCTCG 420
ACATTGCGCC CCGCGACTC GCGCAGAGCG GCGCTGGCAG AGGAGTGTCC GGCAGGAGGG 480
CCAAAGCCCG CTGTTGGGTT TGGACACGCG AGCAGGGAGG TGGGCGCGAG CGTCCCGCGC 540
TTCCAGACAC CAATGGGAAT CCAATGGGG AAGTCGATGC TGGTGTCTCT CACCTTCTTG 600
GCTTGGCCT CGTGTGCTAT TGTCTCTTAC CGCCCCAGT AGACCTCTGT CCGCGCGGAG 660
CTGTGGGACA CCTTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA 720
AGCGGTGTGA GCGGTGGCAG CCGTGGCATC GTTGAAGAGT GCTGTTTCCG CAGCTGTGAC 780
CTGGCCCTCC TGGAGACGTA CTGTGCTACC CCGCCCAAGT CCGAGAGGGA CGTGTGAGCC 840
CCTCGAGCCG TGCTTCGGGA CACTTCCCC AGATACCCC TGGGCAAGTT CTTCCAATAT 900
GACACTGGA AGCAGTCCAC CAGCGCGCTG CGCAGGGGCC TGCCTGCCCT CCGCTGTGCC 960
CGCGGGGTC AGTGTCTGCG CAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACGTCACTCT 1020
CCCCGATTG CTCTACCCAC CCAAGACCCC GCGCCCCCCC AGAGATGGCC 1080
AGCAATCGGA AGTAGCAAAA ACTGCCGCAA GTCTGCAGCC CGCGGCCACC ATCTGCAGC 1140
CTCTCTCTGA CCAAGGAGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACAGT 1200
CCCCCTGGGG CTCTCTCTGA CCCAGTCCCC GTGCCCCGCC TCCCCGAAC AGGCTACTCT 1260
CCTCGGCCCC CTGATCGGG CTGAGGAAGC ACAGCAGCAT CTTCAACAT GTACAAAATC 1320
GATTGGCTTT AAACACCTT CACATACCTT CCCCC

Seq ID NO: 199 Protein sequence
Protein Accession #: NP_000603.1

1 11 21 31 41 51

MGIPMGKSM | VLLTFLAPAS | CCIAAYRPS | TLGGELVD | LQFVCGDRGF | YFSRPASRVS 60
 RRSRGIVEEC | PFRSCDLALL | ETYCATPAKS | ERDVSTPPTV | LPDNFPYFPV | GKFPQYDTWK 120
 QSTQRLRRGL | PALLRRRGH | VLAKELEAFR | EAKRHRPLIA | LPTQDPAHGG | APPEMASNRK

Seq ID NO: 200 DNA sequence
 Nucleic Acid Accession #: AK057131.1
 Coding sequence: 61..1146

1 11 21 31 41 51
 AGTCTGGGGG TTTAGGTGAG AACTACCCCG GTAGCCTGAC AGCAGGAGCT CGAGAGAAGC 60
 ATGGCTCAGC GGTGCGTTTG CGTGCTGGCC CTGGTGGCTA TGCTGCTCCT AGTTTTCCT 120
 ACGCTCTCCA GATCGATGGG CCGGAGGAGC GGGGAGCATC AAAGGGGCTC GCGAATCCCT 180
 15 TCTCAGTTCA GCAAGAGGGA ACGGCTGGCG ATGAAAGAGG CGCTGAAAGG TGCCATCCAG 240
 ATTCCAACAG TGACTTTTAG CTCTGAGAAG TCCAATACTA CAGCCCTGGC TGAGTTGCGA 300
 AAATACATTC ATAAAGTCTT TCTACAGTG GTACAGACCA GCTTTATCCA GCATGAAGTC 360
 GTGAAGAGT ATAGCCACCT GTTCACTATC CAAGGCTCGG ACCCCAGCTT GCAGCCCTAC 420
 CTGCTGATGG CTCACTTTGA TGTGTTGCTT GCCCTGAAG AAGGCTGGGA GGTGCCCCCA 480
 20 TTCTCTGGGT TGGAGGCTGA TGGGCTCATC TATGGTTGGG GCACACTGGA CGACAAGAAC 540
 TCTGTGATGG CATTACTGCA GGCCTTGGAG CTCCTGCTGA TCAGGAAGTA CATCCCCGGA 600
 AGATCTTCTT TCATTCTCTT GGGCCATGAT GAGGAGTCAT CAGGACAGG GGTCTCAGAG 660
 ATCTCAGCCC TGCTACAGTC AAGGGGCGTC CAGCTAGCCT TCATTGTGGA CGAGGGGGGC 720
 25 TTGATCTTGG ATGATTTCAT TCCTAACTTC AAGAAGCCCA TGGCCTTGAT TGCAGTCTCA 780
 GAGAAGGGTT CCAAGAACCT CATGCTGCAA GTAAACATGA CTTCAGGCCA CTCTTCAGCT 840
 CCTCCAAGAG AGACAAGCAT TGGCATCCTT GCAGCTGCTG TCAGCCGATT GGAGCAGACA 900
 CCAATGCCCTA TCATATTGGA AAGCGGGACA GTGGTGAAGT TATTGACGA ACTGGCAAAT 960
 GAGGTTTATG GAGAGAAATC CCTTAAACCA TGCAATAATC AGGACCAACA CGGCACCTAC 1020
 30 CATATTCAAA GCAGGGGTCA AGTTCAATGT CATCCCCCAG GTGGCCAGG CCAAGTCAAA 1080
 CTTCGCGATT CACCTGGGAC AGACAGTCCA AGAGGTCTTA GAACCTCAGA AGAATCATGT 1140
 GGCATGATAA AGAGTCCAGT TCCATGTGTT GAGTGCTTTT GACCCCTCC CCGTCAGGCC 1200
 TTCTGATGAC AAGGCTTGG GCTACCAGCT GCTCCGCGAG ACCGTACAGT CCGTCTTCCC 1260
 GGAAGTCAAT ATTACTGCCC CAGTTACTTC TATTGGCAAC ACAGACAGCC GATTCTTTAC 1320
 35 AAACCTCACC ACTGGCATCT ACAGGTTCTA CCCCATCTAC ATACAGCCTG AAGACTTCAA 1380
 ACCGATCCAT GGAGTCAACG AGAAAATCTC AGTCCAGGCC TATGAGACCC AAGTGAAT 1440
 CATCTTTGAG TTGATTGAGA ATGCTGACAC AGACCAAGGAG CCAAGTTTCT ACCTGCACAA 1500
 ACTGTGAGGT CAAGGGGCTT GCTGGGTTAG GCATGCCCGA CCCCAGGACA GGAATAACCC 1560
 AAGGGGGAAA GCTAGTGTG ATGAAACTTT TGATCAAAAC CACATTGTAA AACATTGCCC 1620
 40 ATCTGCTTGG CTCACTCTTA AACTCTCCCA AGAACAGGC CGGGGTAAGG TAAAGTCAGC 1680
 AGAAATCTGG CTCTCCCTT CCTCCCGACA TCTGCATCCC TTGATCCACT GGCATTGTCT 1740
 GCCCTCTTGT CCTTATCTG TCTTATGCTG GTTATTTCAC TGCTTCACCT TCCAGGCTTG 1800
 ACTTAACAAA TGTAATTTG AGAAATCTCA ACCAGTTGTT ACCTGATAGG AGTCTTTAAT 1860
 TTAGGCACCT CTGCTGGGGA TGCTTTCTCC AGAGCTTATA TATTCTTCT TACTAGAACT 1920
 45 TTCTTCCCC TTTTATTTCC CTCTCTTCTT GGACTCATGA GCTGTCTCTT CATCTCTCCT 1980
 CTCTCTCTCG CATCTCTCCC CTACTCTTC AATTATTTCT ACTTCTGGAC CTGGACTTAC 2040
 CCAAACCTGT ATACTACCAT AATTGTCAAC ATAATCAGTC AAATAAAGT ATCTGTGCAT 2100
 C

Seq ID NO: 201 Protein sequence
 Protein Accession #: BAB71368.1

1 11 21 31 41 51
 MAQRVCVCLA LVAMLLLVFP TVSRSMGPRS GEHQASRIP SQFSKEERVA MKEALKGAIQ 60
 55 IPTVTFSEK SNTTALAEPF KYIHKVPFTV VSTFSIQHEV VEEYSHLFTI QGSDPSLOPY 120
 LLMAHFDVVP APEEGWVPP FSGLERDGI VYWGTLDDKN SVMALLQALE LLLIRKIYPR 180
 RSFFISLGH EESSGTGAQR ISALLQSRGV QLAFLVDEGG FILDDPIFNP KKPILAIIVS 240
 EKGSMNLMQL VNMTSGHSSA PPKETSIGIL AAASRLERQT PMPFIIFGSGT VVTVLQQLAN 300
 60 EVYGEKSLNQ CNNQDHRGTH HIQSRGQVQC HPFSGPGHSQ LPDSEWTDSP RGPRTREHEC 360
 G

Seq ID NO: 202 DNA sequence
 Nucleic Acid Accession #: NM_004217.1
 Coding sequence: 58..1092

1 11 21 31 41 51
 GGCCGGGAGA GTAGCAGTGC CTGGACCCC AGCTCTCTCT CCCCCTTCTC TCTAAGGATG 60
 GCCCAGAAAG AGAACTCCTA CCCCCTGGCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
 70 AGCACCTTGC CCCAGGAGT CCTCCGGAAG GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
 ATGAGCCGCT CCAATGTCCA GCCACAGCT GCCCTGGCC AGAAGGTGAT GGAGAATAGC 240
 AGTGGGACAC CGACATCTT AACCGGGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT 300
 CCTCTGGGCA AAGGCAAGTT TGGAAACGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
 75 ATCGTGGCGC TCAAGTCTT CTTCAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
 CTGGCGCAGG AGATCGAAAT CCAGGCCCAC CTGCACCATC CCAACATCTT CGGTCTCTAC 480
 AACTATTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CCGCGGGAG 540
 CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTTGACGAGC AGCGAACAGC CAGGATCATG 600
 GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATTTA CAGAGACATA 660
 80 AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTGGGCTGG 720
 TCTGTGATGA CGCCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCTTGGA CTACCTGCC 780
 CCAGAGATGA TTGAGGGGCG CATGCACAAT GAGAAGGTGG ATCTGTGTTG CATTGGAGTG 840
 CTTTGCTATG AGCTGCTGGT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC 900
 TATCGCCGCA TGTCAAGGT GGACCTAAG TTCCCGCTT CTGTGCCAC GGGAGCCAG 960
 GACCTCATCT CCAACTGTCT CAGGCATAAC CCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020

TCAGCCACC CTGGGTCG GGCACCTCT CGGAGGGTGC TGCCCTCCCTC TGCCCTTCAA 1080
 TCTGTGCGCT GATGGTCCCT GTCAATCACT CGGGTGGGTG TGTTTGTATG TCTGTGTATG 1140
 TATAGGGGAA AGAAGGGATC CTAACCTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
 TTAATAAAGG CTGAAGCTTT TTGT

Seq ID NO: 203 Protein sequence
 Protein Accession #: NP_004208

1 11 21 31 41 51
 MAQKENSYPW PYGRQTAPSG LSTLPQVRVLR KSPVTPSALV LMSRSNVQPT AAPGQKVMEN 60
 SSGTDPILTR HPTIDDFEIG RPLGKGFN VYLAREKKSH FIVALKVLPK SQIEKEGVEH 120
 QLRREIEIQA HLHHPNLR YNYFYDRRI YLILEYAPRG ELYKELQKSC TFDQRTATI 180
 MEELADALMY CHGKVIHRD IKPENLLGL KGBELKIADFG WSVHAPSLRR KTMCGTLDYL 240
 PPEMIEGRMH NERVDLCWIG VLYVELLVGN PPFESASHNE TYRRIVKVDL KPPASVPTGA 300
 QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPSPAL QSVA

Seq ID NO: 204 DNA sequence
 Nucleic Acid Accession #: AK055663
 Coding sequence: 38..1423

1 11 21 31 41 51
 AGAACGGCTT CCGCGGGGAG CTGTGCAGCT CTTATCATG GGGACAATTC ATCTCTTTTCG 60
 AAAACACCAA AGATCCCTTT TTGGCAAGTT GTTACGGGAA TTAGACTTG TAGCAGCTGA 120
 CGGAAGGTCC TGAAGATAC TGCTCTTTGG TGAATAAAC TTGATATGTA CTGGCTTCT 180
 GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACCT ACCTGACCAT 240
 TTTTGATCTT TTTAGTTTAA TGACATGTT AATAAGTTAC TGGTAACAT TGAGGAAACC 300
 TAGCCCTGTG TATTCATTTG GGTGTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCTCCAC 360
 AGCTCTGGCA CAGTTGGGAG CTCTCTTTAT ATTAAGAGAA AGTGAGAAC GCTTTTGGG 420
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTGTGGCTC TTGTTTTCAA 480
 CCTGTTCAG ATGCTTTCTA TTCGAATAA ACCTTTGTCT TATGTCTCAG AAGCTGTCTAG 540
 TACGAGCTGG CTTCAGAGC ATGTGTCAGA TCTTAGTCGA AGCTTGTGTG GAATTATTCC 600
 GGGACTTAGC AGTATCTTCC TTCCCGAAT GAATCCATTT GTTTGATTTG ATCTTGTCTGG 660
 AGCATTGTCT CTTTGTATTA CATATATGCT CATTGAAATT AATAATTATT TTGCGTAGA 720
 CACTGCCCTC GCTATAGCTA TTGCTTGAT GACATTGGC ACTATGTATC CCATGAGTGT 780
 GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATTGTCT AGTTGGACAA 840
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTTAGAA GTCCGAAATG AACATTTTGG 900
 GACCTTAGCT TTTGGCTCAT TGGCTGGATC AGTGATGTA AGAATTCGAG GAGATGCCAA 960
 TGAACAAATG GTTCTGTCTC ATGTGACCAA CAGGCTGTAC ACTTAGTGT CTACTCTAAC 1020
 TGTCAAAAT TTCAAGGAT ACTGGATTAG GCTGCTCTTA TTGTCTGGGC CTGTTGCAGC 1080
 CAATGTCTTA AACTTTTCTAG ATCATCAGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140
 TGATTGAAC CCAGTTACAT CAATCCAGC TAAACCTAGT AGTCCACCTC CAGAAATTTT 1200
 ATTTAACTG CTGGGAAAA ATGTGAACCC AGTTATTCTT CTAACACAC AAACAAGGCC 1260
 TTATGTTTGT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT 1320
 TGGAGTTTTC GAAATGGAG CAACTCAAGG ATTGAGGACT GGTTTACAA ATATACCAAG 1380
 TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT 1440
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAATCCAACT TTGCATTGAC 1500
 TGTTTAATCA TGTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACAT TCATGAAACC 1560
 TATGAACTA TATTTTGTGA AAATGTATTT GTGACAGTGA AATCCTGCTA AATGTTAAAG 1620
 GCTTTAAAT GCTTCTCTTT AGAAAATGTG TTCTTTTAAA TTGTGATTTT GGTATCTTTG 1680
 GTTTTGTAGT TGACTGCACT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT 1740
 AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTCTTT TCCGAGACGG AGTCTTGTCT 1800
 TGCCACTGTG CCGGCCCAAT ACATTATTAT TAACCTAAGG CTGTACTTTA TTAAGGCTTC 1860
 CTTAGTTTGT GTTTTGTGTT GTTTTGTGAG ATGGAGTCTC ACTCTGTGCG CCAGGCTGGA 1920
 ATGCACTGGC ATGATCTCAG CTCACCTGCA CCTCTGCTC CTGAGTTCAA ATGATTCTCC 1980
 TGCCCTAGCC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCC AGCTAATTTT 2040
 TGTATTTTGA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAATCTCTG 2100
 ACCCTCAGAT CACCCACCT TAGCCTCCCA AAGTGTCTGG ATTAGTGTG AGCCACCGCA 2160
 CCTGGCCGAT ATTTTCTTTA ATGAAATTTA TAAATATGCT TCTTGAATAA TACACATTTT 2220
 GGGAAAGCGA AAAATGTCTG TTCAAAAGT AAAGTCTCT TTTATAGCTT TTCCAACTTT 2280
 AATTGCTAAA TTTTCTTTG AGGTCTCTCT GAATTATGTC TTACAACTA AAAGCAAAAA 2340
 TTTTTCAGAG AAATTTTGGG ATACATTCTA TCTAGACCAA TTTGAATTTT TAATTATCAA 2400
 GATTTTGTGT AAAGTTCTCT TCCTTTAAAA ATTTTAGTAC ATTTGTAAAT

Seq ID NO: 205 Protein sequence
 Protein Accession #: BAB70980.1

1 11 21 31 41 51
 MGTIHLFRKP QRSFPGKLLR EPRLVAADRR SWKILLFGVI NLICTGFLLM WCSSTNSIAL 60
 TAYTYLTIFD LPSLMTCLIS YWVTLRKPS VYSPGFERLE VLAVFASVLA AQLGALFILK 120
 ESAERFLQEP EIHTQRLVVG TFVALCFNLF TMSLRNKP AYVSEAASTS WLQEHVADLS 180
 RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFADVTA SAIAIALMTF 240
 GTMYPMYSYS GKVLQQTTPF HVIGOLDKLI REVSTLDGVL EVRNEHFVTL GFGLAGSVH 300
 VRIRDANEQ MVLARVITNL YTLVSLTLVQ IFKDDWIRPA LLSGFVAANV LNFSDHVVIP 360
 MFLKGTDDLL NPVTSTPAKP SSPPEPFSFN TPGKVNVPVI LLNTQTRPYG PGLNHGHTPY 420
 SSMLNQGLGV PGIGATQGLR TGPTNIPSRV GTNNRIGQPR P

Seq ID NO: 206 DNA sequence
 Nucleic Acid Accession #: NM_016361.1
 Coding sequence: 397..1662

1 11 21 31 41 51

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GGAACTCAGG	GCGGGCTCCT	GTTCCTTCAA	GAGTGCTGGA	GGCCAAACTT	GAATACAAG	60
TTTAATGTTC	CTCGTCGGGC	AAAAGATAAG	GATCCGATCT	CCCCGGCCCC	GGTGTGCAGC	120
AGGAGCGACC	AACCCGAGCC	CGGGTTAAAA	CTCCCAGGGA	CTCTTCGCTG	CTGCCACCTC	180
TTGTTCTCTC	CCCCGTTCOC	ACTCGGGGTC	TCCCTCAGGG	COGGGAGGCA	CAGCGGTCCC	240
TGCTTGCTGA	AGGGCTGGAT	GTACGCATCC	GCAGGTTCCO	GCGGACTTGG	GGGGGCGCGC	300
TGAGCCCCGG	CGCCCCGAGA	AGACTTGTGT	TTGCCTCCTG	CAGCCTCAAC	CCGAGGCGAG	360
CGAGGGCCTA	CCACCATGAT	CACTGGTGTG	TTCAGCATGC	GCTTGTGGAC	CCCAGTGGGC	420
GTCTGACCT	CGCTGGCGTA	CTGCTGACAC	CAGCGGGGGG	TGGCCCTGGC	CGAGCTGCAG	480
GAGCGCGATG	GCCAGTGTCC	GGTGGACCGC	AGCCTGTCTG	AGTTGAAAT	GGTGAGGTTC	540
GTGTTTCGAC	ACGGGGCTCG	GAGTCTCTCT	AAGCCGCTCC	CGCTGGAGGA	GCAGGTAGAG	600
TGGAAACCCC	AGCTATTAGA	GGTCCCACCC	CAAACCTCAGT	TTGATTACAC	AGTCACCAAT	660
CTAGCTGGTG	GTCCGAAACC	ATATTCTCCT	TACGACTCTC	AATACCATGA	GACCAACCTG	720
AAGGGGGGCA	TGTTTGCTCG	GCAGCTGACC	AAGGTGGGCA	TGCAGCAAT	GTTCGCTTG	780
GGAGAGAGAC	TGAGGAAGAA	CTATGTGGAA	GACATTCCTC	TTCTTTACCC	AACCTTCAAC	840
CCACAGGAGG	TCTTTATTCC	TTCCACTAAC	ATTTTTCGGA	ATCTGGAGTC	CACCCGTTGT	900
TTGCTGGCTG	GGCTTTTCCA	GTGTCAGAAA	GAAGGAGCCA	TCATCATCCA	CACTGATGAA	960
GCAGATTGAG	AAATCTTGTA	TCCCAACTAC	CAAAGCTGCT	GGAGCCTGAG	GCAGAGAACC	1020
AGAGGCCGGA	GGCAGACTGC	CTCTTTACAG	CCAGGAATCT	CAGAGGATTT	GAAGAAAGTG	1080
AAGACAGGGA	TGGGCATTGA	CAGTAGTGAT	AAAGTGGACT	TCTTCATCCT	CCTGGACAAC	1140
GTGGCTGCCG	AGCAGGCACA	CAACCTCCCA	AGCTGCCCCA	TGCTGAAGAG	ATTGTCACGG	1200
ATGATCGAAC	AGAGAGCTGT	GGACACATCC	TTGTACATAC	TGCCCAAGGA	AGACAGGGAA	1260
AGTCTTCAGA	TGGCAGTAGG	CCCATTCCTC	CACATCCTAG	AGAGCAACCT	GCTGAAAGCC	1320
ATGGACTCTG	CCACTGCCCC	CGACAAGATC	AGAAAGCTGT	ATCTCTATGC	GGCTCATGAT	1380
GTGACCTTCA	TACCGCTCTT	AATGAACCTG	GGGATTTTTG	ACCACAAATG	GCCACCGTTT	1440
GCTGTTGACC	TGACCATGGA	ACTTTACCAG	CACCTGGAAT	CTAAGGAGTG	GTGTTGTCAG	1500
CTCTATTACC	ACGGGAAGGA	GCAGGTGCCG	AGAGGTTGCC	CTGATGGGCT	CTGCCGCTG	1560
GACATGTTCT	TGAATGCCAT	GTCACTTTAT	ACCTTAAGCC	CAGAAAAATA	CCATGCATCT	1620
TGCTCTCAAA	CTCAGGTGAT	GGAAGTTGGA	AATGAAGAGT	AACCTGATTA	TAAAGCAGG	1680
ATGTGTTGAT	TTTAAATAA	AGTGCCTTTA	TACAAAAAAA	AAAAAAAAAA	A	

Seq ID NO: 207 Protein sequence
Protein Accession #: NP_057445.1

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1	11	21	31	41	51	
MRLWTFVGV	LSLAYCLHQR	RVALAELQEA	DGQCFVDRSL	LKLMVQVVF	RHGARSPLKP	60
LPLEEQVEMN	PQLEVPPTQ	QFDYTVNLA	GGPKPYSPYD	SQYHETTLKG	GMPAGQLTKV	120
GMQMFALGE	RLRKNYVEDI	PFLSPTFNPO	EVFIRSTNIF	RNLESTRCLL	AGLFQCQKEG	180
PILIHTEAD	SEVLYPNYQS	CWSLRQRTRG	RRQTASLQPO	ISEDLLKVKD	RMGIDSSDKV	240
DFPILLDNVA	ABQAHNLPSC	PMLKRFARMI	BQRAVDTSLY	ILPKEDRESL	QMAVGPFPLHI	300
LBSNLLKAMD	SATAPDKIRK	LYLYAAHDVT	FIPLLMTLGI	FDHKNPPFAV	DLTMEYQHL	360
ESKEWFWQLY	YHGKQVPRG	CPDGLCLPDM	FINAMSVYTL	SPEKYHALCS	QTQVMEVGNE	420
E						

Seq ID NO: 208 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1	11	21	31	41	51	
TTTGAAGGGG	TGGTGGGGCG	AGTTTAATTC	ATAAAGAAGC	CTCCTGATCA	GAAAGGGGCC	60
TAACAGCCTG	CCCTTGGAGA	GAAGTCCTTC	CTTGAGGATA	AGGCCTCCCA	GGGGAGGAGG	120
TGCTGGGGGC	CAGTGTTAGG	CTTCAAGCCA	TCCCTGGAGG	CCAGTCTCTG	GCTCAGCAAG	180
TAGTGGCAGA	GCTGTGAGTG	ATGAGTGGGA	TGGCCTTCTC	AGGTACAGGA	CTGTGCTGCT	240
TCTGGCTGCT	TCTGCATTTC	CATTTGCCAC	TCAGAACTGC	CGGATCCCA	GCAATGGCCA	300
GGAGCCCTCC	GCAGATCAGT	CCGCTCAGCT	GCAGGTTTTT	CCAGTCATAG	TAGAAGGGAT	360
CGTCTTTAAT	GGCAAAATGG	TCATTGGCTT	CCAAGGCAAT	CAGGCCAATG	GTGTGACTCT	420
GCAGGTTCTC	CACTGCTCCT	TCACAGTGT	CCTGCGAGGT	CACCTTGGCG	AGGGCTCACC	480
TGAGCTGGCA	GCGCAG					

Seq ID NO: 209 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..564

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1	11	21	31	41	51	
ATGGAGCCCT	GGGCGTGGCT	GCAGGGTTTA	AAGAGCCGAC	CCACGTGCCC	AGCAGCCTCC	60
TCAGATCCGT	TCTCTGGCT	GCCAGCTCAG	GACACTGGTG	AAGGAGCAGT	GAGGAACCTG	120
CAGAGTCACA	CAGTTGGCCT	GACTGCCCTG	GAAGCCAATG	ACCCATTTCG	CAATAAGAC	180
GATCCCTTCT	ACTATGACTG	GAAGAACTTG	CAGCTGAGCG	GACTGATCTG	CGAGGGCTC	240
CTGGCCATTG	CTGGGATGCG	GGCAGTTCTG	AGTGGCAAT	GCAATGCAA	GAGCAGCCAG	300
AAGCAGCACA	GTCTGTGACC	TGAGAAGGCC	ATCCCACTCA	TCACTCCAGG	CAGATTCTC	360
ACCTTGCCCA	AATCAATAA	ACCTTTATCT	CCAAGCACTT	TGTCTTGGT	GTGTTGGCATC	420
AGCTACACAT	CAGTCTTCOG	AGTGCCCTCT	TCTGCTCCC	TGTACCTGCG	CATTCTGGT	480
GATGCTGCTG	CCCTCAGATC	AGGCCATCCA	AGCATGCAGA	ACATAAGCAT	GCAGAACACT	540
GGACGGAAGG	GCTGTACCTA	ATGA				

Seq ID NO: 210 Protein sequence
Protein Accession #: FGENESH predicted

80

1	11	21	31	41	51	
MEPWANLQGL	KSRPTCPAAS	SDPFSALPAQ	DTGEGAVRNL	QSHTVGLTAL	EANDPFPAKD	60
DFPYDWNKWL	QLSGLIQGL	LAIAGIAAVL	SGKCKCKSSQ	KQHSVPPEKA	IPLITPGRFL	120

TLAKSNKPLS PSTPVLVFGI SYTSVFRVPL SASLYPAIPG DAAALTSGHP SMQNISMQNT 180
GTKGCT

Seq ID NO: 211 DNA sequence

Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..318

1 11 21 31 41 51
10 ATGCCCGGCC ACCCGCTCTG TGAAGTGAGG AGCACCTCTG CCGGCTGCC CGTCTGGGA 60
AGTGAGGAGC GCCTCTGCCC GGCTGCCACC CGTCTGTGA GTGCTGCTG CGCTGGGCCC 120
AGGCCGCCCG TGCCCTTGCCA GGCCCTCCGG CCCCCACCT TCCACCCAG GGCCTGTCTC 180
TCACCCAGG GTTCCATCTC CCTAGTTTCC ACCAGAGACT GGGTCTTCAT TCTCACCTG 240
15 CTACACAGCC CCTACCAGAA CGTCTGAAA TGCAAACTTA ACAACTGTCT CACCCAGCA 300
GGAACCTCCC CAGGCTCCCG GGCCCTCTGC GGGGTGCGG GCCTCACTCT TCGCGCCCAT 360
CCCTCCGCCC TGACCGCCCT GAGCTCGCCC CCAGTGTCTG CCCTTCACG CCAGTTATCC 420
CTCCAGCCT CCAAGTCCC CGTTACCGAA GACCGCCACC ATCAOGACAT AGCGCAGCAC 480
ATATGGGACA CTGGTGAAGG AGCAGTGAGG AACCTGCAGA GTCACACAGT TGGCTGACT 540
GCCTTGGAAG CCAATGACCC ATTGCGCAAT AAAGACGATC CCTTCTACTA TGACTGGAAA 600
20 AACCTGCAGC TGAGCGGACT GATCTCGCGA GGGCTCTCTG CCATGTCTG GATCGGGCA 660
GTCTGTAGTG GCAAAATGCAA ATGCAAGAGC AGCCAGAAGC AGCACAGTCC TGTACCTGAG 720
AAGGCCATCC CACTCATCAC TCCAGGCGAA TTTCTACCT TGGCCAAATC AAATAAACCT 780
TTATCTCCAA GCACCTTTGT CTGGTGTGTT GGCATCAGT ACACATCAGT CTTCCGAGT 840
25 CCTCTTCTG CGTCCCTGTA CCCTGCCATT CCTGCTGATG CTGCTGCCCT CACATCAGGC 900
CATCCAAGCA TGCAGAACAT AAGCATGCAG AACACTGGAA CGAAGGGCTG TACCTAA

Seq ID NO: 212 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
30 MPGHVPCVSR STSARLPRIG SEERLCFAAT PSVSACCAGP RFPVPCQALR PPTFHPRACS 60
SPQGSISLVS TRDWVFILTL LHSFYQNVLK CKPNNCLTPA GNSPGSRAPC GVAGLTIRAH 120
35 PSALTALSSP PVLALHVQLS LPASKVPVTE DRHHHDIAQH IWDTEGAVR NLQSHSTVGLT 180
ALEANDPFAN KDDPPFYDWK NLQLSLGICG GLLAIAGIAA VLSGKCKCKS SQKQHSVPVE 240
KAFLITPGR FLTLAKSNKP LSPSTPVLVF GISYTSVFRV PLSASLYPAI PGDAAALTSG 300
HPSMQNISMQ NTGTGCT

Seq ID NO: 213 DNA sequence

Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1758

1 11 21 31 41 51
45 ATGATGGGGT CTCATGTTGC CCAGGCTGGT CTGAACTCC TGGGCTCGAG TGACCCCTCCT 60
GCCTTGGCCT CCGAAAGTGC TGGGATTACA GGACTGTTAT TACAGGAATC CATAACACTG 120
GAGGATGTGG CTGTGACTT CACTTGGGAG GAGTGGCAAC TCCTGGGCGC TGCTCAGAAG 180
GACCTGTACC GGGATGTGAT GTTGGAAGAC TACAGCAACC TGGTGGCAGT GGGGTATCAA 240
50 GCCAGCAAAC CGGATGCACT CTTCAAGTTG GAACAAGGAG AACAACTGTG GACAATTGAA 300
GATGGAATCC ACAGTGGAGC CTGTTCAAGT TCTCCAAAGG TCCCGTTCTC CATTTTCTCA 360
TCTGTGCCCT TCACTCTTCA AAATTGCGCT CATTCTAACA TATGGAAGT TGATCATGTG 420
CTGGAGCGCT TGCAGAGTGA AAGCCTGGTG AACAGAAGGA AACCATGTCA TGAACATGAT 480
GCATTTGAAA ATATTGTTCA TTGCAGCAAA AGTCAGTTTC TGTAGGGCA AAATCATGAT 540
55 ATATTGACT TACGTGGAAA AAGTTTGAAA TCCAAATTAA CTTTAGTTAA CCAGAGCAAA 600
GGCATGAAA TAAAGAACTC TGTGTAGTTT ACTGGAATG GGGACTCCTT TCTTCATGCT 660
AACCATGAAC GACTTCATAC TGCAATTAAA TTCCTGCAA GTCAAAAACAT CATCAGCACT 720
AAGTCCCAAT TCATCAGTCC CAAGCATCAG AAAACACGAA AATTAGAGAA GCATCATGTG 780
TGCAAGTAAT GTGGGAAAGC CTTTATCAAG AAGTCTTGGC TAACGTATCA CCAGGTAATG 840
60 CATAAGGAG AGAAACCCCA CAGATGTAGT CTATGTGAGA AAGCCTTCTC CAGAAAGTTC 900
ATGCTTACTG AACATCAGCG AACTCATACA GGAGAAAAC CTTATGAATG CCCTGAATGT 960
GGCAAGCCT TTCTCAAGAA ATCAAGGCTC AACATACATC AGAAAACACA TACCGAGAG 1020
AAACCTTATA TATGCAAGTA ATGTGGAAAA GGCCTCATCC AGAAAGGAAA TCTCATGTGA 1080
CACCAGCGAA TTCATACAGG TGAGAAACCT TATATATGCA ATGAATGTGG AAAAGGGTTC 1140
65 ATTCAAGAA CGTGTCTCAT AGCACATCAG AGATTTCACA CAGGAAGAGC GCCCTTTGTG 1200
TGCAAGTAAT GTGAAAATTC CTGTTCTCAG AAATCAGGTC TCATTAAACA TCAAGAAATT 1260
CACACAGGAG AGAAACCCCT TGAATGTAGT GAATGTGGGA AAGCCTTAG CACAAAGCAA 1320
AAGCTCATGT TCCATCAAAG GACTCATACA GGAGAGAGAC CCTATGGCTG TAAOGAGTGT 1380
GGGAAAGCGT TTGCGTATAT GTCTGTCTG GTTAAGCATA AGAGAATACA CACAAGGGAG 1440
70 AAACAAGAGG CAGCCAAAGT GGAATAATCCT CCTGCAGAGA GGCACAGCTC ATTACACACC 1500
AGTGATGTCA TGCAGGAGAA AAACCTCTGCT AACGGGGCGA CTACACAAGT GCCTTCTGTG 1560
GCCCCTCAGA CATCATTAAA CATCAGCGGC CTCCTCGCAA ACAGGAACGT AGTCCTTGTG 1620
GGACAGCCAG TGGTCAGATG TGCAGCCTCA GGAGATAACA GAGGATTGTC ACAGGACAGA 1680
75 AACCTTGTGA ATGCAGTGAA TGTGTTGTGT CCTTCCGTGA TCAATTATGT CTTATTTTAT 1740
GTTACAGAAA ACCCATAG

Seq ID NO: 214 Protein sequence

Protein Accession #: FGENESH predicted

1 11 21 31 41 51
80 MMGSHVAQAG LELLGSSDFP ALASESAGIT GLLQESITL EDVAVDPTWE EWQLGAAQK 60
DLYRDMLEN YSNLVAVGQ ASKPDALFKL EQGEQLWTIE DGIHSGACSG SPKVPFSIFS 120
SVPTTLQCL HSNIKVDHV LERLQSESLV NRRKPCHEHD AFENIVHCSK SQFLLGQNH 180
IFDLRGKSLK SNLTLVNQSK GYEIKNSVEF TNGDGSFLHA NHERLHTAIK FPASQKLIST 240

5 KSPISPKHQ KTRKLEKHV CSECGKAFIK KSWLTDHQVM HTGKPHRCS LCEKAPSRKF 300
 MLTEHQRTHT GEKPYBCPEC GKAPLKKSRL NIHQKTHTGE KPYICSECGK GFQKGNLIV 360
 HQRIHTGEKP YICNECGKGF IQKTCILAHQ RFHTGKTFFV CSECGKSCSQ KSLGIKHQRI 420
 HTGKPFBCS ECGKAPSTKQ KLIVHQRTHT GERPYGCNEC GKAPAYMSCL VKHRIHTRE 480
 KQEAQVENP PAERHSSLHT SDVMQEKNSA NGATTQVPSV APQTSINISG LLANRNVVLV 540
 GQPVVRCAS GDMRGPAQDR NLVNAVNVVV PSVINVLVLY VTEMP

Seq ID NO: 215 DNA sequence

Nucleic Acid Accession #: NM_032190.1

Coding sequence: 502..1332

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1	11	21	31	41	51	
GATTCCGTGT	TCTTGGCCAT	GTTAGCCATA	ATATCCTGTG	CAGTATGTTT	TTCCTGTGCA	60
GAGGCAAAAA	CATATTGGGC	ATATGTTCCC	AAGCCCCCAG	CAGTATGACC	CATACTTTGG	120
AGTGACACTC	CTCCTAAGAT	TTATCATGAT	TAAGGAGCAT	GGGCTCCAG3	ACCCCTAACT	180
CCACCTGACA	TAGAACAGTT	AGACTCTCAG	AATAATGTCA	TTAATTATAC	CGCTCCATTG	240
GAAGGACTTC	CTTTGTGTGT	CACCACAAAG	ACATCACTCA	GCCATAGCTG	TCTTACAGTT	300
CAAGCTCACA	CTTGTGTGAG	TCACTATGGG	AAAATCATGT	ACTTATTAAG	TCTTGGTTAT	360
ATTAATGTAA	CCGGTGTGCT	AACCAACCAT	TCCTGGCCCA	ATCGCCTTCA	TTGTGCTGAC	420
TATACAGAAT	GGATTCCCTT	CAATAGTTC	TACCCCCCTC	CATAGACCCA	GTGTCTTGGC	480
CCACTGGCTA	GAAAACAATC	TATGTTAACT	GGAGACATTG	TGGATTGGGG	ACCTAAAGGC	540
CAATTAGATG	GAAAAGAAGA	AAATCAGAAA	TCGTGGCACA	AACCTTGTCT	GCATTGTGTG	600
CAAGCTTTTA	ATGCTTCTTC	TTTATATAAC	ACTGGGATCC	AATCCCAATC	GGCGGCCGAG	660
ATTGCTTGGC	ATGGAGCAGG	CTTTAGCCCG	CCTCTTCTCT	AGTGGCATT	TCTAGGGAGG	720
AAAGGACCAA	TTCAAAGAT	GATATGGAAG	GCAGCATTCC	CATTATGAA	TGGCAACATC	780
TGGGTTGCCA	TAATACTATC	CAATAATAGC	AATAGTAAGC	AACACAGTCT	TAATGTTACA	840
TTTGTAAAGA	ATATCACCAAC	TCAATTATCA	GTTTGTGTTT	TTAATCTTAA	TGTGTTTTTG	900
GCAGCTAAGA	AGGACAGAGT	CCAGGTAAAC	AATACCCAAT	TGACCTGTAA	ATCTTGCCAG	960
TTATATCACT	GCATTATATC	TAGCACATTC	CAACACATA	ATATCTCTAC	TTTGATGATT	1020
TTAGGTTGCA	TCCTGGGCT	ATGGATTCTT	GTTAATCTGT	CTGAGCCATG	GGCTGCCACA	1080
ATTGCTTTAC	ATTTGTGAA	ACTTCTTCTA	ACTCAGTTTA	CTCATTTGTG	COGTAGAGGC	1140
TTAGGCTAGA	TAATTTTTGC	TATTGTTTAC	TTGGTTCACAC	TAATAATTTC	TGTTGTGATG	1200
TCCTCTGTAG	CTTTGCATAG	TTCTATTCAA	ACAGCTCAGT	ATGTGGAGAA	CTGGACACGC	1260
ACAGTCAACC	AAGGTTGGCT	ACTTGAGAAT	AAAATTAAAC	CTGAGTTACA	AACGGAAGTG	1320
GCAGTGTAT	AATCCACGAT	TCTATGGTTA	GGGGAACRAG	TACAAAGCTT	GCAATTGCAG	1380
CAGTAATGTG	GTGTGTCATT	TAATCACACT	CATATTTGTG	TAACCAACTT	AGAATATAAC	1440
CAAGTGAGT	ATCCATGGGA	TCTTGTGAAA	GCCCCATTGC	AGGGAGCTTT	CACATCCGAC	1500
ATCACCTTGT	ATATTGGTGA	ATTACAAAAC	AAAATTCTTG	ATTTAAATAA	ACAAATTCCA	1560
GAGTTTCAGC	CTTCTTTAGA	AGACTGGACT	GAATCCAGC	AAGGCCTGGA	GAGCGTCAAC	1620
CTTGTGACCT	ATCTAAAGCA	CCACATTAAC	ATCTTATATA	TAGTTCCTTG	AATAATGTTG	1680
TTTGTCTCT	GTCTTCTGTT	CATAGTCTGT	AAAATCGGAT	GGACTGCCAA	TGGGAGAATG	1740
AAAGCTACCC	AGCCTGGCCT	TACATTCCTT	CACCTAATAC	ATAAACAAGA	AGGGGGAAAT	1800
GTTGGGAGCG	AAAAGGCCCA	AAGGGATGCT	GACCACTCA	GCATCCACT	GGAGGCTACA	1860
TGATCAAACA	GCAAACGTGT	TATCATGAAT	ACAGAATGTG	GGCAAACCTG	CTTCTGTGCC	1920
TGCCAGAAAG	GTTTGTCTGAG	GGCCATCGCT	CCCTGGCCCC	GGCTCCTTGA	GGTTATCTAC	1980
TGGGACATCT	AGAGCCTATT	GTTGAGGAA	TGCAGTCTTG	CAAGCCTACT	CTGGACCGAG	2040
CAGCTGACCT	CTTCTCCAC	ACCCCTTCTC	ACTATCTCTT	TTGCCATAA	AATATGGAGG	2100
GCTGTGTAAA	GCTCAGGGCC	CTTGTCCACT	AGAGGCAAGG	TGTCCTCTGA	CCCTTCTTCC	2160
AAACAT						

Seq ID NO: 216 Protein sequence

Protein Accession #: NP_115566.1

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 60

1	11	21	31	41	51	
MLTGDIVDWG	PKGQLDGKEE	NQKSWHKLCW	HWQAFNASS	LYNTGIQSQS	AAQIAWHGAG	60
PFPPLPQWYH	LGRKGPIQKM	IWKAAFPFMN	GNIWVAIILS	NNSNSKQHSI	NVTFVKNIIT	120
QFTVCVFNPY	VFLAAKQDL	QVNNITQLTK	SCQLYHCINH	STLQTHNIST	LMILGCIPLG	180
WIPVNLSEFW	AATIALHFVK	LLLTQFTHCV	RRGLGMIIFA	IVYLVTLIIS	VVMSSVALHS	240
SIQTAQVVEN	WRTVYNQWML	LENKINTELO	TEVAVL			

Seq ID NO: 217 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..1566

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1	11	21	31	41	51	
ATGGTGAACC	CCAAATCCAC	TTCTCCCTC	TTCAGTTTAT	GTITTTTGTCT	CCTGAGGAGT	60
CAGAACCTGT	GGGTGAAGA	GCAAATTCAC	TGCAAAAACA	TATTGGGCAT	ATGTTCCCAA	120
TCCCCCAGCA	GTATGGCCCTA	TACTTTGGAG	CTCACTCCTC	CTGAGATTTA	TCAGATCAG	180
GGAGAGTGGG	CTCCAGGACC	CCTAACTCCC	CGTGACATAG	AAAAAGTTAGA	CTCTCAGAAC	240
AATGTCAATTA	ATTATACCAAC	TCCACTGGAA	GGACTCCCTT	TGTTTATCAC	CACAAGAGCG	300
TGGCTCAGCC	ATAGCTGTCT	TGCAATTCAC	GCTCAACAT	GGTTAGTCA	CTATGGAAAA	360
ATTATGTACT	TATTAGTCT	TGGTTCATT	AATGTAACCT	GTGTGCTAAC	CAATCATTC	420
CAGTCCAGTC	ACCTTAATTG	TGCTGATTAT	ACAGAAATGGA	TTCCATTCAA	TAGTTCCTAC	480
CCCACTCTGT	GAACCCAGTG	TCTTGATCCA	CTGGCTAGTA	AACAATATAT	GTCAACTGAA	540
GACACTGTGG	ATTGGGAACC	TAAAGGTCAA	TTAGATGGAA	AAGGTGAAG	TCAGAAATCA	600
TGGCACAAC	TTCACTGGCA	TTGGGGCCAA	GCTTTTAATG	CTTCTCTCTT	ATACAACAGC	660
AGAATCCAA	CCAGTCTGC	TGCTCAGATT	GCTTGGCATG	GAGCAGGCCT	TAGCCCACT	720
CTTCTCTAGT	TGCATTATCT	GGGGAGGAAA	GGACCAATTC	AAGAACTAT	ATGGAAGGCA	780
GCACTCCCAT	TTATGAATGG	CAACATCTGG	ATTGGAACAC	TGTCTAATAA	TAGCAATAGT	840
AAGCAACACA	GTCTTAATGT	TGCATTGTGA	AAGAATATCA	CCACTCAGTT	TACAGTTTGT	900
GTTTTAAATC	CTTATGCCTT	TTTGGCAGCT	AAGAAGAACC	AGCTTCAGT	GGAGAAGTGG	960

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ACACGCACAG CTGACCAAGC GAGGCTACTT CAGAATAAAA TTAACACTGA GTTACAAACT 1020
GAAGTGGCAA TGTGAAATC CATGGTTCCTG TGGTTAGGAG AACAGGTACA AAGCTTGCA 1080
TTGCAGCAGC AATTGGGTCA TCATTTTAAT CACATTGATA TTTGCGTAAC TAACCTCAGAA 1140
TATAACCTAA GTAGATATCC GTGGACCTT GTGAAAGCCC ATTTGCAAG AGCTTTTACA 1200
TCCAACATCA CCTTTGATAT TGGTGAATTA CAAAAAATA TTATTGATT AAATAGGCAA 1260
ACTCAAGAT TTACGCCTTC TTTAGAAGAC TGGACCGAAT TCCAGGAAG CCTGGAGAGC 1320
CTCAACCTT GACCTATCT AAGGCACAC ATTAACATCT TATATGTAGT TCTTGAATA 1380
ATGTTGTTT GTCTCTGTCT TCGGTTTATA GTCTGTAAAA TCGGATGGAC CACCAATTGG 1440
AGAAATGAGC CCTCCAGCC CAGCCTTACA TTCCTTCAAT TAATACATA ACAGAAAGGG 1500
GGATATGCAG GGAGCCAAAG GCCTGTGGGA CGTGACCAAC TCAGCATCT GCTGGAGGCT 1560
ATATGA
  
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Seq ID NO: 218 Protein sequence

Protein Accession #: FGENESH predicted

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1      11      21      31      41      51
|      |      |      |      |      |
MVNPKSTSSL FRLCFLLLRS QNLNVEBQIQ CKNILGICSQ SPSSMAYTLE LTPPEIYHDQ 60
GEWAPGLPLP RDIEKLDSON NVINYTTPLS GLPLFITTKT SLSHSCLAIQ AQTWLSHYGK 120
IMVLLGLGSI NVTVGLTNHS QSSHPNCADY TEWIFPNSSY PTLWTQCLDP LASKQYMSYE 180
DTVDWEFKQG LDGKGBSSQKS WHKLHWHWRQ AFNASSLYNS RIQSQSAAQI ANHGAGFSPF 240
LPQLHYLGRK GPIQETIWK A LPPMNGNIW IGTLSNNNS KQHSLNVAVF KNITTQPTVC 300
VFNPYAFLLA KQQLQVENV TRTADQARLL QNKINTELQT EVAMLKSMVL WLGEQVQSLQ 360
LQQQLRHHFN HIHICVTNSE YNQSEYPWDL VKAHLQGAFT SNITPDIGEL QNKIIDLNRQ 420
TOEFQPSLED WTEFQEGLES LNPWTYLRHH INILYVVLGI MLFCLCLRFI VCKIGWTTNW 480
RMRASQPSLT FQQLIHKQKG GYAGSQRPVG RDQLSILLEA I
  
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Seq ID NO: 219 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 1..900

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1      11      21      31      41      51
|      |      |      |      |      |
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120
CCCGTGCGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTGTGT AGGTACGTTT AATCGCCCGT GCGCGCGCGT 240
GGCTGCGCGC GGGCTGTGCA CCGGGGAGCT GGGGCGGGCG TCTCGGGGGG AGGGCGCAGA 300
GGACCCCGGG GAGGAGACTG GAGCAGGCCC CGAGGTGGCG CTGGTGCGGC CCAGGACGCT 360
CTTCTAACT CAGGCTCTCC CCGCCCCGCC CTGCACTGC AGTCTCTGGT GGATGGAGCT 420
CCGGTGCGCA TTGAGCTCTG GGACACAGCG GGACAGGAGG ATTTGACCG ACTTCGTCTC 480
CTTTGCTACC CGGATACCGA TGTCTTCTGT GGTGCTTCA GCGTGGTGCA GCCCAGCTCC 540
TTTCAAAACA TCACAGAGAA ATGGCTGCCC GAGATCCGCA CGCACAAACC CCAGGCGCCT 600
GTGCTGCTGG TGGGCACCCA GGCCGACCTG AGGGACGATG TCAAGTACT AATTCACTGT 660
GACCAGGGGG GCCCGGAGGG CCGCGTGCCC CAACCCAGG CTGAGGCTCT GGCCGAGAAG 720
ATCCGAGCCT GCTGCTACCT TGAGTGCTCA GCCTTGACGC AGAAGAAGTT GAAGGAAAGT 780
TTTGACTCG GTATTCTCAG TGCCATTGAG CACAAGGCC GCGTGGAGAA GAAACTGAAT 840
GCCAAGGTTG TCGCACCCCT CTCGCCGCTG CGCTGGAAGA AGTCTTCTG CTTCGTTTGA
  
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Seq ID NO: 220 Protein sequence

Protein Accession #: FGENESH predicted

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1      11      21      31      41      51
|      |      |      |      |      |
MPPRELSEAE PPPLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIVS YTCNGYPARY 60
RPTALDTFSG TVVQSPVFRP GCGGAVHRGA GAGVSAGGRR GPRGGDWSRP RGGAGAAQDA 120
LPNSGSPRPA PAVQVLVDGA FVRIELWDTA GQEDPDLRS LCYPDTDVFL ACFSVVQPS 180
FQNIETKWL P EIRTHNPQAP VLLVGTQADL RDDVNVLIQL DQGGREGFPV QPQAQGLAEK 240
IRACCYLECS ALTQKNLKEV FDSAILSABE HKARLEKKLN AKGVRTL SRC RWKPFPCFV
  
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Seq ID NO: 221 DNA sequence

Nucleic Acid Accession #: XM_063832.2

Coding sequence: 1..711

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1      11      21      31      41      51
|      |      |      |      |      |
ATGCCGCCGC GGGAGCTGAG CGAGGCCGAG CCGCCCCCGC TCCGGGCCCC GACCCCTCCC 60
CCGCGGCGGC GTAGCGCGCC CCCAGAGCTG GGCATCAAGT GCGTGCTGGT GGGCGACGGC 120
GCGGTGGGCA AGAGCAGCCT CATCGTCAGC TACACCTGCA ATGGGTACCC CGCGCGCTAC 180
CGGCCCACTG CGCTGGACAC CTCTCTGTGT CAAGTCTGTG TGGATGGAGC TCCGGTGCGC 240
ATTGAGCTCT GGGACACAGC GGGACAGGAG GATTTTGACC GACTTCGTTT CCTTTGCTAC 300
CCGATACCG ATGTCTTCTT GCGTGCTTTC AGCGTGCTTC AGCCGAGCTC CTTTCAAAAC 360
ATCACAGAGA AATGGCTGCC CGAGATCCGC ACGCACAAAC CCCAGGCGCC TGTGCTGCTG 420
GTGGGCACCC AGGCCGACCT GAGGACGAT GTCAAGTAC TAATTAGCT GGACCAAGGG 480
GGCGGGAGG GCCCGGTGCC CCAACCCAG GCTCAGGCTC TGGCCGAGAA GATCCGAGCC 540
TGCTGCTACC TTGAGTGCTC AGCCTTGACG CAGAAGAACT TGAAGGAAGT ATTTGACTCG 600
GCTATTCTCA GTGCCATTGA GCACAAAGCC CGCTGGAGA AGAAACTGAA TGCCAAAGGT 660
GTGGCACCC TCTCCGCTG CCGCTGGAAG AAGTCTTCTT GCTTCGTTTG A
  
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Seq ID NO: 222 Protein sequence

Protein Accession #: XP_063832.1

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1      11      21      31      41      51
|      |      |      |      |      |
  
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MPPRELSEAB PPFLRAPTPP PRRRSAPPEL GIKCVLVGDG AVGKSSLIYS YTCNGYPARY 60
 RPTALDTFVS QVIVDGAQVR IELNDTAGQE DFDRLRLSLCY PDTDVFLACF SVVQFSSPQN 120
 ITERKWLPEIR THNPQAPVLL VGTQADLRDD VNVLIQLDQG GREGVPVPQO AQGLABKIRA 180
 CCYLECSALT QKNLKEVFDS AILSAIEHKA RLEKKLNAGK VRTLSRCRWK KFFCFV

Seq ID NO: 223 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1161

10 1 11 21 31 41 51
 | | | | | |
 ATGAATGGCG ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 60
 TTCGAGATG ACTTCATTGC CAAGGTGTGG CGCCCGGTGT TGGGGCTGGA GTTTATCTTT 120
 15 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCCTGGAAA 180
 TCCAGCCGGA TTTTCTGTG CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240
 CCGTTCTGTA TGAACACTA TGTGCGGGT TCAGACTGGA AGTTTGGGGA CATCCCTTGC 300
 CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
 AATTGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTGTGG CCTAACAGTC 480
 20 CACCTCCTGA AGAAGAAGT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540
 AGCATCTGCC ATACCTTCCG GTGGCAGGAA GCTATGTTCC TCCTGGAGTT CCTCCTGCC 600
 CTGGGCATCA TCTGTCTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
 25 GTCATCTGCT TCCTTCCAG CGTGGTGTG CGGATCCGCA TCTTCTGGCT CCTGCACTC 780
 TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840
 AGCTTCACT ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900
 TTTCCCACT TCTTCTCCAC TTTGATCAAC CGCTGCCCTC AGAGGAAGAT GACAGGTGAG 960
 CCAGATAATA ACCGAGCAC GAGCGTGGAG CTCACAGGGG ACCCAACAA AACAGAGGCG 1020
 30 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080
 ACCTCAAATA ACCATTCCAA GAAGGGACAT TGTACCAAG AACAGCATC TCTGGAGAAA 1140
 CAGTTGGGAT GTTGATCGA G

Seq ID NO: 224 Protein sequence
 Protein Accession #: Eos sequence

35 1 11 21 31 41 51
 | | | | | |
 MNRHHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEFIP GLLENGLALM IPCFHLKSNK 60
 SSRIFLNLVA VADFLLIICL PFVMDYYVRR SDWKPGDIPC RLVLPMFAMN RQGSIIPLTV 120
 40 VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKLLIQ NGPANVCISF 180
 SICTHFWHBE AMFLLEPLP LGIILFCSAR IISLRLQRM DRHAKIKRAI TPIMVVAIVF 240
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMSMLD PVVYFSSPS 300
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV E LTGDPNKTG APEALMANS EPWSPSYLGP 360
 TSNHSHKKGH CHQEPASLEK QLGCCE

Seq ID NO: 225 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1092

50 1 11 21 31 41 51
 | | | | | |
 ATGAATGGCG ACCATCTGCA GGATCACTTT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 60
 TTCGAGATG ACTTCATTGT CAAGGTGTGG CGCCCGGTGT TGGGGCTGGA GTTTATCTTC 120
 55 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCCTGGAAA 180
 TCCAGCCGGA TTTTCTGTG CAACCTGGCA GTGGCTGACT TTCTACTGAT CATCTGCCTG 240
 CCGTTCTGTA TGAACACTA TGTGAGGCGT TGGGACTGGA AGTTTGGGGA CATCCCTTGC 300
 CGGCTGATGC TCTTCATGTT GGCTATGAAC CGCCAGGGCA GCATCATCTT CCTCACGGTG 360
 GTGGCGGTAG ACAGGTATTT CCGGGTGGTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
 AATCGGACAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTATTGG CCTGACAGTC 480
 60 CACCTCCTGA AGAAGAAGAT GCGATCCAG AATGGCGGTG CAAATTGTG CAGCAGCTTC 540
 AGCATCTGCC ATACCTTCCA GTGGCAGGAA GCCATGTTCC TCCTGGAGTT CTTCCTGCC 600
 CTGGGCATCA TCGTGTCTG CTCAGCCAGA ATTATCTGGA GCCTGCGGCA GAGACAAATG 660
 GACCGGCATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATCGTCTTT 720
 65 GTCATCTGCT TCCTTCCAG CGTGGTGTG CGGATCCGCA TCTTCTGGCT CCTGCACTC 780
 TCGGGCAGCG AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGCGTCTT TATCACTCTC 840
 AGCTTCACT ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900
 TTTCCCACT TCTTCTCCAC TTTGATCAAC CGCTGCCCTC AGAGGAAGAT GACAGGTGAG 960
 CCAGATAATA ACCGAGCAC GAGCGTGGAG CTCACAGGGG ACCCAACAA AACAGAGGCG 1020
 70 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1080

Seq ID NO: 226 Protein sequence
 Protein Accession #: Eos sequence

75 1 11 21 31 41 51
 | | | | | |
 MNRHHLQDHF LEIDKKNCCV FRDDFIVKVL PPVLGLEFIP GLLENGLALM IPCFHLKSNK 60
 SSRIFLNLVA VADFLLIICL PFVMDYYVRR SDWKPGDIPC RLVLPMFAMN RQGSIIPLTV 120
 80 VAVDRYFRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKMPIQ NGGANLCSF 180
 SICTHFWHBE AMFLLEPLP LGIILFCSAR IISLRLQRM DRHAKIKRAI TPIMVVAIVF 240
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SFTYMSMLD PVVYFSSPS 300
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV E LTGDPNKTG APEALMANS EPWSPSYLGP 360
 TSP

Seq ID NO: 227 DNA sequence
Nucleic Acid Accession #: NM_006018
Coding sequence: 61..1224

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5      1      11      21      31      41      51
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CGCCACTTTG CTGGAGCATT CACTAGGCGA GCGCTCCAT CGGACTCACT AGCCGCACTC 60
ATGAATCGGC ACCATCTGCA GGATCACITT CTGGAAATAG ACAAGAAGAA CTGCTGTGTG 120
TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCGGTGTG TGGGCTGGA GTTTATCTTT 180
10    GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACTCAA GTCTGGAAA 240
TCCAGCCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 300
CCGTTCTGTA TGGACTACTA TGTGCGGCGT TCAGACTGGA ACTTTGGGGA CATCCCTTGC 360
CGGCTGGTGC TCTTCATGTT TGCCATGAAC CGCAGGGCA GCATCATCTT CCTCACGGTG 420
GTGGGGTAG ACAGGTATTT CCGGTGGTC CATCCCAACC AGCCCTGAA CAAGATCTCC 480
15    AATTGGACAG CAGCCATCAT CTCTTGCCTT CTGTGGGCA TCACTGTGG CCTAACAGTC 540
CACCTCTGTA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 600
AGCATCTGCC ATACCTTCGG GTGGCAGGAA GCTATGTTCC TCTTGGAGTT CCTCTGCCCC 660
CTGGGCATCA TCTGTCTG TGACGCCAGA ATTATCTGGA GCCTGGGCA GAGACAAATG 720
GACCGGATG CCAAGATCAA GAGAGCCATC ACCTTCATCA TGGTGGTGGC CATGCTCTTT 780
20    GTCATCTGCT TCCTTCCCA GCGTGTGTG CCGATCCGCA TCTTCTGGCT CCTGCACACT 840
TCGGGCACGC AGAATTTGTA AGTGTACCGC TCGGTGGACC TGGCGTTCTT TATCACTCTC 900
AGCTTCACCT ACATGAACAG CATGCTGGAC CCGGTGGTGT ACTACTTCTC CAGCCCATCC 960
TTTCCCACTT TCTTCTCCAC TTTGATCAAC CGCTGCCTCC AGAGGAAGAT GACAGGTGAG 1020
CCAGATAATA ACCGAGCAC GAGGTGTGAG CTCACAGGGG ACCCAACAA AACACAGAGC 1080
25    GCTCCAGAGG CGTTAATGGC CAATCCCGT GAGCCATGGA GCCCTCTTA TCTGGGCCCA 1140
ACCTCAAATA ACCATTCCAA GAAGGACAT TGTCAACAAG AACACGATC TCTGGAGAAA 1200
CAGTTGGGCT GTTGCAATCGA GTAAATGTCA TGGACTCGGC CTAAGGTTTC CTGGAACCTC 1260
CAGATTGAGA GAATCTGATT TAGGAAACCT GTGGCAGATG AGTGGGAGAC TGGTTGCAAG 1320
GTGTGACCA AGGAATCTCT GAGGAACAGA GAGTAAAGCT TCTAGGCATC TGAAACTTGC 1380
30    TTCATCTCTG ACCTCTGCG GACTGAAGAT GGCCTAATTG TAGGCTTTTC TGCTGAGCAG 1440
AGTTGAGGCC AGAGATCTAC TTGTGACTTG TTGGCTTCT TCCACATCT GCCTCAGACT 1500
GGGGGGGGCT CAGCTCTCG GGTGATATCT AGCCTGCTTG TGAGCTCTAG CAGGGATAAG 1560
GAGAGCTGAG ATTGGAGGGA ATTGTGTTGC TCCTGGAGGA AGCCCGGCA TCATTAAACA 1620
35    AGCCAGTAGG TCACCTGGCT TCCGTGGACC AATTCATCTT TCAGACAGC TTAGAGAGAA 1680
TGGACTCAGG GAAGAGACTC ACATGCTTTG GTTAGTATCT GTGTTTCCG TGGGTGTAAT 1740
AGGGGATTAG CCCAGAAAG GACTGAGCTA AACAGTGTTA TTATGGGAAA GGAAATGGCA 1800
TTGCTGCTTT CAACCAAGCA CTAATGCAAT CCATTCTCT CTGTTTATA GTAACTAAG 1860
GGTTGAGCAG TTAACACGCG TTCAGGATAG AAAGCTGTTT CCCACCTGTT TCGTTTACC 1920
40    ATTAACAGGG AAACGTGCTT CTGCCACG GGTAGAGGGG GTGACGTTT CTCTGGTTC 1980
CTTCGCTTGT GTTCTGTAC TTACAAAAA TCTACCATT CAATAAATT TGATAGGAGA 2040
CAAAAAAAA A

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Seq ID NO: 228 Protein sequence
Protein Accession #: NP_006009.1

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45      1      11      21      31      41      51
|      |      |      |      |      |
MNRHQLDHF LEIDKKNCCV FRDDPIAKVL PPVLGLEFIF GLLGNGLALM IFCFHLKSWK 60
SSRIFLNLVA VADFLLIICL PFVMDYVVR SDWNPDIIPC RLVLFMFAMN RQGSIIPLTV 120
50    VAVDRYPRVV HPHHALNKIS NWTAAIISCL LWGITVGLTV HLLKKLLIQ NGPANVCISF 180
SICHTFRWHE AMFLLEFLLP LGIILFCSAR IISLRQRQM DRHAKIKRAI TFMVVAIVF 240
VICFLPSVVV RIRIFWLLHT SGTQNCBVYR SVDLAPFITL SFTYNNMLD PVVYFSSPS 300
PFNFFSTLIN RCLQKMTGE PINNRSTSVB LTGDPNKTGR APEALMANSQ EPWSPSYLSP 360
55    TSNHSHKKGH CHQEPASLEK QLCCIE

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Seq ID NO: 229 DNA sequence
Nucleic Acid Accession #: NM_014398.1
Coding sequence: 64..1314

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60      1      11      21      31      41      51
|      |      |      |      |      |
GGCACCGATT CGGGGCTGCG CGGACTTGG CGSCAGCTG CAGAACCTCG CCCAGGCCCC 60
ACCATGCCCC GGCAGCTCAG CGCGGCGGCC GCGCTCTTGG CGTCCCTGGC CGTAATTTTG 120
65    CACGATGCGA GTCAAATGAG AGCAAAAGCA TTTCAGAAA CCAGAGATTA TTCTCAACCT 180
ACTGCAGCAG CAACAGTACA GGACATAAAA AAACCTGTCC AGCAACAGC TAAGCAAGCA 240
CCTCACCAAA CTTTAGCAGC AAGATTCTAT GATGGTCTAT TCACCTTTCA AACAGCGGCC 300
ACAGTAAAAA TTCCAACAAC TACCCAGCA ACTACAAAA ACACCTGCAAC CACCAGCCCA 360
ATTACCTACA CCTGGTTCG AACCCAGGCC ACACCAACA ACTCACACAC AGCTCCTCCA 420
70    GTTACTGAAG TTACAGTCGG CCTAGCTTAT GCCCTTATT CACTGCCACC CACCATCACC 480
CCACCAGTGC ATACAGCTGG AACCAGTTCA TCAACCGTCA GCCACACAC TGGGAACACC 540
ACTCAACCCA GTAACAGAC CACCTTTCCA GCAACTTTAT CGATAGCACT GCACAAAGC 600
ACAACCGGTC AGAAGCCTGA TCAACCCACC CATGCCCCAG GAACAAAGGC AGCTGCCACC 660
AATACCAACC GCACAGCTGG ACCTGCCTCC ACGGTTCTGT GGCACCCCT TGCACTCAG 720
CCATGTCAG TCAAGACTGG AATTATCAG GTTCTAAAG GAAGCAGACT CTGTATAAAA 780
75    GCAGAGATGG GAGATGAGCT GATTGTTCAA GACAAGGAGT CGGTTTTTTC ACCTCGGAGA 840
TACTTCAACA TCGACCCCAA CGCAACGCAA GCCTCTGGGA ACTGTGGCAC CCGAAATACC 900
AACCTTCTGT TGAATTTTCA GGGCGGATT GTGAATCTCA CATTACCAA GAGTGAAGAA 960
TCATATTATA TCAATGAAGT GGGAGCCTAT TTGACCGTCT CAGATCCAGA GACAGTTTAC 1020
80    CAAGGAATCA AACATGCGGT GTGATGTTT CAGACAGCAG TCGGCAATC CTTCAGTGC 1080
GTGAGTGAAC AGAGCCTCCA GTTTCAGCC CACCTGCAGG TGAACCAAC CGATGTCCAA 1140
CTTCAGCCT TTGATTTTGA AGATGACCAC TTTGGAAATG TGGATGAGTG CTCTCTGAC 1200
TACACAAATG TGCTTCTGTT GATTGGGGCC ATCGTGGTTG GTCTCTGCTT TATGGGTATG 1260
GGTGTCTATA AAATCGGCT AAGGTGTCAA TCACTGGAT ACCAGAGAT CTAATGTTG 1320
CCCGGGGGA ATGAAATAA TGAATTTAG AGAATCTTT CATCCCTTCC AGGATGGATG 1380

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5 TTGGGAAATT CCTCAGAGT GTGGGTCCTT CAAACAATGT AAACCACCAT CTTCTATTCA 1440
 AATGAAGTGA GTCAATGTGT ATTTAAGTTC AGGCAGCACA TCAATTTCTA AATACITTTT 1500
 GTTTATTTTA TGAAAGATAT AGTGAGCTGT TTAATTTCTA GTTTCCTTTA GAATATTTTA 1560
 GGCACACAAA GTCAACATTT GAGATATGTT GAATTAACAT AATATATGTA AAGTAGAATA 1620
 AGCCTTCAAA TTATAAACCA AGGCTCAATT GTAACATAA CTACTGTGTG TGCAATTGAAG 1680
 ATTTTATTTT ACCCTGTATC TTAACAAAGC CTTTGCTTTG TTATCAAATG GACTTTCAGT 1740
 GCTTTTACTA TCTGTGTTT ATGGTTTCAT GTAACATACA TATTCTGTGT GTAGCACTTA 1800
 ACTCCTTTTC CACTTTAAAT TTGTTTTTGT TTTTGAGAG GGAGTTTCAC TCTTGTCAAC 1860
 CAGGCTGGAG TACAGTGGCA CGATCTGGC TTATGGCAAC CTCGCGCTCC CGGGTTCAAG 1920
 10 TGATTCTCCT GCTTCAGCTT CCCGAGTAGC TGGGATTACA GGCACACACT ACCACGCTTG 1980
 GCTAATTTTT GTATTTTAT TATAGACGGG TTTCAACATG TTGGCCAGAC TGGTCTTGAA 2040
 CTCCTGACCT CAGGTGATCC ACCCACTCA GCCTCCCAAA GTGCTGGGAT TACAGGCATG 2100
 AGCCATTGGC CCGGGCCTTA AATGTTTTT TTAATCATCA AAAAGAACA CATATCTCAG 2160
 GTTGICTAAG TGTTTTTATG TAAACCAAC AAAAGAACA AATCAGCTTA TATTTTTAT 2220
 15 CTGATGACT CCGCTCCAG AATTGCTAGA CTAGAATAA GGTGGCTACA GATGGTAGAA 2280
 CTAAACAATA AGCAAGAGAC AATAAATAAT GCCCTTAAT ATTAACAAGG TGCCAGAGTC 2340
 TAGGCTAAGC ACTTATCTA TATCTCAATT CATCTCACA ACTTATAAGT GAATGAGTAA 2400
 ACTGAGACTT AAGGGAACAT AATCACTTAA ATGTCACTG GCTAACTGAT GGCAGAGCCA 2460
 20 GAGCTTGAAT TCATGTTGTT CTGACATCAA GGTCTTTGTT CTTCTCCCTA CACCAAGTTA 2520
 CCTACAAGAA CAATGACACC ACACCTGACC TGAAGGCTCA CACCTCATAC CAGCATACGC 2580
 TCACCTTACA GGAAGATGGG TTTATCCAGG ATCATGAGAC ATTAGGGTAG ATGAAAGGAG 2640
 AGCTTTGACG AATAACAAAT AGCCTATCCT TAATAAATCC TCCACTCTCT GGAAGGAGAC 2700
 TGAGGGGCTT TGTAAACAT TAGTCAGTTG CTCATTTTAA TGGGATTGCT TAGCTGGGCT 2760
 25 GTAAAGATGA AGGCATCAAA TAAACTCAAA GTATTTTAA ATTTTTTGA TAATAGAGAA 2820
 ACTTGCTTAA CCAACTGTTT TTTCTTGAGT GTATAGCCCC ATCTTGTTGT AACCTGCTGC 2880
 TTTCTGCACT CATATCCATA TTTCTTATG TTTCTTATG TCTGTAGAGC AGCCTGCCAA 2940
 GAATTTTAT TCTGCTGTTT TTTTGCTGCT TAAAGAAAGG AACTAAGTCA GATGTTTAA 3000
 AGAAAGTCC ACATAACCCT AGAATCTTA GTCAAGGAAT AATCAAGTC AGCCTAGAGA 3060
 30 CCATGTTGAC TTTCTCATG TGTTCCTTAA TGACTCAGTA AGTTGGCAAG GTCTGACTT 3120
 TAGTCTTAAT AAAACATTGA ATTGTAGTAA AGGTTTTTGC AATAAAAACT TACTTTGG

Seq ID NO: 230 Protein sequence

Protein Accession #: NP_055213.1

35 1 11 21 31 41 51
 MPRQLSAAAA LFASLAVILH DGSQMRKAF PETRDYSQPT AAATVQDIKK FVQQPARKAP 60
 HQTLLARFMD GHIFQTAAT VKIPTTTPAT TKNTATTSPI TYTLVTQTAT PNNSHTAPFV 120
 40 TEVTVGPSLA PYSLPPTITP PAHTAGTSSS TVSHTTGNTT QPSNQTLTLP TSLIALHKST 180
 TGQKPDQPTH APGTTAAAHN TTRTAAPAST VPGPTLAPQP SSVKTIYQV LNSRLCIKA 240
 BMGIQLIVQD KESVFSPPRY FNIDPNATQA SGNCGTRKSN LLLNFGGGFV NLFTTKDEBS 300
 YYISEVGAYL TVSDPETVYQ GIKHAVVMFQ TAVGHSFKCV SEQSLQLSAH LQVKTTDVQL 360
 QAFDFEDDHP GNVDECSSDY TIVLPVIGAI VVGLCLMGMG VYKIRLRQCS SGYQRI

Seq ID NO: 231 DNA sequence

Nucleic Acid Accession #: NM_005409.3

Coding sequence: 94..378

50 1 11 21 31 41 51
 TTCCTTTTCT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CACAGCACCC AGCAGCACCA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 55 TGCTTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAAGTAACA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAAT 300
 AAAGGACAAC GATGCTTAAA TCCCAAATCG AAGCAAGCAA GGCTTATAAT CAAAAAGATT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 60 AGACTTTTCT ATGGTTTTGT GACTTTCRAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGAG ACCAAAAACA GAAATACAGT CTTCTGAAAT GAATGACAA CAGAATTCCA 600
 CTGCCCAAAG GAGTCCAGCA ATTAATATGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTTACCATC GGAATTTACA AAGTGCTTTC ACGTTCTTAC TTGTTGTATT ATACATTCAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 65 GAGAACAATT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGGTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTTCC 960
 CCAAAATATG TGTAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 70 TGGGATACAG GCAACAGTGC ACATATTTCA TAACCAAATT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATC CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 TGTACTTTTT GTTTGTATAC GTTTGTATAA ATGATAGCAA TATCTGGAC ACATTTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAAAT TATACCTAGC 1320
 AATCACTTTT ACTTTTTGTA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTCTT 1380
 75 TGTTCATGTC CTATATACAG TAAAAATTA GATATCTCAA GACTAGTTTA AAGAAATCAA 1440
 GTCTTTTATT TCTCTAATAA ACTACCACAA CCTTCTTTT TTAATAAAAA AAA

Seq ID NO: 232 Protein sequence

Protein Accession #: NP_005400.1

80 1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVQ GPPMFKRGRG LCIGPGVKAV KVADIEKASI MYPNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNP

Seq ID NO: 233 DNA sequence
Nucleic Acid Accession #: NM_000577.1
Coding sequence: 41..520

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5      1      11      21      31      41      51
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GGCAAGAGGG GAAGACCTCC TGTCCTATCA GGCCTTCCCC ATGGCTTTAG AGACGATCTG 60
CGACCCCTCT GGGAGAAAAAT CCAGCAAGAT GCAAGCCTTC AGAATCTGGG ATGTTAAACCA 120
GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCCGGA TACTTGCAAG GACCAAAATGT 180
CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGCAATT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCCTT 360
CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCTGCC CCGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
CGTCATGGTC ACCAAATTCT ACTTCCAGGA GGACGAGTAG TACTGCCAG GCCTGCCTGT 540
TCCCATTTCT GCATGGCAAG GACTGCAGG ACTGCCAGTC CCGCTGCCCC AGGGCTCCCG 600
GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCACAACAA 660
CTTGGTCAAA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGTGTC CTCAGAAATG 720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTGCA CAAAGCCCTT CCATGTGCC 780
TCTGCACTCA GGATCAAAAC CCGACCACCT GCCCAACCTG CTCTCCTCTT GCCACTGCCT 840
CTTCTCCTCT CATTCACACT TCCCATGCC TGGATCCATC AGGCCACTTG ATGACCCCCA 900
ACCAAGTGGC TCCACACCCC TGTTTTACAA AAAAGAAAAG ACCAGTCCAT GAGGGAGGTT 960
TTTAAGGGTT TGTGGAATAA GAAAATTAGG ATTTCAATGAT TTTTITTTTT CAGTCCCGGT 1020
GAAGGAGAGC AGTTTCTCAG GAGATTATGT TCTTTCGGGG AGAGGCTGAG GACTTAAAT 1080
ATTCTGTCAT TTGTGAAATG ATGTGAAAG TAAAGTGTAG CTTTTCCTCT CTTTTCCTC 1140
TTTTTTTGTG ATGTCCCAAC TTGTAAAAAT TAAAGTTAT GGTACTATGT TAGCCCATTA 1200
ATTTTTTTTT TCCTTTTAAA ACACTTCCAT AATCTGGAAT CCTCTGTCCA GGCCTCTGCT 1260
CCGAGCCTCC AAGCTCCATC TCCACTCCAG ATTTTITACA GCTGCCTGCA GTACTTTACC 1320
TCCTATCAGA AGTTTCTCAG CTCCTCAAGGC TCTGAGCAAA TGTGGCTCCT GGGGTTCTT 1380
TCTTCTCTGT CTGAAGGAAT AAATTGCTCC TTGACATTGT AGAGCTCTGT GCACTTGGAG 1440
ACTTGTATGA AAGATGGCTG TGCCTCTGCC TGTCTCCCC ACCAGGCTGG GAGCTCTGCA 1500
GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCCAAGCA CCTAGCCTCG 1560
CTCTTGGCAG GTACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAAAGT TCCCTACTTC 1620
CTGTGACTTC AGCTCTGTTT TACAATAAAA TCTTGAAAAAT GCCTAAAAAA AAAAAAAA 1680
AAAAA

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Seq ID NO: 234 Protein sequence
Protein Accession #: NP_000568.1

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40     1      11      21      31      41      51
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MALETICRPS GRKSSRMQAF RIWDVNQKTF YLRNNQLVAG YLQGPVNLE EKIDVVPPIEP 60
HALFLGIHGG RMCLSCVKSQ DETRLQLEAV NITDLSNRK QDKRPAFIRS DSGPTTSFES 120
AACPGWFLCT AMEADQFVSL TNMPDEGVMV TKFYFQDEE

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Seq ID NO: 235 DNA sequence
Nucleic Acid Accession #: NM_001840.1
Coding sequence: 149..1567

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50     1      11      21      31      41      51
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GGGGACTACG GAGAGCTCTG CAGGGAGCCG AGGCCCCCGC CCGGGCCAAG GGAGCTTCTG 60
TCCCGAGGAC CAGGGGATGC GAAGGGATTG CCCCCTGTGG GTCACTTTCT CAGTCATTTT 120
GAGCTCAGCC TAATCAAGA CTGAGTTAT GAAGTCGATC CTAGATGGCC TTGAGATAC 180
CACCTTCCGC ACCATCACCA CTGACCTCCT GTACGTGGGC TCAATAGACA TTCAGTACGA 240
AGACATCAAA GGTGACATGG CATCCAAATT AGGGTACTTC CCACAGAAAT TCCCTTTAAC 300
TTCTTTTAGG GGAAGTCCCT TCCAAGAGAA GATGACTGCG GGAGACAACC CCCAGCTAGT 360
CCAGCAGAGC CAGGTGAACA TTACAGAATT TTACAACAAG TCTCTCTCGT CCTTCAAGGA 420
GAATGAGGAG AACATCCAGT GTGGGGAGAA CTTCTATGAC ATAGAGTGT TCATGGTCTC 480
GAACCCAGC CAGCAGCTGG CCATTGCACT CCTGTCCCTC ACGCTGGGCA CCTTCAAGGT 540
CCTGGAGAAC CTCCTGGTGC TGTGCTCAT CTCTCACTCC CGCAGCCTCC GCTGCAGGCC 600
TTCTTACCAC TTCTATCGGC GCCTGGCGGT GGCAGACCTC CTGGGGAGTG TCATTTTGT 660
CTACAGCTTC ATTGACTTCC ACGTGTCCA CCGCAAGAT AGCCGCAAG TGTTTCTGTT 720
CAAACTGGGT GGGGTCAAG CTTCTTCCAC TGCTTCGTG GGCAGCTGT TCCTCAGCG 780
CATCGACAGG TACATATCCA TTCACAGGCC CCTGGCTTAT AAGAGGATTG TCACAGGCC 840
CAAGCCCGTG GTGGCGTTTT GCCTGATGTG GAACATAGCC ATTGTGATCG CCGTGTCTGC 900
TCTCTGGGC TGAAGTGGC AGAAACTGCA ATCTGTTTGC TCAGACATT TCCACACAT 960
TGATGAACCT TACCTGATGT TCTGGATCG GGTCAACAGC GTACTGCTTC TGTTTATGTT 1020
GTATGGTAC ATGTATATT TCTGGAAGGC TCACAGCCAC GCCGTCCGCA TGATTACAGC 1080
TGGCACCCAG AAGAGCATCA TCATCCACAC GTCTGAGGAT GGAAGGTAC AGGTGACCCG 1140
GCCAGACCAA GCCCGCATGG ACATTAGGTT AGCCAAGACC CTGGTCTGTA TCCTGTGTTG 1200
GTGATCATC TGCTGGGCGC CTCTGCTGCA AATCATGGTG TATGATGTCT TTGGGAAGAT 1260
GAACAAGCTC ATTAAGACGG TGTTCGATT CTGCAGTATG CTCTGCTGTC TGAATCTCAC 1320
CGTGAACCCC GTCACTATG CTCTGAGGAG TAAGGACCTG GCACAGCTT TCCGAGCAT 1380
GTTTCCCTCT TGTGAAGGCA CTGCGCAGCC TCTGGATAAC AGCATGGGGG ACTCGGACTG 1440
CCTGCACAAA CAGCACAACA ATGCAGCCAG GTTTCACAGG GCCCGAGAAA GCTGCATCAA 1500
GAGCAAGGTC AAGATTGCCA AGGTAACCAT GTCTGTGTCC ACAGACAGCT CTGCCAGGCC 1560
TCTGTAGGCC TGATGCCTCC CTGGCAGCAC AGGAAAGAAA TTTTITTTTT TAAGCTCAAA 1620
ATCTAGAAGA GTCTATTGTC TCCTTGGTTA TATTTTTTTA ACTTTACCAT GCTCAATGAA 1680
AAGGTGATTG CCACATGTCA CTTATTGCT TAGTTTCCGT TTGGGCTAAT CTTCCGGGGT 1740
TGTAGGAAA CCTTT

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Seq ID NO: 236 Protein sequence
Protein Accession #: NP_001831.1

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1      11      21      31      41      51
|      |      |      |      |      |
5  MKSILDGLAD TTFRTITDDL LYVGSNDIQY EDIKGDMASK LGYFPQKFFL TSFRGSPFQE 60
    KMTAGDNPOL VPADQVNITE PYNKSLSSFK ENEENIQOGB NFMDIECFMV LNPSQOLAIA 120
    VLSLTLTGFT VLENLLVLCV ILHSRSLRCR PSYHFIGSLA VADLLGSVIF VYSFIDFHV 180
    HRKDSRNVPL FKLGGVTASP TASVGSFLFT AIDRYISIH  PLAYKRIVTR PKAVVAPCLM 240
    WTIAIVIAVL PLLGWNCEKL QSVCSDFPH IDETYLMPWI GUTSVLLLF  VYAYMYILWK 300
    AHSHAVRMIQ RGTQKSIH  TSEDGKVQVT RPDQARMDIR LAKTLVLILV VLIICWGPLL 360
10  AIMVYDVFQG MNKLIKTVFA FCSMLCLLNS TVNPITIALR SKDLRHAFRS MPSCCEGTAQ 420
    PLDSMGDSD CLHKHANNA  SVHRAESCI KSTVKIAKVT MSVSTDTSAE AL

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Seq ID NO: 237 DNA sequence

Nucleic Acid Accession #: NM_016083.2

Coding sequence: 64..1482

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1      11      21      31      41      51
|      |      |      |      |      |
20 GATTGCCCCC TGTGGGTCAC TTTCTCAGTC ATTTTGAGCT CAGCCTAATC AAAGACTGAG 60
    GTTATGAAGT CGATCCTAGA TGGCCTTGCA GATACCACT TCGCACCAT CACCCTGAC 120
    CTCCTGTACG TGGGCTCAAA TGACATTCAG TACGAAGACA TCAAAGGTGA CATGGCATCC 180
    AAATTAGGGT ACTTCCACCA GAAATTCCTT TTAACCTTCT TTAGGGGAAG TCCCTTCCAA 240
    GAGAAGATGA CTGCGGGAGA CAACCCCCAG CTAGTCCAG CAGACCAGGT GAACATTACA 300
    GAATTTTACA ACAAGTCTCT CTGTCCTTC AAGGAGAATG AGGAGAACAT CCAGTGTGGG 360
25 GAGAACTTCA TGGACATAGA GTGTTTCATG GTCTGAACC CCAGCCAGCA GCTGGCCATT 420
    GCAGTCTGT CCCTCACGTG GGGCACCTTC ACBGTCTTGG AGAACCTCCT GGTGCTGTGC 480
    GTCATCTCTC ACTCCCGCAG CCTCCGCTGC AGGCCTTCTC ACCACTTCAT CGGCAGCTGC 540
    GCGGTGGCAG ACCTCCTGGG GAGTGTCTAT TTTGTCTACA GCTTCATTGA CTTCACGCTG 600
    TTCCACCGCA AAGATAGCCG CAACGTGTTT CTGTTCAAAC TGGGTGGGGT CACGGCTCTC 660
30 CTCACCTGCT CCGTGGGCAG CCGTCTCTC ACAGCCATCG ACAGGTACGT ATCCATTAC 720
    AGGCCCTTGG CCTATAAGAG GATTGTCAAC AGGCCCAAG CCGTGGTGGC GTTTTGCTG 780
    ATGTGGACCA TAGCCATTGC GATCGCGGTG CTGCTCTCC TGGGCTGGAA CTGCGAGAAA 840
    CTGCAATCTG TTTGCTCAGA CATTTTCCCA CACATTGATG AAACCTACCT GATGTTCTGG 900
    ATCGGGGTCA CCAGGCTACT GCTTCTGTTT ATCGATGATG CGTACATGTA TATTCTCTGG 960
35 AAGGCTCACA GCCACGCGGT CGCATGATT CAGCGTGGCA CCCAGAAGAG CATCATCATC 1020
    CACACGCTCG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG CATGGACATT 1080
    AGGTTAGCCA AGACCTCTGT CCTGATCCTG GTGGTGTGA TCATCTGCTG GGGCCCTTTG 1140
    CTTCGCAATC TGGTGTATGA TGTCTTTGGG AAGATGAACA AGCTCATTAA GACGGTGTTC 1200
    GCATTCTGCA GTATGCTCTG CCTGCTGAAC TCCACGTAAC ACCCATCAT CTATGCTCTG 1260
40 AGGAGTAAGG ACCTGCGACA CGCTTCCCG AGCATGTTTC CCTCTTGTGA AGGCACTGCG 1320
    CAGCCTCTG ATAACAGCAT GGGGGACTCG GACTGCTGCG ACAAACACGC AAACAATGCA 1380
    GCCAGTGTTC ACAGGGCCGC AGAAAGCTGC ATCAAGAGCA CGGTCAAGAT TGCCAAGGTA 1440
    ACCATGCTCG TGTCCACAGA CAGCTGCGC GAGGCTCTGT GAGCCTGATG CCTCCCTGGC 1500
    AGCACAGGAA AAGAATTTT TTTTAAAGC TCAAAATCTA GAAGAGTCTA TTGCTCTCTT 1560
45 GGTATATATT TTTTAACTTT ACCATGCTCA ATGAAAAGT GATTGTCAAC ATGATCATCT 1620
    ATCAGTTTGC TAATGTTTCC ATAGTTTAGG TACTCAAAC CTATTCTCCA GGGGTTTACA 1680
    GTGAAGAAAG CCTGTGTGTT AAGTGAAGTGA ACGATCCTTC AAAGCTCTCA TGAATAGGTA 1740
    GGGAAACCTT TGGCTACACA ATTGGAAGTC TAAGAACCCA TGGAAAAATG CCATCAAATG 1800
    AATAATGCTT TGTGAACCA AACTTCACT ATAATGTGAA ATGTAACGT CCGTAGTATC 1860
50 AGAGATGTCC ATTTTACAA GTTATAGTAC TAGAGATATT TTGTAAAA  TATTATGTCC 1920
    TGTGAGATGT GTATCAGTGT TTATGTGCTA TTAATATTG TTTAGTTTCA CAAAACGTGA 1980
    AGGTAGACTT TTATGAGAAC AATGGACAAG CAGTGGATAC GTGTCAATGT GTGCATTTT 2040
    TTTCTATATT ATTGCCCATG ATATAACTTT AGAAATAAAC CTTAATATTT CTTCAAATAT 2100
    CTCTATTAA TTTTGAACCT GAAATAACCG TAAAGGTTTA TTTTCTGTT ACCTCAACAA 2160
55 GAAGAAATTTG AAGACTTCAA AATATTGAGC AGAATTCATT CATACTTAAA AATTTATTAG 2220
    CCCTGCATT TCATAGGAAG ACACATTATC TTCTGGACTA TAGCTGTTCT AATGGATTAT 2280
    AATCAGAAAG GAAGAGAGCA AGCATATTGA CTTTTTTGA GCGACATCTC TGACTTTCTT 2340
    TAGTCTTTAG CTATTACTGG ATCTCTTAAG ACAGCATGTG TTAATCTTAA TGTATATCGT 2400
    TATCACTGTG CAGTTGCTGT TTACTTGAAT AGTATTGTGT TCTATATTC CAGGTTTAA 2460
60 TAGATTTCAT GCCTGGGTGG CCAACAACA GTCTTCATT TTTTAAATG AAAAGAAGTA 2520
    GTGTCTGATC CAGTAAATTT ATACTGTGTG TGAAGTGAAG TATAAATGTG TGTATGTGTG 2580
    TTTCTGTCCG TAACTGTTAC AGTAATGTCA TAAAGTGAGA AAACGTGTAC CAAGTATAAA 2640
    CTTTTACCAC TTGCTGCACT CTGACATAG GATTCACTT CTAAATTTGA GTTCTTCTG 2700
    TAATCTTGTT GATAAAATA CTGACTCCAA CCATTCAAAA ATTTACACCC ATCCTCTCTT 2760
65 AAGAGATTGG ATCAAGTATT ACTAAATTGA CCTTTAGGTA TTACACAAGA CCAAGTCTTA 2820
    GCAAAAAATA ATGACAGGCA TCCAAGGAAG GGATGTATT GTAGTGTATT TGCCAGGAAA 2880
    GGAGAGTACT TTGGTTTCTG AGCACCGAAT ATTGAGCAAT ATGTCACTCA CTAAGAGGAA 2940
    GACAGTTCTA CAGAAAAACA AATGTAACA TTTTCAATA CGGTGTGTAG ATAGATGCA 3000
    CTATATACAT CAGTTTAAAG TAGGACTATC ACACCCAGCC CATGTGGCTA AAAAAGCTGA 3060
70 ATCAGACAGT GGATGAGACA CACAACGGCA GTGAAGAACC GATACACTTG GCATTGACGT 3120
    CTAGCTATGC TGTATCTGTG CTTTGGCCAC ATGCCCTTGG TGACAGCTGA GCACCCAGCT 3180
    CTGTCTTGGT AGGTTTGGGC TAAGGAACAA ATCTCTCTT TGCTGTGTGT TAGCAGATA 3240
    CACTCAAGCA TGAAGATAAA CACAGCTGCT TTCTTCTTAC ACCCGGCTCT CATGCTCTT 3300
    AATGGCGCCA TGGGTGCTTG TTGGGCTTT TTCCAGTAAG GAATGATATT GCTGAAGAA 3360
75 CTACTTAACC CTGACAAATT TTAATTATAA TCTCTCTTA TACAGATAAA ACATGACTCC 3420
    TACAAGGCCC CAAGGTTTAC ATAGTCTGAA GTGAAGTACA GAGCTGGCAT CTATCTGGTG 3480
    ATTTCTAGCT CTGAGATAC CCAAGCAGCC TGATGGGGCA GTTCCCTCTT TTAAGGTTCA 3540
    CGCTCAAGG CAGGATGTGG CTTATGAGAT ACTTGTCAAT GTCTGTCTGC ACACCTTGAA 3600
    TCTGCTCTGT GGTCTCCCTTA CTTTACTCT CTGTCTGTG CAGATGAAGG CTCAGGCTGC 3660
80 TAGAGGATTA GTAAGATCTC TTTCTAAAGA CAGGAGAGAT TATTTACAAG AAGAACTCAC 3720
    CAGGTTTATG TTTGCAATTA AGAATTGCCA GTCTTTTGTG CTGCATCATC TTGAACATTA 3780
    ATCCACATGT TTCAGAGCTC ACCAGGCAGT ACCAATGCTC TTTTCAAGC TATGAAGAGC 3840
    TAGAGAAATT CTTGTTATGG TAGAAAAATT TCACGGTTCA TTTTGAAGC TGCATTTGTG 3900
    CGTATGCAGT GTAGATTTTA TAGTGTGTG TGCTTTCAAG ATCTAAATCA TATATAATAA 3960

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ATTAAGGGAC AATGGGGCTG ACAGCACTAA ACTTGGTGCT TATTGATATT CTAAGAAATA 4020
 TCTGTGAAAT ATCATCAGT ATGTTATACA ACCTTCATTT AAAAAGGTTT AAAACTAGTT 4080
 AGATTCACTT TGACACTTTT CATATCATTT CTTAACCCAA GTGACGAAAA CATGTGCCCC 4140
 AATGAATATA CTCATTAGAA TTACCAATTG TTAATATCAC TCATTAAATTA ACCCCATAAT 4200
 TAGATCCATT AATTAAATG ATTTAAATTT AAGTAAGTTT TATAAGGTCT GACATCAGAG 4260
 GTATCTTACT TTCTCTGAG GATGATGTAC TTGCCCTGAC CATGCATTTT ACCATCACAC 4320
 ATGTTTCAGAA AGGGCCAAAT TCCCAACCTG CTCATTTTIT TTTTATCAG AGTCATGATG 4380
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 ATGTTTAGAG AGTGGCCTAC AAATCAGTAA TTTTCGGGTG GGAGAGTTTC TTTACATTGC 4980
 CGTGGCATCT TAAAGGCTAT CTTCATGTAA ATTGACTGTA CTAGGCCTAC TGGGGATCAG 5040
 AGTTCCTCAAG AAGAGAAACC TTTCTTGTG TCTGGATTCA AATTATTTC CAATGTTTCA 5100
 AGCGGAAAC ATGACTCTTT ATTTCTGTA AATCTAACAT TATTACTTTT CCTCTTAGAA 5160
 GAATATTGTA TTGTATAGAT TTTGTGAGC TGGTAACATC GTTGCAACCA CTGCAATATC 5220
 TTCTTTAGAG ATCTGTATGA TACTTTGTAT ACAAGTACTG GTAAGATTGT TATTAAATGT 5280
 AGCTTCAGTC ATTAATTTAT TATAGCAAG TAGTACTTCT TCTGTAATAT TTACAATGTA 5340
 TTAAGCCAC AGTATATTTT ATTTCAATGT AATTAACTG TTAACCTATT CAAAGAGAAA 5400
 ACATCTCATC ATGTCTATTG TCCAAAGTTA CCTGGAATCA AATAAAAAAT CTAGATTACC 5460
 ATGAAGACA TA

Seq ID NO: 238 Protein sequence
 Protein Accession #: NP_057167.1

1 11 21 31 41 51
 MKSILDGLAD TTFRTITDL LYVGSNDIQY EDIKGDMASK LGYFPQKFPF TSFRGSPFQF 60
 KMTAGDNPLQ VPADQVNITE FYNKSLSSFY ENEENIQCGE NFMIDIECFMV LNPSQQLAIA 120
 VLSLTGTGTF VLENLLVLCV ILHSRSLRCP SYHFIGSLA VADLLGSVIP VYSFIDPHVF 180
 HKRDSRNPLF FKLGGVTASL TASVGSFLFT ALDRYVSIHR PLAYKRIVTR PKAVVAFCLM 240
 WTIAIAIAVL PLLGWNCEKL QSVCSDFPHI IDETYLMEFWI GVTSVLLLFV VYAYMYILWK 300
 AHSVAVRMIQ RGTQKSIITH TSDEGKVQVT RPDQARMDIR LAKTLVLILV VLIICWGPLL 360
 AIMVYDVFGK MNKLIKTVFA PCSMLCLNST TVNPIIYALR SKDLRHAFRS MPFSCBETAQ 420
 PLDSMGDSDC LHKHANNAA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE AL

Seq ID NO: 239 DNA sequence
 Nucleic Acid Accession #: NM_033181.1
 Coding sequence: 17..1252

1 11 21 31 41 51
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 CTGTACGTGG GCTCAATGA CATTCACTAC GAAGACATCA AAGGAGAATG AGGAGAACAT 120
 CCAGTGTGGG GAGAACTTCA TGGACATAGA GTGTTTCATG GTCCGAACCC CCAGCCAGCA 180
 GCTGGCCATT GCAGTCCTGT CCTCAGCCTC GGGCACCTTC ACGTCTCTGG AGAACCTCCT 240
 GGTGCTGTGC GTCACTCTCC ACTCCCGCAG CCTCCGCTGC AGGCCTTCTC ACCACTTCAT 300
 CGGCAGCCTG GCGGTGGCAG ACCTCCTGGG GAGTGTGATT TTTGTCTACA GCTTCATTGA 360
 CTTCACAGTG TTCCACCGCA AAGATAGCCG CAACGTGTTT CTGTTCAAACT TGGGTGGGGT 420
 CACGGGCTCT TCACTGTGCT CCGTGGGCAG CCTGTTCTCT ACAGCCATCG ACAGGTACAT 480
 ATCCATTCACT AGGCCCTCTG CCTATAAGAG GATTGTCACT AGGCCCAAGG CCGTGTGTGG 540
 GTTTTGCTCG ATGTGGACCA TAGCCATTGT GATCGCCGTG CTGCCTCTCC TGGGCTGGAA 600
 CTGCGAGAAA CTGCAATCTG TTTGCTCAGA CATTTCCTCA CACATTGATG AAACCTACCT 660
 GATGTTCTGG ATCGGGGTCA CCAAGCTACT GCTTCGTGTC ATCGTGTATG CGTACATGTA 720
 TATTCTCTGG AAGGCTCACA GCCACGCGCT CGCATGATT CAGCGTGGCA CCCAGAAGAG 780
 CATCATCATC CACAGCTCTG AGGATGGGAA GGTACAGGTG ACCCGGCCAG ACCAAGCCCG 840
 CATGGACATT AGGTTAGCCA AGACCTGGT CCTGATCCTG GTGGTGTGTA TCATCTGCTG 900
 GGGCCCTCTG CTGCAATCA TGGTGTATGA TGTCTTGGG AAGATGAACA AGCTCATTA 960
 GACGGTGTGT GCATTCTGCA GTATGCTCTG CCTGCTGAAC TCCACCGTGA ACCCCATCAT 1020
 CTATGCTCTG AGGAGTAAGG ACCTGGGACA CGCTTTCGG AGCATGTTTC CCTCTTGTGA 1080
 AGGCACTGCG CAGCCTCTGG ATAAACAGAT GGGGACTCG GACTGCTGCA ACAACACAGC 1140
 AAACAATGCA GCCAGTGTTC ACAGGGCCGC AGAAAGCTGC ATCAAGAGCA CGGTCAAGAT 1200
 TGCCAAAGTA ACCATGTCTG TGTCCACAGA CACGTCTGCC GAGGCTCTGT GA

Seq ID NO: 240 Protein sequence
 Protein Accession #: NP_149421.1

1 11 21 31 41 51
 MALQIPPSAP SPLTSCMAQ MTPSTKTSKE NEENIQCGEN FMDIECFMV LNPSQQLAIAV 60
 LSLTLGTPTV LLENLLVLCV LHSRSLRCP SYHFIGSLAV ADLLGSVIP VYSFIDPHVF 120
 RKDSRNPLF KLGGVTASPT ASVGSFLFTA IDRYISIHRL LAYKRIVTRP KAVVAFCLMW 180
 TIAIVIAVLP LLGWNCEKLQ SVCSDFPHI DETYLMEFWI VTSVLLLFV VYAYMYILWKA 240
 HSHAVRMIRQ GTQKSIITHT SEDGKVQVTR RPDQARMDIR ARTLVVLILV LIIICWGPLLA 300
 IMVYDVFGMK MNKLIKTVFA PCSMLCLNST VNPPIIYALR KDLRHAFRS MPFSCBETAQ 360
 LDNSMGDSDC LHKHANNAA SVHRAAESCI KSTVKIAKVT MSVSTDTSAE L

Seq ID NO: 241 DNA sequence
 Nucleic Acid Accession #: NM_003596.1

Coding sequence: 82..1194

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5	GTAGACTGTC	CATGGCCTGA	ACATTTTCOG	AAAATCATT	TGAGCAAAAT	ATCTGTTTAA 60
	TAACAAGATA	ACCACATCAA	GATGGTTGGA	AAGCTGAAGC	AGAACTTACT	ATTGGCATGT 120
	CTGGTGATTA	GTTCTGTGAC	TGTGTTTAC	CTGGGCCAGC	ATGCCATGGA	ATGCCATCAC 180
	CGGATAGAGG	AACGTAGCCA	GCCAGTCAAA	TTGGAGAGCA	CAAGGACCAC	TGTGAGAACT 240
10	GGCCTGGACC	TCAAAGCCAA	CAAAACCTTT	GCCTATCACA	AAGATATGCC	TTTAATATTT 300
	ATTGGRGGTG	TGCCTCGGAG	TGGAACCACA	CTCATGAGGG	CCATGCTGGA	CGCACATCCT 360
	GACATTGCGT	GTGAGAGGGA	AACCAGGGTC	ATTCCTCCGAA	TCCTGGCCCT	GAAGCAGATG 420
	TGGTCACGGT	CAAGTAAAGA	GAAGATCCGC	CTGGATGAGG	CTGGTGTTC	TGATGAAGTG 480
	CTGGATTCTG	CCATGCAAGC	CTTCTTACTA	GAATTTATCG	TTAAGCATGG	GGAGCCAGCC 540
15	CCTTATTTAT	GTAATAAAGA	TCCTTTTGCC	CTGAATCTTT	TAACTTACCT	TTCTAGGTTA 600
	TTCCCCAATG	CCAAATTTCT	CCTGATGGTC	CGAGATGGCC	GGGCATCAGT	ACATTCAATG 660
	ATTCTCGAAT	AAGTTACTAT	AGCTGGAATT	GATCTGAACA	GCTATAGGGA	CTGTTTGACA 720
	AAGTGGAAAT	GTGCTATAGA	GACCATGTAT	AACCAAGTGA	TGGAGGTTGG	TTATAAAAAAG 780
	TGCATGTTGG	TTCACTATGA	ACAACTGTGC	TTACATCCTG	AACGGTGGAT	GAGAACACATC 840
20	TTAAAGTTCC	ATGGAACCCAC	TCAGTATTGC	ACCATGAAGA	GATGATTGGG	900
	AAAGCTGGGG	GAGTGTCTCT	GTCAAAAGTG	GAGAGATCTA	CAGACCAAGT	AATCAAGCCA 960
	GTCAATCGAG	GAGCTCTATC	AAAATGGGTT	GGGAAGATAC	CGCCAGATGT	TTTCAAGACA 1020
	ATGGCAGTGA	TTGCTCCTAT	GCTTGCCCAAG	CTTGATATG	ACCCATATGC	CAACCCACCT 1080
	AACCTACGAA	AACCTGATCC	CAAAATTTAT	GAACACATC	GAAGGTCTTA	TAAGGGAGAA 1140
25	TTCCAACATC	CTGACTTTCT	TAAAGAAAAA	CCACAGACTG	AGCAAGTGGG	GTAGCAGAAC 1200
	CAGGAGCCTC	TTCCATACAT	GAGGAAAGAT	TGCTGCCTTT	TCAGCAGAAAG	GGAAATTCCT 1260
	AGGATTGGCT	GTCCCTTGCC	AAGCTTGCTG	GAGCGTCTGC	ACCTTGGCTG	CGCGGCTGCT 1320
	GCAITTGCCA	GTTTCCCTCC	ACTGAGAGGA	TGGAGGTGTC	CGCACAGCTT	TGGGCTCGT 1380
	GAGGATCTGC	CCTCCTGAGC	AAAGAGCTCT	TGATCCCGAT	TTCATGCACA	GGCCTGCATG 1440
30	AAGGAGCCCA	GAAAGAACAT	GTGTTTCTGT	TTAAACTCC	TCTTGTCTCT	TTTTCTTACA 1500
	TTATGACGTT	TGTTTCAAG	GAGAGGGTTT	AAAAATGGGA	TCCTGTAAGC	AGACTTGGCG 1560
	AGTCTCCTTT	TGAATAGGT	TGTTCTGTACA	TGTTCTAATG	TTTTGTAGAA	CAAGTGTGCC 1620
	TGTTTAAAGT	TATGATGTG	AATAATATTA	AATATCCTAA	TTATTTAATT	CATTGTATTG 1680
	TTTCTGAGAA	GTTGGGAAAT	TACCATTATA	CATTTACAAC	CTAATGACTT	TTGTATTTTA 1740
35	TTTTTCAAAA	TAAAGCTTT	CAATGTGA			

Seq ID NO: 242 Protein sequence
Protein Accession #: NP_003587.1

1	11	21	31	41	51	
40	MVGLKQLNLL	LACLVISSVT	VFYLGQHAME	CHHRIEERSQ	PVKLESTRRT	VRTGLDLKAN 60
	KTFAYHKDMP	LIFIGGVFRS	GTTLMRAMLD	AHPDIRCGEE	TRVIPRIILAL	KQMWRSRSKE 120
	KIRLDEAGVT	DEVLDASAMQA	FLLEIIVKGG	EPAPYLCKND	PPALKSLTYL	SRLPFNAPKL 180
	LMVRDGRASV	HSMTSRKVTI	AGFDLNSYRD	CLTKWNRAIE	TMYNQCMVEG	YKKCMLVHYE 240
45	QLVLHPERWM	RTLKFLQIP	WNHSLVHHEE	MIGKAGGVSL	SKVERSTDQV	IKPVNVGALS 300
	KWVGKIPPDV	LQDMAVIAPM	LAKLGYDPYA	NPPNYGKPD	KIIENTRRVY	KGEFQLPDPL 360
	KEKPQTEQVE					

Seq ID NO: 243 DNA sequence
Nucleic Acid Accession #: NM_001492.3
Coding sequence: 1395..2513

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	CGAGCGGGCG	GTATGGCGGC	GGCGGGGCCC	CGCGCGGGCC	CGAGCGGCCC	CGAGCCCATG 120
	CCGAGCTACG	CGCAGCTAGT	GCAGCGCGGC	TGGGGCAGCG	CGCTGGCGGC	GGCGCGGGGC 180
	TGCACGGACT	GGCGCTGGGG	GCTGGCGCGT	CGCGGCTGGG	CTGAGCACGC	GCACTTGGCG 240
60	CGCGCGGAGC	TGCTGCTGCT	GGCGCTGGGC	GGCGCTGGGC	GGAGCGGCGT	GGCGTGGCG 300
	GCCACTGGCG	GCCTCTTTCC	GGCGCTGGGC	AAGCGGTGCT	GCCTCCAGCC	CAGAGATGCC 360
	GCCAAGATGC	CGAGAGCGCG	TTGGAAGTTT	CTCTTCTACC	TGGGCGAGCT	GAGCTACAGT 420
	GCCTACCTGC	TGTTTGGCAC	CGACTACCCC	TTCTTCCATG	ACCCACCATC	TGCTTCTTAC 480
	GACTGGAGCG	CGGGCATGGC	AGTGCCACGG	GACATTGCAG	CGCCCTACCT	GCTCCAGGGA 540
65	AGCTTCTATG	GCCACTCCAT	CTACGCTACG	CTATACATGG	ACACCTGGCG	CAAGGACTCG 600
	GTGGTCATGC	TGCTCCACCA	CGTGGTCACT	CTCATCTCTA	TGCTCTCTCT	CTACGCTTTC 660
	CGGTACCAACA	ATGTGGGCAT	CCTTGTGCTC	TTCTTGCACG	ATATCAGTGA	CGTGCAGCTT 720
	GAGTTCACCA	AGCTCAACAT	TTACTTCAAG	TCCCGCGGCG	GCTCCTACCA	TCGGCTGCAT 780
	GCCTTGGCAG	CAGACTTGGG	CTGGCTCAGC	TTGGGCTTCA	GCTGGTCTTG	GTTCCGCTTC 840
70	TACTGGTTCC	CGCTCAAGGT	CCTGTATGCC	ACCACTCACT	GCAGTCTGCG	CACGGTGGCT 900
	GACATCCCTC	TCTACTTCTT	CTTCAATGCG	CTCTGCTGCG	TGCTCACTCT	TATGAACCTC 960
	TACTGGTTCC	TGTACATCGT	GGCGTTTGCA	GCCAAGGTGT	TGACAGGCCA	GGTGCACGAG 1020
	CTGAAGGACC	TGCGGGAGTA	TGACACAGCC	GAGGCCACGA	GCCTGAAGCC	CAGCAAAAGCC 1080
	GAGAAGCCAC	TGAGGAACGG	CCTGTGTAAAG	GACAAGCGCT	TCTGAACCCC	TGGGCCCCGC 1140
75	CCCGTGGAG	CCCGCCCCAC	CCCGAATACC	CCCGCCACGC	TCCCGTCTCT	TGGCGGCCCC 1200
	TCCACCCCTC	CCAACCTGTC	TCTCTAGGGG	CCCGCCACGC	CTCCCTGGGG	ACCCCGCCCC 1260
	CTCATCTGTC	CTCCATTTC	CCCGCAAGCC	CCCGAGGACC	CCTGCCCCCT	CGGGGACACC 1320
	GGCCCCGCCC	TCAGCCCACT	GGTCCCCGGC	CGCGCGGAC	CCTGCGCACT	CTCTGGTCAT 1380
	GGCTGGGAG	GAGATGCCA	CGCGCGCAGC	AAGGTCCCTG	CGGCAACCA	CTCTCTCTCC 1440
80	TCTGGGCTCC	GCTGCTGCC	TGCTGCCCC	TGAACCGGCG	CCCGTGGCCC	CCAGGCCAGG 1500
	CGCGCGCTCC	GCTCCAGGCT	CTAGGACTGC	GCGATGAGCC	CCAGGTGGCC	CCAGGCTTCC 1560
	GGCGGTTTCC	CCCGGTCAAT	TGGCGCTGT	TTGACGCGCG	GGACCCCGAG	GAGACCAAGT 1620
	CTGGCTCGCG	GCGGACGCTC	CCAGGGGTCA	CCCTGCAACC	GTGCCACGTT	GAGGAGCTGG 1680
	GGGTCCGCGG	AAACATCGTG	CGCCACATCC	CGGACCGCGG	TGCGCCACCC	CGGGCTCGGG 1740
	AGCCTGTCTC	GGCGCGGGG	CATTGCCCTG	AGTGGACAGT	CGTCTTGCAC	CTGTGGGCTG 1800

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TGGAAACCCG TGAGCGCCCG AGCCGGGCCC GCCTGGAGCT GCGTTTCGCG GCGGCGGCGG 1860
 CGGACGCCCC GGAGGGGCGC TGGGAGCTGA GCGTGGGCGA AGCGGGCCAG GGCGCGGCGC 1920
 CGGACCCCGG GCGGTGTCTG CTCGCCAGT TGGTGCCTCG CCTGGGCGCG CCAGTGGCGG 1980
 CGGAGCTGCT GGGCGCGCGT TGGGCTCGCA ACGCCTCATG GCGCGCGCAG CTCGCGCTGG 2040
 CGCTGGCGCT ACGCCCGCGG GCGCTGCGCG CCTGCGCGCG CCTGGCCGAG GCCTCGCTGC 2100
 TGCTGGTGAC CCTCGACCGG GCGCTGTGCC ACCCCTGGC CGGCGCGCGG CGCGACGCGG 2160
 AACCCGTGTT GGGCGGCGGC CCCGGGGGCG CTTGTGCGCG GCGGCGGCTG TACGTGAGCT 2220
 TCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCGCGG CGGCTTCCTG GCCAACTACT 2280
 GCCAGGTCGA GTGCGGCGTG CCCGTGCGCG TGTGCGGGTC CGGGGGGCGG CGGCGCTCA 2340
 ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCGGCCCC GGGAGCCGCG GACCTGCCTC 2400
 GCTGGGTGCC CGCGCGCGCT TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG 2460
 TGGTGTCTGG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG 2520
 CGGGCAGGGA CGGGGCCCC ACAATAAATG CCGGTGGTC TGCTC

Seq ID NO: 244 Protein sequence
 Protein Accession #: NP_001483.2

1 11 21 31 41 51
 20 MFPFQQGPGC KHLILLALL LPSLPLTRAP VPPGPAALL QALGLRDEPQ GAPRLRPVPP 60
 VMKRLFRRRD PQETRSGRSRR TSPGVTLQPC HVEELGVAGN IVRHIPDRGA PTRASEPVSA 120
 AGHCPSEWTVV FDLSAVEPAE RPSRARLELR PAAAAAAPE GGWELSAQA GQAGADPGP 180
 VLLRLQVLPAL GPPVRAELLG AAWARNASWP RSLRLALALR PRAPAACARL AEASLLLVTL 240
 DPLRLCHPLAR PRDAEPVLG GPPGGACRAR RLYVSEFREV WHRWIAPRG FLANYCQGGC 300
 25 ALPVALSGSG GPPALNHAUL RALMHAAPG AADLPCCVPA RLSPISVLFP DNSDNVVLRLQ 360
 YEDMVDECG CR

Seq ID NO: 245 DNA sequence
 Nucleic Acid Accession #: NM_021267.1
 Coding sequence: 17..1125

1 11 21 31 41 51
 35 ACGCGGGGCG CGCGGCTCGG TCGGCTACCG CGGGCGGGCG CAGGCGACGG GCACGGCGGG 60
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 CGAGCTACCG CGAGCTAGT GCGAGCGCGG TGGGGCAGCG CGCTGGCGCG GCGCGGGGCG 180
 TGCAOAGACT CGCGCTGGGG GCTGGCGCGT CGCGCGCTGG CTGAGCACGG GCACCTGGCG 240
 CGGCGCGGAG TGCTGCTGCT GCGCGCTGCG GCGCTGGGCT GGACCGCGCT GCGCTCGCGG 300
 GCGACTGCGC GCTCTTTTCG GCGCGTGGCG AAGCGGTGCT GCGTCCAGCC CAGAGATGCC 360
 40 GCCAAGATGC CGGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCAGCTG GAGCTACAGT 420
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 45 CGGTACCACA ATGTGGGCAT CTTTGTGCTC TTCTGCAAG ATATCAGTGA CGTGCAGCTT 720
 GAGTTACACA AGCTCAACAT TTACTTCAAG TCCCGGCGCG GCTCTTACCA TCGGCTGCAT 780
 GCGTTGGCAG CAGACTTGGG CTGCTCAGC TTGCGCTTCA GCTGGTCTCG GTTCCGCTTC 840
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 CCGCGTGGAG CGGCGCCACG CCGCAATACC CCGGCCACGG TCCCGTCTCT TGGCGCGCCC 1200
 55 TCCACCCCTC CCACTCTTGC TCTCTAGGG CCGCGGCCAC CTCCCTGGGG ACCCGCGCCC 1260
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 70 TGCTGGTGAC CCTCGACCGG GCGCTGTGCC ACCCCTGGC CGGCGCGCGG CGCGACGCGG 2160
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 TCGCGAGGTT GGGCTGGCAC CGCTGGGTCA TCGCGCGCGG CGGCTTCTCT GCCAACTACT 2280
 GCCAGGTCGA GTGCGGCGTG CCGGTGCGCG TGTGCGGGTC CGGGGGGCGG CCGGCGCTCA 2340
 ACCACGCTGT GCTGCGCGCG CTCATGCACG CGGCGGCCCC GGGAGCGCGC GACCTGCCTC 2400
 75 GCTGGGTGCC CGCGCGCGCT TCGCCCATCT CCGTGCTCTT CTTTGACAAC AGCGACAACG 2460
 TGGTGTCTGG GCAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG

Seq ID NO: 246 Protein sequence
 Protein Accession #: NP_067090.1

1 11 21 31 41 51
 80 MAAAGPAAGP TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60
 LLLALGALGW TALRSATAR LFRPLAKRCC LQPRDAAKMP ESANKFLPYL GWSYSAYLL 120
 FGTDYPPFPH PPSVFPYDWP GMAYPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180

LHHVVTLILI VSSYAPRYHN VGILVLFPHD ISDVQLEPTK LNIYFKSRGG SYHRLHALAA 240
 DLGCLSPGFS WFWRLYNFP LKVLVATSHC SLRTPVDIPP YFFFNALLLL LTLNMLYNFL 300
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5 Seq ID NO: 247 DNA sequence
 Nucleic Acid Accession #: NM_002081.1
 Coding sequence: 222..1898

10 1 11 21 31 41 51
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 CGGGACCTTG GCTCTGCCCT TCGCGGGCGG GAACTCGCA GGACCGGCGC AGGATCCGAG 180
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 15 GCTGGTGGCT GCTATGTGCG GCGGCAGCGC TGGTCCGCTG CCGCGCGCGG GACCGCGCCA 300
 GCAAGAGCCG GAGCTGCGGC GAGGTCCGCC AGATCTACGG AGCCAGGGGC TTCAGCCTGA 360
 GCGAGCGTCC CAGAGCGGAG ATCTCGGGTG AGCACTGCG GATCTGTCCC CAGGGCTACA 420
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 20 TGATGACCA CTTCAGCAC CTGCTGAACG ACTCGGAGCG GACGCTGCAG GCCACCTTCC 600
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 AGCTGGCGCT GTACTACGCG GGTGCCAAC TGCACTTGA GAGAGCGCTG GCGGAGTTCT 720
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 25 GAGAGCTGCG CTTGCGGGCC ACCCGTGCCT TCGTGGCTGC TCGCTCCTTT GTGCGAGGCC 900
 TGGGCGTGGC CAGCGACGCT GTCCGGAAG TGGCTCAGGT CCGCTTGGGC CCGGAGTGTCT 960
 CGAGAGCTGT CATGAGCTG GTCTACTGTG CTCACTGCTT GGGAGTCCCC GCGCGCAGGC 1020
 CTGCGCTGGA CTATTGCGGA AATGTGCTCA AGGCTGCTCT TGCCAAACAG GCGGACCTGG 1080
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 30 CATCGGGTGT GAGAGTGTTC ATGGGCGAGG TGACACGCTG GCTGGCGGAG GCCATCAACG 1200
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 35 TGAGCACTGC CAGTGATGAC CGCTGCTGGA ACGGATGTC CAGAGGCGCG TACCTCCCCG 1500
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 40 GCTCCAGCTC CCGGAGCGCC TTGACCATG CCTCCGAGG CCGTGTGAG CAGGAAGGAC 1800
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 TCCTGGCCCT TACAGTAGCC AGGCCCGGT GGCCTTAAC GCCCAAGGC CCGAGGACA 1920
 GAGGCCAAGG ACTGACTTTC CCAAAATAC AACACAGAG ATATTTAATT CACTCAGCC 1980
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 45 GTCCAGGCC CAGGCGTGGC CTGCGCTGCC TTTCTGCTT TTAATTTGT ATGAGGTCCT 2100
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 CTACAGAGGA GGCCTCAAG CAACCGCTG GAGCCACAG CAGGCTGTG CTCTCTCTCC 2280
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 50 CTTCCAGAGA AGCCCCGAC GGCCTGTCTG GGTGTGCGC ATCCAGGTC TGGCAGAGCC 2400
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 55 GAGGCGAGCG TGGGCTCTGC CAATGTGGGC TGCCCCCGC ACACAGGCTC CACAGGGCAG 2700
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 CAGGCTCAG AGTGACCTTC GGTGTCAAC TGCTCAGAG GATGTGTGTG GCTGTGAGA 2880
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 60 GCAAGGGGAG CTGATAGTT AAGGGCTTT CCAACATGC ATCCATTAC TGACACTTCC 3000
 TGCTCTGTT CATGGAGAGC TGTTCGCTCC TCCAGATGG CTTCGAGGC CCGCAGGGCC 3060
 CACCTTGAG CCGTGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCCAGGC 3120
 CTGCAAGGCG CCTCTTCCC TCCTGTGCCC CAGCTGCCAG GTGCGCTGG GAGGGGTGG 3180
 TGTGTTGTG GGAAGGGGTC CTGAGGGGG AGGAGGACTT GGAGGGTCTG GGGGCACTG 3240
 65 TCCTGAAGCG ACTGACCTTC AGGAGGCGC TTAGTGTGC TTTGCTTTTC ATCACGCTCC 3300
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 CTGACTTTAG ATGTTTTGGG ATCAGGAGCC CCAACACAG GCAAGTCCAC CCCATAATA 3420
 CCTGCCAGT GCCAGGTTGG GCTGGGACT CTGGCAGT GATGCCGCGC GCCAGGACAG 3480
 CAGCACTCCC GCTGCACACA GACGCGCTAG GGTGGGCTC CAGACCCAC CCTACGCTCA 3540
 70 TCTCTGGAAG GGGCAGCCCT GAGTGGTCA TGGTCAGGGC AGTGGCCAAG CCGTCTGTGT 3600
 CCTTCTCCA CAGGTCCCC CCAACGCTCA GTGTCAGGGC GTGACGTGTG TTCTTTGAG 3660
 TCCTGTATG AATAAAGGC TGAACCTA AA

75 Seq ID NO: 248 Protein sequence
 Protein Accession #: NP_002072.1

1 11 21 31 41 51
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 80 ICPQGYTCTT SEMSENLANR SHAELBTALR DSSRVLAQML ATQLRSPDDH FQHLNDSE 120
 TLQATFPFAP GELYTONARA FRDLYSELRL YRQANLHLE ETLAEFWARL LERLPKQLHP 180
 QLQLPDDYLD CLGKQAEALR PFGEAPRELR LRATRAFVAA RSFVQGLGVA SDVVRKVAQV 240
 PLGFECSRAV MKLVYCAHCL GVPGARPCPD YCRNVLKGCL ANQADLDAEW RNLLDSMVL 300
 TDKFNFTSGV ESVIGSVHTM LABAINALQD NRDTLTAKVI QGCGNPKVNP QGPGPEEKRR 360

RGKLAPRERP PSQTLEKLVS EAKAQLRDVQ DFWSLPGTL CSEKMLSTA SDDRCWNGMA 420
 RGRYLPFVVMG DGLANQINNP EVEVDITKPD MTIRQQIMQL KIMTNRLRSA YNGNDVDFPD 480
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5 Seq ID NO: 249 DNA sequence
 Nucleic Acid Accession #: NM_001492.3
 Coding sequence: 8..1864

10 1 11 21 31 41 51
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 GCGGGGTCCA GGCCCTGGGG CCCCGGGGTC CCCCTGCAGC GCCCGGCTCC CCTGCGGCCT 180
 15 CTCTTTCAGA GTCTGCTGA AGCCTGGGCT CTCAGAGGAG GCCGCGAGT CCGCGTGC 240
 CCTGGGGGCG GCGCTAGTG CGCGCGGACC GGTCTACACC GAGCAGCCCG GAGCGCCCGC 300
 GCCTGATCTC CCATGCCCCG ACGGGCTCTT GCAGGTGCCC TTCGGGAGCG CCTGGCCTGG 360
 CACCTTCTCT TTCACTATCG AACCTGGAG AGAGGAGTTA GGAGACACAGA TTGAGAGGCC 420
 CGCTTGAGAG CTCTGCGGCG GCGTGGCTGG CAGGCGGCGC TTGGCAGCGG GAGGCCCGTG 480
 GGCCCGGAGC ATTACGCGCG CAGCGGCTCG GAGCTGCGC TTCTCGTACC GCGCGCGCTG 540
 20 CGAGCGGCTT GCGGTGGGA CCGCGTGAC GCGCCTCTGC CGTCCGCGCA GCGCCCCCTC 600
 GCGGTGCGGT CCGGAGATGC GCCCTGCGCG ACCGCTCGAG GACGAATGTG AGCGCGCGCT 660
 GGTGTGCGGA GCAAGGCTGCA GCCCTGAGCA TGGCTTCTGT GAAACACCCG GTGAATGCCG 720
 ATGCTAGAGG GGTGAGACTG GACCCCTCTG CACGGTCCCT GTCTCCACCA GCAGCTGCCT 780
 25 CAGCCCGGAG GCGCGTCTCT CTGCTACCAC CGGATGCCTT GTCCCTGGGC CTGGGCCCTG 840
 TGACGGGAAC CCGGTGTCGA ATGAGGCGAG CTGTAGTGAG ACACCCAGGT CCTTTGAAATG 900
 CACCTGCCCG CGTGGGTCTT ACGGGCTGCG GTGTGAGGTG AGCGGGGTGA CATGTGCAGA 960
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 CTGCCACTGC CCACCTGGTT TCCAAGGCTC CAACTGTGAG AAGAGGGTGG ACCGGTGCA 1080
 30 CTGCGAGCCA TGGCGCAATG GCGGACTCTG CTTGGACCTG GGCCACGCCG TGGCTGCGCG 1140
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 TGCTCAAGGC GCGCGCTGCT ACGCCCACTT CTCGGGCTCT GTCTGCGCTT GCGCTCCCGG 1380
 35 CTACATGGGA GCGCGGTGTG AGTTCCCACT GCACCCGAG GCGCAAGCG CCTTGCCTCG 1440
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 ACTGCTCGTG GCGCGGCGCG TGGCGGCGCG TGCGCTCTTG CTGGTCCAGG TGGCGCGCGG 1560
 TGGCACTTCC CAGGATGCTG GGTCTGCTT GCTGCTGGG ACCCGGAGC CGTCACTCCA 1620
 CGCACTCCGA GATGACTCA ACAACCTAAG GACGAGGAG GGTTCGGGG ATGGTCCGAG 1680
 40 CTGCTCCGTA GATTGGAATC GCCCTGAAGA TGTAGACCTT CAAGGGAATT ATGTATATC 1740
 TGCTCTCTCC ATCTACGCTC GGGAGGTAGC GACGCCCCCT TCCCCCGCG TACACACTGG 1800
 GCGCGCTGGG CAGAGGCAGC ACCTGCTTTT TCCTTACCTT TCCTGATTC TGTGGTGA 1860
 ATGAATTGGG ATGAATCTCT GGAAGGTTTT AAGCCCATTT TCAGTCTTAA CTTACTTTCA

45 Seq ID NO: 250 Protein sequence
 Protein Accession #: NP_058637.1

1 11 21 31 41 51
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 MVSPRMSGLL SQTIVILALIF LPQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCRLFF 60
 50 RVCLKPGLSE EAASPCALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDWPPTFF 120
 SFIIETWREE LGDQIGPAW SLLARVAGRR RLAAGGPNAR DIQRAGAWEL RFSYRARCPE 180
 PAVGTACTRL CRPRSAFSPRC GPGLRPAAPL EDECEAPLVC RAGCSPEHGF CEQPGECRL 240
 EGWTGPICTV PVSTSSCLSP RGPSSATTGC LVPGPGRCDG NPCANGSGCS ETPRSFECTC 300
 PRGPIGLRCE VSGVTCADGP CPNGGLCVGG ADPDSAYICH CPPGQGSNC EKRVDRCSLQ 360
 55 PCRNGLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGGTCVEGG GAHRCSCLAG 420
 FGGRDCRERA DPCAARCAH GGRCAHFSG LVCAAPGYM GARCEPFVHP DGASALPAAP 480
 PGLRPGDPQR YLLPPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTPPSVHAL 540
 PDALNNLRQT EGSGDGPSSS VDWNRPEVDV PQGIYVISAP SIYAREVATP LFPPLHTGRA 600
 60 QQRQHLFFPY PSSILSVK

Seq ID NO: 251 DNA sequence
 Nucleic Acid Accession #: CAT cluster

65 1 11 21 31 41 51
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 GCTTCAATTC CTTATATGAC TTCAGACTGG AGAAGCCTGT TAAACCACTG TTAGTTTCAG 180
 70 TTAGAAAGTC TGAGAGACTT TATACATAAA TTCTCAATT GGTGCTGTA CACGTGCCAG 240
 AGTTTACTA CTGTAGTGAC CGTTGAGAAG ACCCTTGTIT ATTACATTG GAAGCACTGT 300
 TTGTGCAAAC AACCTTTCAT TGTAAAGTGC CTGTATTCTT TCATTACTT TCATGTCCAG 360
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 75 GTTTACTGAA AGCACTCAAT GAAGTCAAT TACTGAAGCT TTTGCTACA TCTTGTCTCT 540
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 TGCCATTGTC ATATCAAACT TGCTTTGTAT CATACTAATG TTACATAACT TATGATCA 660
 TAAAAATACA TTTCATGTTT AAAAAAATA AAAAAAATA

80 Seq ID NO: 252 DNA sequence
 Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 | | | | | |
 AGGTACTGCC AGAAAGGATC AGGACCTGGA GTCTGGCAAG AGGAAGACAG AGGCTGTGT 60

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GGGAAGCGAG TTGTTATCTT TGGTTATCTA GCTGTATGAG TGTATTGGTC TTCATAAAGC 120
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AGAAGTGTAT AGTGATAATG AGTAAAGATG CATGTGCAGT TTGTTCTATT TTAAGGCCAA 420
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CCTATAGAGT ACAGCCCTGT TGGGGGGTGG GGGTATGAAA AAAACATCAA GTGCACACAC 1200
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AACAATATGA TAAAAAGTTT GTTTTGAAT AGTCTCAGCT AGATGGGTCT AAATAGCCAT 1740
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TCTTCCACGT GGCCTAGATT ATTGACAAAT CCAAATATAC AATTTTCTTT TAAAGTAGT 1980
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CTGTACAGCT GCCAGAGTTT TACTACTGTA GTGACGGTTG AGAAGACCTT TGTATTATTA 2160
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CTGGAGAAAC TATTTGTTTA CTGAAAGCAC TCAATGAAGT CAAATTACTG AAGCTTTTGC 2400
CTACATCTTG GTCTTTTATG TAAATATGTT AAATATAACA TCTAAGGAAA ATAAACAATA 2460
TTATAATTAT GTGTTTGCCA TTGTCATATC AAACTTGCTT TGTATCATAC TAATGTTACA 2520
TAACCTATCG ATCAATAAAA ATACATTCA ATGTT

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45 Seq ID NO: 253 DNA sequence
Nucleic Acid Accession #: NM_001650.2
Coding sequence: 40.1011

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60
65
70
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1 11 21 31 41 51
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AGGCGGTGGG GTAAGTGTGG ACCTTTGTGT ACCAGAGAGA ACATCATGGT GGCTTTCAAA 120
GGGCTCTGGA TCAAGCTTTT CTGAAAGACA GTCCAGCGCG AATTCTCTGC CATGCTTATT 180
TTTGTCTCTC TCAGCCTGGG ATCCACCATC AACTGGGGTG GAACAGAAAA GCCTTTACCG 240
GTGACATAGG TCTCATCTCT CCTTGTCTTT GGACTCAGCA TTGCAACCAT GTGTCAGTGC 300
TTTGCCATA TCAGCGGTGG CCACATCAAC CCTGCAGTGA CTGTGCCAT GGTGTGCACC 360
AGGAAGATCA GCATGCCCAA GTCTGTCTTC TACATGCGAG CCCAGTGCCT GGGGGCCATC 420
ATTGAGATCA GAATCTCTTA TCTGGTCACA CTCGCCAGTG TGGTGGGAGG CCGGGAGTGC 480
ACCATGGTTC ATGGAATCTT TACCGCTGGT CATGGTCTCC TGGTTGAGTT GATAATCACA 540
TTTCAATTGG TGTTTACTAT CTTTGCCAGC TGTGATTCCA AACGAGCTGA TGTCACTGGC 600
TCAATAGCTT TAGCAATTGG ATTTCTGTGT GCAATTGGAC ATTTATTTCG AATCAATTAT 660
ACTGGTGCCA GCATGAATCC CGCCCGATCC TTTGGACCTG CAGTTATCAT GGGAAATTTG 720
GAAAACCAAT GGATATATTG GGTGGGGCCC ATCATAGGAG CTGTCTCTGC TGGTGGCCTT 780
TATGASTATG TCTTCTGTCC AGATGTTGAA TTCAAACGTC GTTTTAAAGA AGCCTTCAGC 840
AAAGCTGCCC AGCAACAAAA AGGAAGCTAC ATGGAGGTGG AGGACACAG GAGTCAGGTA 900
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GTCTAAACAA TAAATATTTC ATAATTACA AAGGAGGAAC GGAAGAAACC TATTGTGAAT 1200
TCCAAATCTA AAAAAAGAAA TATTTTAAAG ATGTTCTTAA GCAATATAT ACCTATTTTA 1260
TCTAGTTACC TTTCATTAA ACCTAATTTT AACGTTGTGT CAAGATTGGT TTAAGTCTTG 1320
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AGTCAATTCT TATTGAATA TTTATTCTAT TAACTGAGT TTAACATGG C

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75 Seq ID NO: 254 Protein sequence
Protein Accession #: NP_001641.1

80

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1 11 21 31 41 51
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GTEKPLPVDL VLISLCFGLS IATMVQCFGH ISGGHINPAV TVAMVCTRKI SLAKSVFYIA 120
AQCGLAIGA GILYLVTPPS VVGLGVTVV HGNLTAGHGL LVELIITPQL VPTIPASCDS 180
KRTDVTGSLA LATGFSVAIG HLFALNYTGA SMNPARSFPG AVIMGNWENH WIYWVGPPIG 240
AVLAGGLLEY VPCPDVEPKR RFKEAFSKAA QQTGSGYMEV EDNRSQVETD DLILKPGVVH 300

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VIDVDRGEK KGRDQSGEVL SSV

Seq ID NO: 255 DNA sequence

Nucleic Acid Accession #: U26742.1

Coding sequence: 325..1449

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CTCAAAACCTC	CTGCGACACC	AATGGACACC	TTCTAAGAGT	TTGGCGAGTC	AGTGACTGAA	180
CGCCCGTCC	ATTCCAAGAT	AAATAGGATT	TACCAATCCT	TGGATGAAGT	GCTTGGGAAG	240
TCITTAAGTG	CCATAATCAA	CTGCCATTTC	AAAGAAATATA	GATGTTTGTG	AAAAGTTCAT	300
GCTGTCCCTT	CATTGAATTT	TAGAATGATT	GAAGATAGTG	GGAAAAGAGG	AAATACCATG	360
GCAGAAAGAA	GACAGCTGTT	TGCAGAGATG	AGGCTCAAG	ATCTGGATCG	CATCOGACTC	420
TCAOCTACA	GAACAGCATG	CAAGCTTAGG	TTTGTTCAGA	AGAAATGCAA	TTTGCACTGT	480
TGGACATAT	GGAATGTCT	AGAAGCATTG	CGGGAAAATG	CTCTGAACAA	CCTGGACCCA	540
AACACTGAAC	TCAACGTGTC	COGCTTAGAG	GCTGTGCTCT	CCACTATTTT	TTACGAGCTC	600
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AACCTCCTGC	TTGCAGCGTT	TGATCCGGAA	GGCATGGTA	AAATTTCACT	ATTGTGCTGT	720
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TCAATGATT	CTGACTCCAG	TGGGTGATG	GTTTATGGAC	GATATGACCA	ATTCCTTCGG	840
GAAGTTCTCA	AACTACCCAC	GGCAGTTTTT	GAAGTCCCTT	CATTGTGTTA	CACAGAACAG	900
TCAGCCAGAT	CTGTGTTCTC	CCAACAGAAA	AAAGTCAGT	TAAATGGTTT	CTTGGACACG	960
CTTATGTCA	ATCCTCCCCC	CGAGTGTCTG	GTCTGGTTGC	CTCTTCTGCA	TCGACTAGCA	1020
AATGTGAAA	ATGTCTTCCA	TCCGGTTGAG	TGTTCTTACT	GCCACAGTGA	GAGTATGATG	1080
GGATTGTGCT	ACGATGTCCA	ACAGTGTGAC	AATTACCAGC	TCTGTGAGGA	CTGCTTCTGG	1140
AGGGGACATG	CCGGTGGTTC	TCATAGCAAC	CAGCACCAAA	TGAAAGAGTA	CACGTCTATG	1200
AAATCACCTG	CTAAGAAGCT	GACTAATGCA	TTAAGCAAGT	CCCTGAGCTG	TGCTTCCAGC	1260
CGTGAACCTT	TGCACCCCAT	GTTCCAGAT	CAGCCTGAGA	AGCCACTCAA	CTTGGCTCAC	1320
ATCGTTGATA	CTTGGCCTCC	CAGACCTGTA	ACCAGCATGA	ACGACACCTT	GTTCTCCCAT	1380
TCGTGTTCCCT	CCTCAGGAAG	TCCTTTTATT	ACCAGGAGCT	CGGACGGTGC	TTTTGGTGGA	1440
TGGGTCTAGA	TGATAACAT	GACTTCTTCT	ACCTTAAAT	ATTCTATAA	TACTTTGAGC	1500
TGTTCTGGTT	CCTCCAGGCT	GCATGGTACC	CATTAAACCA	AAATATGATT	ATTTCCCTTT	1560
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Seq ID NO: 256 Protein sequence

Protein Accession #: AAC50424.1

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PEGHKISVF	AVKMALATLC	GGKIMDKLRY	IFSMISDSSG	VMVYGRYDQF	LREVLKLPFA	180
VFEGPSFQY	EQSARSCFQ	QKVTNLNGFL	DTLMSDPPQ	CLVWLPPLHR	LANVENVFP	240
VECSYCHSES	MMGPRYRCQ	CHNYQLQDC	FWRGHAGGSH	SNQHQMKBYT	SWKSPAKKLT	300
NALSKSLSCA	SSREPLHPMF	PDQPEKPLNL	AHIVDTWPPR	FVTSMNDTLF	SHSVPSGSGP	360
PITRSSDQAF	GGCV					

Seq ID NO: 257 DNA sequence

Nucleic Acid Accession #: NM_004172.1

Coding sequence: 179..1807

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GACTAAAAGC	AATGGAGAAG	AGCCCAAGAT	GGGGGCGAGG	ATGGAGAGAT	TCCAGCAGGG	240
AGTCCGTAAA	CGCACACTTT	TGGCCAAGAA	GAAAGTGCA	AACATTACAA	AGGAGGATGT	300
TAAAAOTTAC	CTGTTTGGGA	ATGCTTTTGT	GCTGCTCACA	GTCAACGCTG	TCAATGTGGG	360
TACAACTCCT	GGATTTACCC	TCCGACCATA	CAGAATGAGC	TACCGGGAAG	TCAAGTACTT	420
CTCCTTTCCT	GGGGAACCTC	TGATGAGGAT	GTTACAGATG	CTGGTCTTAC	CACCTATCAT	480
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GCGAGCTGTA	GTCTATTATA	TGACTACCAC	CATCAITGCT	GTGGTGATTG	GCATAATCAT	600
TGTCATCATC	ATCCATCCTG	GGAAGGGCAC	AAAGGAAAAC	ATGCACAGAG	AAGGCAAAAT	660
TGTACGAGTG	ACAGCTGCAG	ATGCCTTCCT	GGACTTGATC	AGGAACATGT	TCCCTCCAAA	720
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GCCCATCCAG	GCCAAACGAAA	CGCTTGTGGG	TGCTGTGATA	AACAATGTGT	CTGAGGCCAT	840
GGAGACTCTT	ACCCGAATCA	CAGAGGAGCT	GGTCCAGATT	CCAGGATCTG	TGAATGGAGT	900
CAATGCCCTG	GGTCTAGTTG	TCTTCTCCAT	GTGCTTCGGT	TTTGTGATTG	GAAACATGAA	960
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GGTAGCAGTA	ATAATGTGGT	ATGCCCCCGT	GGGTATTCTC	TTCTGTATTG	CTGGGAAGAT	1080
TGTGGAGATG	GAAGACATGG	GTGTGATTGG	GGGGCAGCTT	GCCATGTACA	CGGTGACTGT	1140
CATTGTGGC	TTACTTATT	ACGCAGTCAT	CGTCTTGCCA	CTCCTCTACT	TCTTGGTAAC	1200
ACGGAAAAC	CCTTGGGTTT	TTATTGGAGG	GTTGCTGCAA	GCACTCATCA	CCGCTCTGGG	1260
GACCTCTTCA	AGTTCTGCCA	CCCTACCCAT	CACCTTCAAG	TGCTTGGAA	AGAACAAATG	1320
CGTGACAAG	CGGTTCACCA	GATTCTGTCT	CCCGTAGGGA	GCCACCATTA	ACATGGATGG	1380
GACTGCCCTC	TATGAGGCTT	TGGCTGCCAT	TTTCATTGCT	CAAGTTAACA	ACTTTGAAC	1440
GAACTTCOGA	CAAAATTTATA	CAATCAGCAT	CACAGCCACA	GCTGCCAGTA	TTGGGGCAGC	1500
TGGAATTCCT	CAGGCGGGCC	TGGTCACTAT	GGTCATTGTG	CTGACATCTG	TGGGCTGCC	1560
CAGTGACGAC	ATCAGCTCA	TCATCGCGGT	GGACTGGTTC	CTGGATCGCC	TCCGACCCAC	1620

5 CACCAACGTA CTGGGAGACT CCCTGGGAGC TGGGATTGTG GAGCACTTGT CAGGACATGA 1680
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 10 TCCTATAAAT GTCATTTTTT TATATAAGTT AAAGAGACAA ATAGTAGGCT AAAAAATT 2160
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 15 GGCCTCAGTG TCCTCATCTA TAAATGAGG GACTTCCCTA GAAGTCTTCA TGGTCTCTTC 2460
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 20 CCCAGTTCAT GTCATGAGG GAAGTATCC CTCTTTCTCT ACTCTGGGAA GAATGTCTCC 2760
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 25 AATCATTTCC CCGTGAAGT CTGCTTACCA AAACATAAGA CGACTTATAT ATTGAAAGA 3060
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 30 TTATGAGAAA AAAACAGCAG GGCATTAGT TTCAGGCAAG GCAGCTCCA GGTTTAGAGA 3360
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 ATATACTAAC CATTTCTTAT GGAAGGTCC TGTGGGAGC CCATCCTCTC GCCAAGCCAT 3780
 CACAGGCTCT GCATACACAT GCATCAGTG TGGACTGGGA AGCATTACTT TGTAGATGTA 3840
 TTTTCAATAA AGAAAAAAT AGTTTACAT T

Seq ID NO: 258 Protein sequence
 Protein Accession #: NP_004163.1

45 1 11 21 31 41 51
 MTKSNGEPEK MOGRMERFQQ GVRKRTLLAK KKVQNIKED VKSFLFRNAP VLLTFTAVIV 60
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 MRADVYMTT TIIAVVIGII IVIIHPGKG TKENMHREGK IVRVTAADAF LDLIRNMFPF 180
 NLVEACEKPKF TATYKRSFK VPIQANETLV GAVINNVSEA METLTRITRE LVPVPGSVNG 240
 VNALGLVVPF MCFGFVIGNM KEQQQALREF FDSLNEALMR LVAVIMWYAP VGILFLIAGK 300
 50 IVEMEDMGVI GGQLAMTYVT VIVGLLIHAV IVLPLLYPLV TRKNPWVFIG GLLQALITAL 360
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Seq ID NO: 259 DNA sequence
 Nucleic Acid Accession #: NM_021948.1
 Coding sequence: 48..2783

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 65 TGCAAGGAGT GCTCGGCGGC GCCCTCACCA TCCCTTGCCA CGTCCACTAC CTGCGGCCAC 240
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 70 ACAGCAGOGA CGCTGTGGAG GTCAAGGTCA AAGGGGTGGT CTTTCTCTAC CAGAGGGGCT 540
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5	TCTCAGAAGA	GGAAGGTAAG	GCATTGGAGG	AAGAAGAGAA	ATATGAAGAT	GAAGAAGAGA	1440
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	CACTCTCCCA	GGCGCCAGCA	AGGGCAGTCC	TGCAGCCTGG	TGCATCACCA	CTTCTGTATG	1620
	GAGAGTCAGA	AGCTTCCAGG	CCTCCAAGGG	TCCATGGACC	ACCTACTGAG	ACTCTGCCCA	1680
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	CAGGAAGCTC	CGAGGGTGCC	CCTTCCCTGC	TTCCAGCCAC	ACGGGCCCTC	GAGGGTACCA	1860
10	GGGAGCTGGA	GGCCCCCTCT	GAAGATAATT	CTGGAAGAAC	TGCCCCAGCA	GGGACCTCAG	1920
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15	CACGAAGGAG	CTGGGAGGAG	GCAAGAGACC	AGTGCCTGAT	GTACGGCGCG	CATCTGGCCA	2220
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20	CCTACACCTG	CAAGATGGGG	CTGGTGTCTT	GTGGGCGCGC	ACCGGAGCTG	CCCTTGGCTC	2520
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25	ACCCAGAAGG	AGGTCAGGGG	AGGCTACTGG	GACGCTGGAA	GGCGCTGTTG	ATCCCCCTTT	2760
	CCAGCCCCAT	GCCAGGTCCC	TAGGGGGCAA	GGCCTTGAAC	ACTGCGCGCC	ACAGCACTGC	2820
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Protein Accession #: NP_068767.1

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35	SLALSELRPN	DSGIYRCEVQ	HGIDDSDDAV	EVKVGKVFL	YREGSARYAF	SFSGAQEACA	180
	RIGAHIAIPE	QLYAAYLGGY	EQCDAGWLSD	QTVRYPIQTP	REACYGDMDG	FPGVRYNGVV	240
	DPDDLVDVYC	YAEOLNGELF	LGDPPPEKLT	EEARAYCQER	GASIAITGQL	YAAWDGGLDH	300
	CSPGWLADGS	VRYPITVPSQ	RCGGGLPGVK	TLFLFPNQTG	FPNKHRSFNV	YCFRDSAQPS	360
	ALPEASNPAS	NPASDGLLEI	VTVTETLEEL	QLPQEATESE	SRGAIYSIPI	MEDGGGGSST	420
40	PEDPAEAPRT	LLEFETQSMV	PPTGFSEBEG	KALEEBEEKYB	DEEEKEBEEE	EEVEDEALN	480
	AMPSELSSPG	PEASLPTEPA	AQEESLSQAP	ARAVLQPGAS	PLPDGSEBAS	RPPRVHGPPT	540
	ETLPTPRERN	LASPSPTLV	EAREVGEATG	GPELSGVPRG	ESEETGSSEB	APSLPATRA	600
	PEGTRELEAP	SEDNSGRTP	AGTSVQAQPV	LPTDSASRGG	VAVVPASGDC	VPSPCHNGGT	660
	CLEEEGVRC	LCLPGYGGDL	CDVGLRFCNP	GWDAPQGACY	KHFSTRRSWE	EARTQCRMYG	720
45	AHLASISTPE	EQDFINNRYR	EYQWIGLNDR	TIEGDFLWSD	GVPLLYENWN	PGQPDYFPLS	780
	GENCVVMVWH	DQGQWSDVPC	NYHLSYTCKM	GLVSCGPPPE	LPLAQVFGRP	RLRYEVDTVL	840
	RYRCREGLAQ	RNLPLIRQCE	NGRWEAPQIS	CVPRRPARAL	HPZEDPEGRQ	GRLLGRWKAL	900
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Seq ID NO: 261 DNA sequence
Nucleic Acid Accession #: NM_004386.1
Coding sequence: 2..3967

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	GAAGCTGGGG	TCTGGGTGAG	TGCAGGCTGC	GCTGGCGGAG	CTGGTGCCCC	TGCCCTGTCT	180
	CTTTACCCCT	CAGCCACGGC	CAAGCGCAGC	CCGAGATGCC	CCTCGGATAA	AGTGAGACCA	240
60	GGTGCGGACT	GGTTCGGGCC	AGCGACAGGA	CTTGCCCATC	CTGGTGGCCA	AGGACAATGT	300
	CGTGAGGGTG	GCCAAAAGCT	GGCAGGGAGC	AGTGTCACTG	CCTTCTTACC	CCCGCGCGCG	360
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	CACCCAGTCC	CGTCTGTGTT	GCTATGGCGA	CCGTAGCAGC	CTTCCAGGGG	TTCCGAGCTA	720
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Seq ID NO: 262 Protein sequence
 Protein Accession #: NP_004377.1

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Nucleic Acid Accession #: Eos sequence

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Protein Accession #: Eos sequence

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CCAAACTCTT GGACCTTGTG GTTAGGAAAT TCCTTAACT TCCAGCCATA TGGCATTATC 2400
65 GTGTCTCTTT CTCTCTCTCT CTTGCTCTCT CTCTCTCTCT CTTCCTCTCT CTTCCTCTCT 2460
AATAAGTACT GTTTACTCAT TTAGTTGCTT ATCAAGTACT TATTCTTGTT TTTAAAAAAA 2520
ATTAATGGTA ACTGTATTTT TCTCATTTT AGCATTATTC AAATGTTTAT ATTTTAATAC 2580
CTTTAAACCA CTTTAAAGTT TTTTCATGTT TAATTATAGT TTTAAGAAAA ACTATTTTGA 2640
ACAACCCCAA ATATAGTGCA TCTAGAAACT AATGTATATT TGATTAGACA TCATTTATAG 2700
70 TGGAAACAGTA GACTGTAGTA CATGGTAATT TTTCTTTTAC TATTAAGATA CAATAAAACA 2760
TGACTAATTT TGCTGTCAAA AATGTAAAGA ATAATGATAA ATGGAGTTT TATATTTTAA 2820
CTTTTAAAGT TGCTGTCTT TAATAAGACA AAGCCTTAAG CCTTATGTTA TAATTTTGGT 2880
TCTAAAAACC ATCATTTCAG TATAAGGAAT AAGTATATTT CGTCTCTCTC TTTAGTTTTT 2940
TTCTTCTCTT TTATTTTTAT TTTGAAAAAT TTCTACACCT TCTTTGAATT CCTTGTATGA 3000
75 ATTTTGTGTT TTAGAAGTT AATTGTGTG AAATGAGATT CTTCAAAACG ATGAAACCTC 3060
ATAGCTCTGA GAAAGGTTT TAGGGTTTAA AATTCTAAGC AAAGCGTGAC TATGGCTGAC 3120
AGACTACACA TTTAATTATA CAGCTTCTCT TTCTTAAACA CAGGCAGATT AACCTCATTG 3180
TGGATTGTC TTACAGACCTT AGTCTCTCAG CATGTTTCTT GGTGCCACT CCTGGAAGCC 3240
GCTGTTCCTT TTCTACCTTC TTACAGAGC CCAAGGGCAG GCCTGTGCCC GGGGAAGCAG 3300
CAGCTTGCTG ACATAGTCA GCTGCAAGG CTGAGGAGTG TGCCCTCAGA GAAGCACCGC 3360
COCCTAGCTT TGTGCGCAGC CCTAGAGCCG CAGCTOCCAG GGAATGCTCT TCCCTGGAGG 3420
CAGCCAGAGA GAGGGAGCT GGCAGGTTT TTCAGATTTG TGGCCACTGT TTCTCATTTG 3480
80 CTGTTGACTT GTTTTTATTT CTTAGGCTTT TGCTAGTTTT AGAAAAATAG GAAGCAGCCC 3540
TTGATTTGTT GATTAAGAAC AACATTGAG CGATGATGCA CAACAGTCCA GAAAAATGGG 3600

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5 CGGTGGACAC TTGAGGCTGA GGATGGGAGT TGACATGAGC AGGGAGAGGG AGGTGCGCGC 3660
 TGCTTATCTG TGATTGTGTC TCACCTGAGT GTGGCTGATT GTGTACATCC AGCAGTTACA 3720
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 TCCAAAGAAG TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAATAATA 3840
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 GAAGGATCCT TTTGTAGCAG TGTATTGAA TGTAAACCCC AGCAAAATAT GGCTATATAT 3960
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 10 TTCCATAGGC GTACAAAACA GTATTAAAGC TCAGTGTITT GCATATTGTT AGCATTTACA 4140
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 AAAAATGCTT GGCAAAAAAA ATATAGTGTT AAAATAGGCC AGTGATATTA ATGAGAAAAA 4320
 GAAAGTATGT ATCAGGAATA AAGTGATATT GCATAGGAGT ATTGTATTTT TATGAATTTT 4380
 15 ATGCCAGTTG TTACATGTA CTATATATGT TAAATTAATA AAAATCATGA GAAATG

Seq ID NO: 266 Protein sequence
 Protein Accession #: BAA74900.1

20 1 11 21 31 41 51
 | | | | | |
 PLVINTLKRP NLYPEVILAS WYRIYTKIMD LIGIQTKICW TVTRGEGSLP IESCEGLGDP 60
 ACFYVAVIFI LNLMMALFF IYGYLSGSR LGLLTVLCP PFNHGECTRV MWTPLRESF 120
 SYFPLVLQML LVTHILRAK LVRGLIALC ISNVFMLPW QPAQFVLLTQ IASLFAVYV 180
 25 GYIDICLRK IYIHMISLA LCFVLMFGNS MLLTSYASS LVIIWGILAM KPFLKINVS 240
 ELSLWVIQGC FNLFGTVILK YLTSKIPGIA DDAHIGNLLT SKFFSYKDFD TLLVTCAEF 300
 DFMEXETELR YTKLILLPVV LVVFVAIVRK IISDMWGVLA KQOTHVRKHQ FDHGLVYHA 360
 LQLLAYTAL LILMLRLKLF TPEMCMASL ICSRQLFGWL FCKVHGAIV FAILAAMSQ 420
 GSAHLQTQWN IVGFPSNLPQ EELIEWIKYS TKPDVAFPGA MPTMASVKLS ALRPVNHFH 480
 30 YEDAGLRART KIVYSMSRK AAEVVKRELI KLVNYYILE ESWCVRRSKP GCSMPBEIWDV 540
 EDPANAGKTP LCNLIVKDSK PHFTTVFQNS VYKVLVVKE

Seq ID NO: 267 DNA sequence
 Nucleic Acid Accession #: U26744.1
 Coding sequence: 59..1600

35 1 11 21 31 41 51
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 40 GATGAGGCTC CAAGATCTGG ATGCAATCCG ACTCTCCACC TACAGAACAG CATGCAAGCT 180
 TAGGTTTGTG CAGAAGAAAT GCAATTTGCA CCTGGTGGAC ATATGGAATG TCATAGAAGC 240
 ATTGCGGGAA AATGCTCTGA ACAACCTGGA CCCAACACT GAACTCAAGC TGTCOCGCTT 300
 AGAGGCTGTG CTCCTCACCTA TTTTITACCA GCTCAACAA CGGATGCCAA CCACCTACCA 360
 AATCCATGTG GAGCAGTCCA TCAGCCTCCT CCTTAACCTC CTGCTTGACG CGTTTGATCC 420
 45 GGAAGGCCAT GGTAAAAATT CAGTATTTGC TGTCAAAATG GCTTTAGCCA CATGTGTGG 480
 AGGGAAGATC ATGGACAAAT TAAGATATAT TTTCTCAATG ATTTCTGACT CCAGTGGGGT 540
 GATGCTTTAT GGACGATATG ACCAATTCCT TCGGGAAGTT CTCAAACTAC CCACGGGAAGT 600
 TTTGAGGGGT CCTTCATTG GTTACACAGA ACAGTCAGCC AGATCCTGTT TCTCCCAACA 660
 50 GAAAAAGTGC AGGTTAAATG GTTCTTTGGA CACGCTTATG TCAGATCCTC CCCCAGAGTG 720
 TCTGCTCTGG TTGCTCTTC TGCATGAGT AGCAAAATG GAAAATGTCT TCCATCCGGT 780
 TGAGTGTTC TACTGCCACA GTGAGAGTAT GATGGGATT OGCTACOGAT GCCAACAGTG 840
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 CAACAGCAGC CAAATGAAAG AGTACACGTC ATGGAAATCA CCTGCTAAGA AGCTGACTAA 960
 55 TGCAATTAAG AAGTCCCTGA GCTGTGCTTC CAGCCGTGAA CCTTTGCACC CCATGTTCCC 1020
 AGATCAGCCT GAGAAGCCAC TCAACTTGGC TCACATCGTT GATACTTGGC CTCCAGAGCC 1080
 TGTAAACAGC ATGAACGACA CCTGTCTCTC CCACTCTGTT CCTCCTCAG GAAGTCTCTT 1140
 TATTACCAAG AGCATGCTTG AGAGTTCAAA CCGGCTTGAT GAAGAACACA GGCTAATTGC 1200
 CAGGTATGCG GCAAGGCTGG CAGCAGAGTC CTCTCTGCT CAGCCACCTC AGCAGAGAAG 1260
 60 TGCTCTGAC ATCTCTTTCA CCATCGATGC GAATAAGCAG CAAAGGCAGC TGATTGCTGA 1320
 GCTAGAAAAC AAGAACAGAG AAATCTTACA GGAGATCCAG AGACTTCGGC TAGAGCATGA 1380
 ACAAGCTTCT CAGCCACAGC CAGAGAAGGC ACAGCAAAAC CCCACCTGTC TGGCAGAACT 1440
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 COGGAGAGAG CTAATGGTCC AGTTGGAGGG TCTCATGAAG CTACTAAAGG AAGAAGAACT 1560
 65 GAAGCAGGGA GTAAGTTATG TCCCTACTG CAGGTCTTAA CTAACAGTGG AGGGGCTGTC 1620
 CGACCTGCGG TTTTCTCATT GCTTTTGCTC TAATGTATGT TCATGCTTCA GTTTGAAAAG 1680
 AGAAAAAAGT CATACTAATT TGCTTCTTTT TCAATGTAGT GCTTGAATTG AGATATATAA 1740
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 70 TTCAAACCAAG TCTTAGCTTT TCAAGTTGTT GATCAGACCC TTCTCTTAAC AGAGAGATAC 1920
 CACAGTCACT AGAGATACCC TGAGGTTTCAT GTCATCCCAA AACCACAGC ACTCAGAAGC 1980
 TAACCTCTAC ACCCACTCAC ACTGTAGATA TTCAGTTGGG TTTCAATTTA CTGAAAACCT 2040
 GTGAAACCTC TTTTATATAA AATCAGGCAA TTAATCCCT TTTCAACACA CAATTAATGA 2100
 GCCTGTCTCC CCATGGCTCA CCAAAATGTG CTCAATTTTG TGAGAGAAG ACTGTACTCC 2160
 75 ATAACTGACT ATTCAAGTCC CATCTTTTGG GCTCTTCCCC AAAGCAGAACT CCTTACTGTT 2220
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 TTGGGCTCGG GAGAGCGAGA GGGTCATTAC ATACTTTTTT TTTTCTGAG AAATAGGGGC 2340
 ATTGTGACTT TATAGCTTAA ACTGGAGCTG TCTGAACCTG TGGTCAGGCT CAAGAGCCAG 2400
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Seq ID NO: 268 Protein sequence
 Protein Accession #: AAC50426.1

1 11 21 31 41 51
 | | | | | |

5 MIEDSGKGRN TMAERQLFLA EMRAQDLDRl RLSTYRTACK LRFVQKKCNL HLVDIMNVIE 60
 ALRENALNNL DPNTLNVSRL LEAVLSTIFY QLNKRMPTTH QIHVEQSISL LNLPLLAAPD 120
 PEGHGKISVF AVIMALATLC GKGIMDKLRY IFSMISDSSG VMVYGRYDQF LREVLKLPTE 180
 VLEGPSFGYT EQSARSCPSQ QKQVTLNGLY DTLMSDPPPO CLVNLPLLHR LANVENVFHP 240
 20 VECYSCHSES MMGFRYRCQQ CHNYQLQDC FWRGHAGGSH SNQHKMEYF SNKSPAKKLT 300
 NALSKSLSCA SSREPLHPMF PDQPEKPLNL AHIVDTNPPR PVTSMNDTLF SHSVPSGSP 360
 PITRSMLESS NRIDBEHRLI ARYAARLAAE SSSSQPPQOR SAPDISFTID ANKQQRQLIA 420
 ELENKREIL QEIQLRLLEH EQASQPTPEK AQONPTLLAE LRLLRQRKDE LEQRMSALQE 480
 SRRELMVQLE GLMKLLKBEZ LKQGVSYVPY CRS

Seq ID NO: 269 DNA sequence
 Nucleic Acid Accession #: NM_001276.1
 Coding sequence: 127..1278

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 TAGCTGGCAC CAGGAGCCGT GGGCAAGGGA AGAGGCCACA CCCTGCCCTG CTCTGCTGCA 120
 GCCAGAAATGG GTGTGAAGGC GTCTCAACA GGCCTTGTGG TCCTGGTGCT GCTCCAGTGC 180
 20 TGCTCTGCAT ACAAACCTGT CTGCTACTAC ACCAGCTGGT CCCAGTACCG GGAAGGCGAT 240
 GGGAGCTGCT TCCAGATGCG CCTTGACCGC TTCCTCTGTA CCCACATCAT CTACAGCTTT 300
 GCCAATATAA GCAACGATCA CATCGACACC TGGGAGTGGG ATGATGTGAC GCTCTACGGC 360
 ATGCTCAACA CACTCAAGAA CAGGAACCCC AACCTGAAGA CTCTCTGTGC TGTGCGAGGA 420
 TGGAACTTTG GGTCTCAAGG ATTTTCCAAG ATAGCCTCCA ACACCCAGAG TCGCCGGACT 480
 25 TTCATCAAGT CAGTACCGCC ATTCCTGCGC ACCCATGGCT TTGATGGGCT GGACCTTGCC 540
 TGGCTCTACC CTGGACGGAG AGACAAACAG CATTTTACCA CCCTAATCAA GGAATGAAG 600
 GCGGAATTAA TAAAGGAAGC CCAGCCAGGG AAAAAGCAGC TCCTGCTCAG GCGAGCACTG 660
 TCTGCGGGGA AGGTCAACCAT TGACAGCAGC TATGACATGG CCAAGATATC CCAACACCTG 720
 GATTTCATTA GCATCATGAC CTACGATTTT CATGGAGCCT GCGTGGGAG CACAGGCCAT 780
 30 CACAGTCCCC TGTTCGAGG TCAGGAGGAT GCAAGTCCCT ACAGATTGAG CAACACTGAC 840
 TATGCTGTGG GGTACATGTT GAGGCTGGGG GCTCCTGCCA GTAAGCTGGT GATGGGCATC 900
 CCGACCTTCG GGAGGAGCTT CACTCTGGCT TCTTCTGAGA CTGGTGTGG AGCCCCAATC 960
 TCAGGACCGG GAATTCACAG CCGGTTCAAC AAGGAGGAGC GGACCCCTGC CTACTATGAG 1020
 ATCTGTACTT TCTCCGCGG AGCCACAGTC CATAGAACC TCAGCCAGCA GGTCCCTAT 1080
 35 GCCACCAAGG GCAACCAAGT GGTAGGATAC GACGACCAGG AAGCGCTCAA AAGCAAGGTG 1140
 CAGTACCTGA AGGATAGGCA GCTGGCAGGC GCCATGGTAT GGGCCCTGGA CCTGGATGAC 1200
 TTCCAGGGCT CTTCTGCGG CCAGGATCTG CGCTTCCCTC TCACCAATGC CATCAAGGAT 1260
 GCACCTCGTG CAACGATGCC CTCGTGTTCT CACACAGCAC GGGGGCCAA GATGCCCGGT 1320
 CCGCCTCTGG CTCCAGCTGG CCGGAGCCT GATCACTGC CTGCTGAGT CCCAGGCTGA 1380
 40 GCCTCAGTCT CCCTCCCTTG GGGCCTATGC AGAGTCCAC AACACACAGA TTTGAGCTCA 1440
 GCCTGTGGTG GCAGAGAGGT AGGGATGGGG CTGTGGGGAT AGTGAGGCAT GCGAATGTAA 1500
 GACTCGGGAT TAGTACACAC TTGTTGATGA TTAATGGAAA TGTTTACAGA TCCCAAGCC 1560
 TGGCAAGGGA ATTTCTTCAA CTCCCTGCC CCTAGCCCTC CTTATCAAGG GACACCATTT 1620
 TGGCAAGCTC TATGACCAAG GAGCCAAACA TCCTACAAGA CACAGTGACC ATACTAATTA 1680
 45 TACCCCTGCG AAGCCAGCT TGAAACCTTC ACTTAGGAAC GTAATCGTGT CCCCTATCCT 1740
 ACTTCCCTTT CCTAATTCCA CAGCTGCTCA ATAAAGTACA AGAGTTTAAC AGTGTGTTGG 1800
 CGCTTTGCTT TGGTCTATCT TTGAGCGCCC ACTAGACCCA CTGGACTCAC CTCCTCCATC 1860
 TCTTCTGGGT TCCTTCTCT GAGCCTTGGG ACCCCTGAGC TGCAGAGAT GAAGGCCGCC 1920
 ATGTT

Seq ID NO: 270 Protein sequence
 Protein Accession #: NP_001267.1

55 1 11 21 31 41 51
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 ISNDHIDTNE WNDVTLYGML NTLKNRNPNL KTLISVGGWN PGSQRFSKIA SNTQSRRTFI 120
 KSVPPFLRTH GFDGLDLAWL YPGRRDQHF TLLIKEMKAE FIKEAQPGKK QLLLSAALSA 180
 60 GKVTIDSSYD IAKISQHLDF ISIMTYDFHG AWRGTTGHS PLFRGQEDAS PDRFENTDYA 240
 VGYMLRLGAP ASKLVMGIFT FGRSFTLASS ETGVGAPISG PGIPGRPTKE AGTLAYYBIC 300
 DFLRGATVER TLGQQVYAT KGNQWVGYDD QBSVKSQVQY LKDRQLAGAM VWALDLDDFQ 360
 GSFCCQDLRF PLTNAIKDAL AAT

65 Seq ID NO: 271 DNA sequence
 Nucleic Acid Accession #: NM_006474.1
 Coding sequence: 181..669

70 1 11 21 31 41 51
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 TCCGGCCCCC CCACCGTCGC GCTCCTCCAG GCTGGGCTG TGGCCGCGGT GCTTTTAATT 120
 TTCCCCAGC TCAGAATCTT GCTGCTCGGC CCCAGGAGA GCAACAACCT AACGGGAACG 180
 ATGTGGAAGG TGTGAGCTCT GCTCTGTGTT TTGGGAAGCG CGTCGCTCTG GGTCTCTGCA 240
 GAAGGAGCCA GCACAGGCCA GCCAGAAGAT GACACTGAGA CTACAGGTTT GGAAGGCGGC 300
 75 GTTGCCATGC CAGGTGCGGA AGATGATGTG GTGACTCCAG GAACCAAGCA AGACCGCTAT 360
 AAGTCTGGCT TGACAACTCT GGTGGCAACA AGTGTCAACA GTGTAACAGG CATTGCGATC 420
 GAGGATCTGC CAACTTCAGA AAGCACAGTC CAGCGCAAG AACAAAGTCC AAGCGCCACA 480
 GCCTCAACG TGGCCACCAG TCACTCCAGC GAGAAAGTGG ATGGAGACAC ACAGACAAACA 540
 80 GTTGAGAAAG ATGGTTTGTG AACAGTGACC CTGGTTGGAA TCATAGTTGG GGTCTTACTA 600
 GCCATCGGTT TCATTGGTGG AATCATCGTT GTGGTTATGC GAAAAATGTC GGAAGGTAC 660
 TCGCCCTAAG GAGCTGAAGG GTTACGCCCT GCTTGCCAAC GTGCTTTAAA AAAAGACCGT 720
 TTCTGACTCT GTGGCCCTGT CCCTGAGCTC GTGGGGAGAA GATGACCCTG GGAACATTTG 780
 CCGGCCCAT CAGATTCCAC GTGACTTTT CGTTTGCCAA ATTAACCGAG GAAAGACCTT 840

TCACCAGATT TGGTTCITAA ACTTT

Seq ID NO: 272 Protein sequence
 Protein Accession #: NP_006465.1

5
 1 11 21 31 41 51
 | | | | |
 MKVSVALLFV LGSASLWVLA EGASTGQPED DTETTGLEGG VAMPGAEDDV VTPGTSEDRY 60
 KSLGTLTVAT SVNSVTGIRI EDLPTSESTV HAQEQSPSAT ASNVTASHST EKVDGDTQTT 120
 10 VKDGLSTVT LVGIIVGVLL AIGFIGGIIV VVMRMSGRY SP

Seq ID NO: 273 DNA sequence
 Nucleic Acid Accession #: CAT cluster

15
 1 11 21 31 41 51
 | | | | |
 GCGGCCGCCA GCTTGCAAG CCGAAGTCTG GCGCGCTCT TCGACTCGCT GCGCCACGTC 60
 CCCGGGGGTG CCGAGCCGGC GGGGGGTGAG GTGGCTGCGC CGGCGGCCGG GCTAGGAGGT 120
 GCGGGCACTG GGGGCGCGGG AGGGGACGTG GCAGGCCCGC CGGGGGCCAC GCGATCCCA 180
 20 GGGGCCAGGA AGGTCCCGCT GCGGGCACGC AATCTGCCTC CGTCTTCTT CACGAGCCCG 240
 TCCGGGCGAG CCGGCGCGGG GTGTGGCCCG TCGGGGCCGG ACCTGAGCTT GGGCGACCTG 300
 GAGAAGGGCG CCGAGGCCGT GGAGTTCTTT GAGCTGCTGG GGGCCGACTA CGGCGCCGGC 360
 ACGAGAGCGG CAGTCTTGCT TGCCGCCGAG CCTCTCGACG TGTTCGCCCG CCGAGCCTCC 420
 GTACTGGCGG GACCCCGGGA GCTGGAGCCC GGCTCTTTG AGCCGCCCGC GCGAGTGGTG 480
 25 GGAACCTTAC TGTACCCGGA GCCCTGGAGC GTCCCGGGCT GCTCCCGGAC CAAAAGAGAC 540
 CCTTGTACTG CCTCCGCGG CGGGTTGACC TTGAACGAGC CCTTGTAGCC CCTGTACCCC 600
 GCGCTGCGGA ATTTCTCCCG CGGGGGAGGA CGGGCCGGGC CATTTGGCTT CTTCGCCGCC 660
 CTCTTTCCA GACTGCGCTT TGC

30
 Seq ID NO: 274 DNA sequence
 Nucleic Acid Accession #: Bos sequence

35
 1 11 21 31 41 51
 | | | | |
 CAAAGAGGCC GGGCTCCAGC TCGGGGGTTC CCCGAGTAC GGAGGCTCCG GCGGGGAACA 60
 COTCAGAGG CTCGCGCGCA AGCAAGACTG CCGCTCCGCT GCGCGGCCCG TAGTCGGGCC 120
 CCAGCAGCTC AAGAAGACTC ACGGCTCCCG CGCCTTCTC CAGGTGCCCC AAGCTCACGT 180
 CCGGCCCGGA CCGGCCACAC CCGCCGCGCG CTGCGCGGGA CGGCTCCGTC AAGAAGGACG 240
 GAGGCAGATT GCGTGCCCGC AGCGGGAACCT TCCTGGCCCC TGGGATCGCC GTGGCCCCCG 300
 40 CCGGCGCTGC CAGTCCCTCT CCGCGGCCCG CAGTGCCCGC ACCTCTAGC CCGGCCCGCG 360
 GCGCAGCCAC CTCACCCCGC GCGGCTCCGG CACCCCGGGC GACGTGGCGC AGCGAGTCGA 420
 AGAGCGCGCG CAGACTTCGG CTTTGCAAGC TGGCGGCCCG

Seq ID NO: 275 DNA sequence
 Nucleic Acid Accession #: NM_001118.1
 Coding sequence: 74..1651

45
 1 11 21 31 41 51
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 50 AGCCAGAGA CACATTGGGG CTGACCTGCC GCTGCTGTCA GTGGGAGGCC AGTGGTGTG 60
 GCCAAGAAGT GTCATGGCTG GTGTGCTGCA CGTTTCCCTG GCTGCTCACT GCGGGGCCCTG 120
 TCGTGGGGGC CGGGGAGAGC TCGCAGAGGC ACGCGCAGCC TCGAAGTCCG CGGCCAGAG 180
 ACACATTGGG GCTGACCTGC CGCTGCTGTC AGTGGGAGGC CAGTGGTGTG GGCCAAGAAG 240
 55 TGTATGGCTT GGTGTGCTGC ACGTTCCCTT GGCTGCTCTC CTCTGCTGTC CTATGGCCCC 300
 TGCCATGCAT TCTGACTGCA TCTTCAAGAA GGAGCAAGCC ATGTGCTGCG AGAAGATCCA 360
 GAGGGCCAAT GAGCTGATGG GCTTCAATGA TTCTCTTCCA GGTGTGCTGT GGATGTGGGA 420
 CAACATCAGC TGTGTGAAGC CCGCCCATGT GGGTGAGATG GTCCCTGGTCA GCTGCCCTGA 480
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 60 TTTTGGTGAC AGTAATCCTT TAGATCTCTC AGACATGGGA GTGGTGAGCC GGAAGTGCAC 600
 GGAGGATGGC TGGTCGGAAC CCTTCCCTCA TTAATTGAT GCCTGTGGGT TTGATGAATA 660
 TGAATCTGAG ACTGGGAGCC AGGATTATTA CTACCTGTCA GTGAAGGCC TCTACACGGT 720
 TGGCTACAGC ACATCCCTCG TCACCCCTCAC CACTGCCATG GTCATCCTTT GTGCTTCCG 780
 GAAGCTGCAC TGCACACGCA ACTTCATCCA CATGAACCTG TTTGTGTGCT TCATGCTGAG 840
 65 GCGATCTCC GTCTTATCA AAGACTGGAT TCTGTATGCG GAGCAGGACA GCAACCACTG 900
 CTTCATCTCC ACTGTGGAAT GTAAGGCGGT CATGGTTTTC TTCCACTACT GTGTTGTGTC 960
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 GTGTGTGACA GTGTGGGCTA CGCTGAGACT CTACTTTGAT GACACAGGCT GCTGGGATAT 1140
 70 GAATGACAGC ACAGCTCTGT GGTGGGTGAT CAAAGGCCCT GTGGTTGGCT CTATCATGGT 1200
 TAACTTTGTG CTTTATTATG GCATTATCGT CATCCTTGTG CAGAACTTC AGTCTCCAGA 1260
 CATGGGAGGC AATGAGTCCA GCATCTACTT GCGACTGGCC CGGTCCACCC TGCTGCTCAT 1320
 OCCACTATTC GGAATCCACT ACACAGTATT TGCTTCTCC CCAGAGAAATG TCAGCAAAAG 1380
 GGAAGAGACT GTGTTGAGC TGGGGCTGGG CTCCTTCCAG GGCTTTGTGG TGGCTGTTCT 1440
 75 CTACTGTTT CTGAATGGTG AGGTACAAGC GGAGATCAAG CGAAATATGC GAAGCTGGAA 1500
 GGTGAACCGT TACTTCGCTG TGGACTTCAA GCACCGACAC CCGTCTCTGG CCAGCAGTGG 1560
 GGTGAATGGG GGCACCCAGC TCTCATCTCT GAGCAAGAGC AGCTCCCAAA TCGCATGTCT 1620
 TGGCTTCCCT GCTGACAACT TGGCCACCTG AGCCATGCTC CCT

Seq ID NO: 276 Protein sequence
 Protein Accession #: NP_001109.1

80
 1 11 21 31 41 51
 | | | | |
 MAGVVHSLA AHCGACFWGR GRLRKGRAAC KSAAQRHIGA DLPLLSVGQ WWPBPMVAG 60

5 VVHVSAAALL LLMFAPAMHS DCIPKKEQAM CLEKIQRANE LMGFNDSSPG CPGMNDNITC 120
 WKPAHVGMV LVSCPELPRI FNPQVWETE TIGESDFGDS NSLDLSDMGV VSRNCTEDGW 180
 SEPPHYFDA CGDEYESBT GDQDYVYLSV KALYTVGYST SLVTLTTAMV ILCRFRKLHC 240
 TRNFIHMLP VSPMLRAISV FIKDWILYAE QDSNHCFIST VECKAVMVFP HYCVVSNYFW 300
 LFIEGLYLET LLVETFFPER RYPYWTYIIG WGTPTVCVTV WATLRLYFDD TGCWDMNDST 360
 ALMWVIKFPV VGSIMVNFVL FIGIIVILVQ KLQSPDMGGN ESSYILRLAR STILLIPLFG 420
 IHYTVAFSP ENVSKRERLV FELGLGSFQG FVVAVLYCFL NGEVQAEIKR KWSNWKVNRV 480
 FAVDPKRRHP SLASSGVNGG TQLSILSKSS SQIRMSGLPA DNLAT

10 Seq ID NO: 277 DNA sequence
 Nucleic Acid Accession #: NM_004000.1
 Coding sequence: 36..1193

15 1 11 21 31 41 51
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 GTGTAGTGGT CTGCTGCTT CTCCAGGAG GATCTGCCTA CAACTGGTT TGCTACTTTA 120
 CCAACTGGTC CCAGGACCGG CAGGAACGAG GAAATTCAC CCCTGAGAAT ATTGACCCCT 180
 20 TCCTATGCTC TCATCTCATC TATTCATTG CCAGCATCGA AAACAACAAG GTTATCATCA 240
 AGGACAAGAG TGAAGTAGT CTCTACCAGA CCATCAACAG TCTCAAAACC AAGAATCCCA 300
 AACTGAAGT TCTCTGTGCC ATTGGAGGGT ACCTGTTTGG TCCCAAAGGG TTCCACCCTA 360
 TGGTGGATTC TTCTACATCA CGCTTGGAA TCCATTAATC CATAATCCTG TTTCTGAGGA 420
 ACCATAACTT TGATGGACTG GATGTAAGCT GGATCTACCC AGATCAGAAA GAAACACTC 480
 25 ATTTCACTGT GCTGATTCAT GAGTTAGCAG AAGCCTTTCA GAAGGACTTC ACAAAATCCA 540
 CCAAGGAAAG GCTTCTCTG ACTGCGGGCG TATCTGCAGG GAGGCAAAAT ATTGATAACA 600
 GCTATCAAGT TGAGAAACTG GCAAAAGATC TGGATTTTCA CAACCTCCTG TCCTTTGACT 660
 TCCATGGGTC TTGGGAAAAG CCCCTTATCA CTGGCCACAA CAGCCCTCTG AGCAAGGGGT 720
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 30 ATAAAGGAAAT GCCATCAGAG AAGGTGGTCA TGGGCATCCC CACATATGGG CACTCCTTCA 840
 CACTGGCCTC TGCAAAAACC ACCGTGGGGG CCCCTGCCTC TGGCCCTGGA GCTGCTGGAC 900
 CCATCAGAGA GTCTTCAAGG TTCTGGCCT ATTATGAGAT CTGCCAGTTC CTGAAAGGAG 960
 CCAAGATCAC GCGCTCCAG GATCAGCAGG TTCCTACGCG AGTCAAGGGG AACCAGTGGG 1020
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Seq ID NO: 285 DNA sequence
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Protein Accession #: NP_001785.2

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Seq ID NO: 287 DNA sequence
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 Protein Accession #: AAD43756.1

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1 11 21 31 41 51
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 70 CACTGCTCTG AGAATTTGTG AGCAGCCCTC AACAGGCTGT TACTTCACTA CAACTGACGA 60
 TATGATCATC TTAATTTACT TATTTCTCTT GCTATGGGAA GACACTCAAG GATGGGGATT 120
 CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG 180
 AGAAGCACGG TCTGGCAAAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT 240
 TGAAGGCGCG CATCTCGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTC 300
 75 TGTCTGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATTT TGAAGCCGAG 360
 GCGCACTGT GGAATTTGAA AACTGGCAT TATTGATTAT GGAATCCGTC TCAATAGGAG 420
 TGAAAGATGG GATGCTTATT GCTACAACCC ACACGCAAG GAGTGTGTG GCGTCTTAC 480
 AGATCCAAAG CAAATTTTAA AATCTCCAGG CTTCCCAAT GAGTAGCAAG ATAACCAAT 540
 CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTATGATT 600
 80 TGACCTTGAA GATGACCCAG GTTGTCTGGC TGATTATGTT GAAATATATG ACAGTTACGA 660
 TGATGTCCAT GCGCTTGTGG GAAGATACTG TGGAGATGAG CTTCCAGATG ACATCATCAG 720
 TACAGGAAAT GTCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGGAGGTTT 780
 CCAAAATCAA TATGTTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAA 840
 TACTACTTCT ACTGAAATA AAAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAA 900
 AAAAAAAGGA TGATCAAAAC ACACAGTGTT TATGTTGGAA TCTTTTGAA CTCTTTGAT 960

5

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CTCACTGTGA TTATTAAACAT TTATTATTA TTTTCTTAAA TGTGAAAGCA ATACATAATT 1020
TAGGGAAATAT TGGAAAATAT AGGAAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
ACTGCATAGA AATAACAAGC GTTAACATT TCAATTTTTT TTCTTTCAGT CATTTTTCTA 1140
TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTCAT TTGAAATTTT GGAATCCTGC 1200
TCTATGTACA GTTTGTATAT ATACTTTTA AATCTTGAAC TTTATAACA TTTTCTGAAA 1260
TCATTGATTA TTCTACAAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
TGTTTTATGC ATTATTTAAG CTTGTCTCTA TTGTTGGAAT TTCAGGTCAT TTTCAATAAT 1380
ATTGTTGCAA TAAATATCCT TGAACACACA AAAAAAAAAA AA

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10 Seq ID NO: 292 Protein sequence
Protein Accession #: Eos sequence

15

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1 11 21 31 41 51
MIIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEP 60
EGGHLATYKQ LEARKRIGFH VCAAGWMAKG RVGYPIVKPG PNCQPGKGTI IDYGI RLNR 120
ERWDAYCYNP HAKCCGGVFT DPKQIFKSPG PFNEYEDNQI CYWHIRLKYQ QRIHLSFLDP 180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
QIKYVAMDPV SKSSQKNTS TTSTGNKNFL AGRFSLH

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20 Seq ID NO: 293 DNA sequence
Nucleic Acid Accession #: NM_007115.1
Coding sequence: 69..902

25

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1 11 21 31 41 51
GAATTCGCAC TGCTCTGAGA ATTTGTGAGC AGCCCCTAAC AGGCTGTTAC TTCCTACAA 60
CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120
GGGATATCAA GGATGGAAAT TTTCATAACT CCATATGGCT TGAACGAGCA GCCGTGTGRT 180
ACCAAGAGAG AGCAGCGTCT GGCAATACA AGCTCACCTA CGCAGAAGCT AAGGCGGTGT 240
GTGAATTTGA AGGCGGCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG 300
GATTTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCATTGTGA 360
AGCCAGGGCC CAATGATGA TTTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA 420
ATAGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGTTGGCG 480
TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAAATGAG TACGAAGATA 540
ACCAAATCTG CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTAC CTGAGTTTTT 600
TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
GTACGATGA TGTCCATGGC TTTGTGGGAA GATACTGTGG AGATGAGCTT CCAGATGACA 720
TCATCAGTAC AGGAATGTCT ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
GAGGTTTCCA AATCAAAATAT GTTGCAATGG ATCCTGTATC CAAATCCAGT CAAGGAAAAA 840
ATACAAGTAC TACTTCTACT GGAAATAAAA ACTTTTATAG TGGAAAGATT AGCCACTTAT 900
AAAAAAAAAA AAGGATGATC AAAACACACA GTGTTTATGT TGGAAATCTT TGGAACTCCT 960
TTGATCTCAC TGTATTATT AACATTTATT TATTATTTT CTAAATGTGA AAGAAATACA 1020
TAATTTAGGG AAAATTTGAA AATATAGGAA ACTTTAAACG AGAAATGAA ACCCTCTATA 1080
ATCCCACTGC ATAGAAATAA CAAGCGTTAA CATTTTCATA TTTTTCCTT TCAGTCATT 1140
TTGTAATTTGT GGTATATGTA TATATGTACC TATATGTATT TGCAATTGAA ATTTTGGAA 1200
CTGTCTTAT GTACAGTTTT GTATTATACT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260
TGAATCATT GATTATTCTA CAAAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320
ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTTTCAG GTCATTTTCA 1380
TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

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50 Seq ID NO: 294 Protein sequence
Protein Accession #: NP_009046.1

55

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1 11 21 31 41 51
MIIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEP 60
EGGHLATYKQ LEARKRIGFH VCAAGWMAKG RVGYPIVKPG PNCQPGKGTI IDYGI RLNR 120
ERWDAYCYNP HAKCCGGVFT DPKRIPKSPG PFNEYEDNQI CYWHIRLKYQ QRIHLSFLDP 180
DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPDDIIS TGNVMTLKFL SDASVTAGGF 240
QIKYVAMDPV SKSSQKNTS TTSTGNKNFL AGRFSLH

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65 Seq ID NO: 295 DNA sequence
Nucleic Acid Accession #: NM_001218.2
Coding sequence: 116..1180

70

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1 11 21 31 41 51
GTACTGCGCA CGGCAACCCAG GCTGCGGCGA CGCGGTCCCG GTGTGCAGCT GGAGAGCGAG 60
CGGCCACCGG GAGCCCCCGG CACAGCCCGC GCCCGCCCCG CAGGAGCCCG CGAAGATGCC 120
CGGCCGACGC CTGCAGCGCG CGGCCGTGCT CCGTCTGGTG ATCTTAAAGG AACAGCCTTC 180
CAGCCCGGCC CCAAGTGAAC GTTCCAAGTG GACTTATTTT GGTCTCTGAT GGGAGAAATG 240
CTGATCCAAG AAGTACCCGT CGTGTGGGGG CCTGCTGCAG TCCCCATAG ACCTGCACAG 300
TGACATCCTC CAGTATGAGG CCAGCCTCAC GCCCTCGAG TTCCAAGGCT ACAATCTGTC 360
TGCCAACAAG CAGTTTCTCC TGACCAACAA TGCCATTCTA GTGAAGCTGA ACCTGCCCTC 420
GGACATGCAC ATCCAGGGCC TCCAGTCTCG CTACAGTGCC ACGCAGCTCG ACCTGCACAG 480
GGGGAACCCG AATGACCCGC ACGGCTCTGA GCACACCGTC AGCGACAGC ACTTCGCCGC 540
CGAGCTGCAC ATTGTCCATT ATAACCTAGA CCTTTATCCT GACGCCAGCA CTGCCAGCAA 600
CAAGTCAGAA GGCCCTGCTG TCCTGGCTGT TCTCATTGAG ATGGGCTCCT TCAATCCGTC 660
CTATGACAAG ATCTTCAGTC ACCTTCAACA TGTAAGTAC AAAGGCCAGG AAGCATTGCT 720
CCCGGATTC AACATTGAAG AGCTGCTTCC GGAGAGGACC GCTGAATATT ACGCTACCG 780
GGGGTCCCTG ACCACACCCC CTTGCAACCC CACTGTGCTC TGGACAGTTT TCCGAAACCC 840
CGTGCAAAAT TCCAGGAGC AGCTGCTGCG TTTGGAGACA GCCCTGTACT GCACACAT 900

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GGACGACCCT TCCCCAGAG AAATGATCAA CAACTTCCGG CAGGTCCAGA AGTTGATGA 960
GAGGCTGGTA TACACCTCCT TCTCCCAAGT GCAAGTCTGT ACTGGGGCAG GACTGAGTCT 1020
GGGCATCATC CTCTCACTGG CCCTGGCTGG CATTCTTGGC ATCTGTATTG TGGTGGTGGT 1080
GTCCATTGGG CTTTTCAGAA GGAAGAGTAT CAAAAAAGGT GATAACAAGG GAGTCATTTA 1140
CAAGCCAGCC ACCAAGATGG AGACTGAGGC CCACGCTTGA GGTCCCGGGA GCTCCCGGGC 1200
ACATCCAGGA AGGACCTTGC TTTGGACCTT ACACACTTGG GCTCTCTGGA CACTTGGCGAC 1260
ACCTCAAGGT GTTCTCTGTA GCTCAATCTG CAAACATGCC AGGCCTCAGG GATCCTCTGC 1320
TGGGTGGCTC CTTCCTTGG GACCATGGCC ACCCCAGAGC CATCCGATCG ATGGATGGGA 1380
TGCACTCTCA GACCAAGCAG CAGGAATTCA AAGCTGCTTG CTGTAAGTGT GTGAGATTGT 1440
GAAGTGGTCT GAATTCTGGA ATCACAACCC AAGCCATGCT GGTGGGCCAT TAATGGTTGG 1500
AAAAACACTT CATCCGGGGC TTTGCCAGAG CGTGCTTTCA AGTGCTCTGG AAAGTCTGCT 1560
GCTTCTCCAA GCTTTCAGAC AAGAATGTGC ACTCTCTGCT TAGGTTTTGC TTGGGAAACT 1620
CAACTTCTTT CCTCTGGAGA CGGGGCATCT CCTCTGATT TCCTTCTGCT ATGACAAAAC 1680
CTTTAATCTG CACCTTACAA CTCGGGGACA AATGGGGACA GGAAGSATCA AGTTGTAGAG 1740
AGAAAAAAGA AAACAAGAGA TATACATTGT GATATATTAG GGACACTTTC ACAGTCTGCT 1800
CCTCTGGATC ACAGACACTG CACAGACCTT AGGGAATGGC AGGTTCAAGT TCCACTTCTT 1860
GGTGGGGAGA AGAAGGAGGA GAGAGCTAGA GGGACAAAGA GAATGAGAAG ACATGGATGA 1920
TCTGGGAGAG TCTCACTTTG GAATCAGAAT TGGAAATCAA TTCTGTTTAT CAAGCCATAA 1980
TGTAAGGACA GAATAATACA ATATTAAATC CAAATCCAACT CTCTGTCTAG TGGAGCAGTT 2040
ATGTTTTATA CTCTACAGAT TTTACAAATA ATGAGGCTGT TCCTTGAAAA TGTGTTGTTG 2100
CTGTGCTCTG GAGGAGACTG GAGTTCGAGG ATGACCCAACT CTGCTTTTGA ATCTGGAGGA 2160
AATAGGCAGA AACAAAATGA CTGTAGAACT TATTCTCTGT AGGCCAAATT TCATTTCAGC 2220
CACTTCTGCA GGATCCCTAC TGCCAACTCT GAATGGAGAC TTTTATCTAC TTCTCTCTCT 2280
CTGAAGATGT CAAATCGTGG TTTAGATCAA ATATATTTCAGTCTATAAAA GCAGGAGGTT 2340
ATCTGTGCGA GGGCTGGGCA TCATGTATTT AGGGGCAAGT AATAATGGAA TGCTACTAAG 2400
ATACTCCATA TTCTTCCCGG AATCACACAG ACAGTTTCTG ACAGGCGCAA CTCTCCATT 2460
TTCTCCCGC AGGTGAGAAC CCTGTGGAGA TGAGTCAGTG CCATGACTGA GAAGGAACCG 2520
ACCCCTAGTT GAGAGCACTT TGCAGTTCCC CGAAGACTTT CTGATTCCCA GTCTCATTTT 2580
GACAGCATGA AATGTCCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTCC TTCTACTCT 2640
CCCTCTGACT CTAAGAAATC TCTCTCTGG AATCGCTTGA ACCCAGGAGG CGGAGGTTGC 2700
AGTAAGCCAA GGTCTATGCC CTGCACTCTA GCCTGGGTGA CAGAGCGAGA CTCATCTCA 2760
AAAAA AAAAA

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35 Seq ID NO: 296 Protein sequence
Protein Accession #: NP_001209.1

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1 11 21 31 41 51
| | | | |
MPRRSLHAAA VLLLVLKEQ PSSPAPVNGS KNTYFGPDGE NSWSKYPSC GLLQSPIDL 60
HSDILQYDAS LTPLEQGYN LSANKQFLLT NNGHSVKLNL PSDMHIQGLQ SRYSATQLHL 120
HWGNPNDPHG SEHTVGGQHF AELHLIVHYN SDLYPDASTA SNKSEGLAVL AVLIEMGSFN 180
PSYDKIFSHL QHVKYKGQBA FVPGFNIEEL LPERTAYYR YRGLSLTPPC NPTVLWTVFR 240
NPVQISQEQE LALETALYCT HMDDPSPREM INNFRQVQKF DERLVYTSFS QVQVCTAAGL 300
SLGILSLAL AGILGICIVV VVSIWLPFRK SIKKGDNKGV IYKPKTKMET EARA

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Seq ID NO: 297 DNA sequence
Nucleic Acid Accession #: NM_006632.1
Coding sequence: 377..1582

50
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60
65
70
75
80

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1 11 21 31 41 51
| | | | |
ACGGGTGCGC CCAAGCGTCC GCCACGCGT CCGGTGCGGG CCAGAGCGCA GGTGTACCTG 60
GGGCGCGTGC TGGAGCACTT GACCGCGAG ATCCTGGAGC TGGCTGGCAA CCGGCGCGC 120
GACAAGAAGA CCCGATCAT CTGTGCGCAC CTGTAGCTGG CCATTGCGCA CGGCGAGGAG 180
CTTAACAAGC TGCTGGGCGA AGTCACCATC GCGCAGGGCG GTGTCTCTCC CAACATTCTAG 240
GGCGTGCTTC TGGCCAGAA GACCAAGAGC CACCACAAGG CCAAGGGTGA AAACCATTC 300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAG CAAGGGAGAG 360
CAAGAAGCCA CAAGATATGC AAGTGGATGA GACACTGATC CCCAGGAAG GTCCAGTTT 420
ATGTTCTGCT CGCTATGAA TAGCCCTGCT CTACATTTC TGCAATTTC CAACGATAGC 480
ACAAAATGTC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACAA GCCCTCAATC 540
CCAGCTCAAT GATTCCTCTG AGGTGCTGCC TGTGACTCA TTTGGTGGCC TAAGTAAAGC 600
CCCAAGAGT CTTCTGCAA AGTCTCAAT ACTGGGGGT CAGTTTGCAA TTTGGGAAAA 660
GTGGGGCCCT CCACAGAAG GAAGCAGACT CTGCAGCATT GCTTTATCAG GAATGTACT 720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCATTAGT GAAACCCCTG GGTGGCCCTT 780
TGTCTTCTAT ATCTTTGGAG GTGTTGGCTG TGTCTGCTGC CTCTCTGTG TTGTTGTGAT 840
TTATGATGAC CCTTTTCTT ATCCATGGAT AAGCACTCA GAAAAAGAT ACATCATATC 900
CTCCTTGAAA CAACAGGTGG GTCTTCTAA GCAGCCTCTT CCCATCAAAG CTATGCTCAG 960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGGT TAGTTAGCAC 1020
AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA 1080
TGGACTTCTA TCTGCCCTTC CTTTATTGTT TGCCTGGGTC ATAGGCATGG TGGGAGGCTA 1140
TCTGGCATGC TTCTTCTTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTGCCAC 1200
AATTTTAGGA AGTCTCCCTT CTTGAGCACT CATTTGTCT CTGCTTACC TCAATTCCGG 1260
CTATATCACA GCACTGCCCT TGCTGACGCT CTCTTGCAGA TTAAGCACAT TGTGTCACTC 1320
AGGGATTTAT ATCAATGTCT TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
ATCAAGAGGA TTCTGAGACA TAGCACTGT CATGTACCC ACTGTCAAGG GATTTCTCT 1440
TAGTCAGGAC CCTGAGTTTG GGTGGAGGAA TGTCTTCTTC TTGCTGTTTG CCGTTAACT 1500
GTTAGACTCA CTCTCTACC TCATATTGG AGAAGCAGAT GTCCAAAGAT GGGCTAAAGA 1560
GAGAAAACCT ACCTGTTTAT GAAGTTATCC CACTTGGAT GGAAAAGTCA TTAGGCACCG 1620
TATTGCATAA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAGAAGAT TTTTCTCT 1680
GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTAT TTTGAGAGAA 1740
ATGTAAAGAT AATAAAAAAT CAAATAAAAT GATAACTAAG AAAAAA AAAAA

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Seq ID NO: 298 Protein sequence
Protein Accession #: NP_006623.1


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1      11      21      31      41      51
|      |      |      |      |      |
5  MQVDETLPKR KGPSLCSARY GIALVLHPCN FTIAQNVIM NITMVMVNS TSPQSQNLDS 60
SEVLVDSFPG GLSKAPKSLP AKSSILGGQF AINBKWGPQ ERRLCSIAL SGMLLGCTPA 120
ILIGGFISET LGWPFVFIYP GVGCVCCLL WFWVIYDDFP SYPWISTSEK EYIISLKKQ 180
VGSSKQPLPI KAMLRSLPIW SICLCPSHQ WLVTMVVYI PTYISSVYHV NIRDNGLLSA 240
LPFIVAMVIG MVGGYLADFL LTKKPRITV RKIATILGSL PSSALIVSLP YLNSGYITAT 300
ALLTSLCGLS TLCQSGIYIN VLDIAPRYSS FLMGASRGFS SIAPVIVPTV SGFLLSQDPE 360
10 FGWRIVFFLL FAVNLLGLLF YLIFGEADVQ EWAKERKLTR L

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Seq ID NO: 299 DNA sequence

Nucleic Acid Accession #: NM_003058.1

Coding sequence: 145..1812

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15      1      11      21      31      41      51
|      |      |      |      |      |
20  GGCCCTGCC TGAAGGCTGG TCACCTGCAG AGGTAAACTC CCTCTTTGA CTCTGGCCA 60
GGGTTTGTGC TGAGCTGGCT GCAGCCGCTC TCAGCCTCGC TCCGGGCAGC TCGGGCAGCC 120
TGGGGCCCTC CTGCTCGCAG GATCATGCCC ACCACCGTGG ACGATGTCTT GGAGCATGGA 180
GGGAGTTTC ACTTTTCCA GAAGCAAATG TTTTCTCTCT TGGCTCTGCT CTCGGCTACC 240
TTGCGGCCCA TCTACGTGGG CATCGTCTTC CTGGGCTTCA CCCCTGACCA CCGCTGCCGG 300
AGCCCCGGAG TGGCCGAGCT GAGTCTGCGC TGGCGCTGGA GTCTCGCAGA GGAAGTGAAC 360
TACACGGTGC CGGGCCAGG ACCTGGGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420
GAGGTGAGCT GGAACCCAGG CACCTTTGAC TGGTGGAGCC CCTGGCCAGC CCGGACACC 480
AACAGGAGCC GCTGCTCACT GGGCCCTGCG CGGACGGCTC GGGTGTACGA GACGCTGGC 540
TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAACT CCTGGATGTT GGACCTATTC 600
CAGTCATCAG TGAATGTAGG ATTCTTTATG GGCTCTATGA GTATCGGCTA CATAGCAGAC 660
AGGTTTGGCC GTAAGCTCTG CCTCCTAACT ACAGTCTCTA TAAATGCTGC AGCTGGAGTT 720
CTCATGGCCA TTTCCCAAC CTATACGTGG ATGTTAATTT TTGCTTAAT CCAAGGACTG 780
GTGAGCAAAG CAGGCTGGTT AATAGCTAC ATCCTGATTA CAGAATTGTT TGGCGGAGA 840
TATCGGAGAA CAGTGGGGAT TTTTACCAA GTTGCTTATA CAGTTGGGCT CCTGGTCTA 900
GCTGGGGTGG CTTACGCACT TCCTCACTGG AGGTGGTTGC AGTTCACAGT TGCTCTGCC 960
AAGTTCTTCT TCTTGTCTTA TTAAGTGTGC ATACCTGAGT CTCGAGGTG GCTGATCTCC 1020
35  CAGAATAAGA ATGCTGAAGC CATGAGAATC ATTAAGCACA TCGCAAAGAA AAATGGAAAA 1080
TCTCTACCCG CCTCCCTTCA GCGCCTGAGA CTTGAAGAGG AAAGTGGCAA GAAATTGAAC 1140
CCTTCATTTC TGAAGTGGT CAGAACTCCT CAGATAAGGA AACATACTAT GATATTGATG 1200
TACAACGTGT TCACGAGCTC TGTGCTCTAC CAGGGCCTCA TCATGCACAT GGGCCTTGCA 1260
GGTGACATA TGTACCTGGA TTTCTTCTAC TCTGCCCTGG TGAATTCCG AGCTGCTCTC 1320
40  ATGATCATCC TCACCATCGA CGCATCGGGA CGCGTTACC CTGGGCTGCG ATCAAATATG 1380
ATTGCGAGGG CAGCCTGTCT GGCCTCAGTT TTTATACCTG GTGATCTACA ATGGCTAAAA 1440
ATTATTATCT CATGCTTGGG AAGAAATGGG ATCACAATGG CCTATGAGAT AGTCTGCCTG 1500
GTCAATGCTG AGCTGTACCC CACATTCATT AGGAATCTTG GCGTCCACAT CTGTTCTCTA 1560
ATGTGTGACA TGTGTTGGAT CATCAAGCCA TTCCTGTCTC ACGGCTCAC TAACATCTGG 1620
45  CTGAGCTCC CGCTGATGGT TTTGGGGTGA CTGGCTTGG TTGCTGGAGG TCTGGTGTG 1680
TTGCTTCCAG AAATAAAGG GAAAGCTTTG CCTGAGACCA TCGAGGAAGC CGAAATATG 1740
CAAGACCAA GAAAAAATAA AGAAAAGATG ATTTACCTCC AAGTTCAGAA ACTAGACATT 1800
CCATTGAACT AAGAAGAGAG ACCGTTGCTG CTGTCATGAC CTAGCTTGA TGGCAGCAAG 1860
ACCAAAAGTA GAAATCCCTG CACTCATCAC AAAGCCATA CAAGTCAACC AAAGTTACCC 1920
50  CTGAGCCCTA TCAACCTAGG TCTACAGCCA GTGGAGTCTA TTGTACACTG TGGAAAAATA 1980
CCCATGGGAC CAGATCCTCT CAAATCTTTC CAGCTCAGTT TATTCTCAGC ATTCCTAGGA 2040
CATTGACAT TGGTTTCTG GAGGTTTCTT TTTCCGATCT TTGATTTT TTAATTTGA 2100
TTCTTTCTCT TGCAATGCTA GCAACCAAGG TACATAGGGG AACTGTGGGG TAGGCAANA 2160
55  AAAATAGAAA AGTGTGAAAA ACAGTAAAGT TGGGAGAGGA GCATCTATTT TCTTAAAGAA 2220
ATAAACACC NAAAAA AAAA AAAA

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Seq ID NO: 300 Protein sequence

Protein Accession #: NP_003049.1

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60      1      11      21      31      41      51
|      |      |      |      |      |
65  MPTTVDDVLE HGGEPHFQK QMFFLLALLS ATPAPIYVGI VFLGFTPDHR CRSPGVAELS 60
LRGWSPAEE LNYTVPGPGP AGEASPRQCR RYEDWNQST FDCVDPLASL DTNRRLPLG 120
PCRDGWVYET PGSSIVTEFN LVCANSWMLD LFQSSVNVGF FIGSMSIGYI ADRPGRKLCL 180
LTTVLINAA GVLMAISPTY TWMLIFRLIQ GLVSKAGWLI GYLITEFVG RRYRRTVGIF 240
YQVAYTVGLL VLAGVAYALP HWRWLQPTVA LPNFFFLYY WCIPESPRWL ISQKNNAEAM 300
RIIKHIAKGN GRSLPASLQR LRLEETGKK LNPSFLDLVR TPQIRKHTMI LMYNWFTSSV 360
LYQGLIMEMG LAGDNLYLDP FYSALVEPPA AFMIILTIDR IGRYPVWAS NMVAGAACLA 420
SVFIPGDLQW LKIIISCLGR MGIIMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480
70  TFFLVYRLTN IWLPLPLAVF GVLGLVAGGL VLLLPETKGR ALPETIEEAE NMQRPRKNKE 540
RMIYLVQVQL DIPLN

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Seq ID NO: 301 DNA sequence

Nucleic Acid Accession #: NM_012206.1

Coding sequence: 52..1131

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75      1      11      21      31      41      51
|      |      |      |      |      |
80  GTTACCCAGC ATTGTGAGTG ACAGAGCCTG GATCTGAACG CTGATCCCAT AATGCATCCT 60
CAAGTGTGCA TCTTAAGCCT CATCTACAT CTGGCAGATT CTGTAGCTGG TTCTGTAAAG 120
GTTGGTGGAG AGGCAGGTCC ATCTGTGACA CTACCCCTGCC ACTACAGTGG AGCTGTGACA 180
TCAATGTGCT GGAATAGAGG CTCATGTTCT CTATTCACAT GCCAAAATGG CATTGTCTGG 240
ACCAATGGAA CCCAGCTCAC CTATCGGAAG GACACACGCT ATAAGCTATT GGGGGACCTT 300
TCAGAAGAGG ATGTCTCTTT GACCATAGAA AATACAGCTG TGCTGACAG TGGCGTATAT 360

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5 TGTGCGGTG TTGAGCACCG TGGGTGGTTC AATGACATGA AAATCACCGT ATCATTGGAG 420
 ATTGTGCCAC CCAAGGTCAC GACTACTCCA ATTGTCCAA CTGTTCCAAAC CGTCACGACT 480
 GTTGCAACGA GCACCACTGT TCCAACGACA AGGACTGTTT CAACGACAAC TGTTCCAACA 540
 ACAATGAGCA TTCCAACGAC AACGACTGTT CGAAGACAA TGACTGTTTC AACGACAACG 600
 AGCGTCCCAA CGACAAAGAG CATTCACAACA ACAACAAGTG TTCCAGTGAC AACCAACGGTC 660
 TCTACCTTTG TTCTCCAAT GCCTTTGCC AGGCAGAAC ATGAACCAAT AGCCACTTCA 720
 CCATCTTCAC CTCAGCCAGC AGAAACCCAC CCTACGACAC TGCAGGGAGC AATAAGGAGA 780
 GAACCCACCA GCTCACCATT GTACTCTTAC ACAACAGATG GGAATGACAC CGTGACAGAG 840
 10 TCTTCAGATG GCCTTTGGAA TAACAATCAA ACTCAACTGT TCCTAGAACA TAGTCTACTG 900
 ACGGCCAATA CCACTAAAGG AATCTATGCT GGAGTCTGTA TTCTGTCTT GGTGCTTCTT 960
 GCTCTTTTGG GTGTATCAT TGCCAAAAAG TATTTCTTCA AAAAGGAGGT TCAACAACATA 1020
 AGTGTTCAT TTAGCAGCCT TCAAATTAAA GCTTTGCAAA ATGCAGTTGA AAAGGAAGTC 1080
 CAAGCAGAAG ACAATATCTA CATTGAGAAT AGTCTTTATG CCACGGACTA AGACCCAGTG 1140
 15 GTGCTCTTTG AGAGTTTACG CCCATGACTG CAGAAGACTG AACAGGTATC AGCAGATCAG 1200
 ATGTCTTTTA GACTCCAAGA CAATTTTCT GTTTCAGTTT CATCTGGCAT TCCAACATGT 1260
 CAGTGACTACT GGGTAGAGTA ACTCTCCAC TCCAACATGT GTATAGTCAA CCTCATCAT 1320
 AATGTAGTCC TAAATTTGTT TGCTAAAAC GGTCTAATCC TTCTGATCAT TGCAGAGTTT 1380
 TCTCTCAAC ATGAACACTT TAGAATTGTA TGTCTCTTT AGACCCATA AATCTGTAT

20 Seq ID NO: 302 Protein sequence
 Protein Accession #: NP_036338.1

25 1 11 21 31 41 51
 MHPQVVLISL ILHLADSVAG SVKVGGEAGP SVTLPCHYSG AVTSMCWNRG SCSLFTQNG 60
 IWTNGTRHT YRKDTRYKLL GDLSRRDVSL TIENTAVSDS GYVCCRVERH GWFNDMKITV 120
 SLEIVPPKVT TTPIVTTVPT VITVRTSTTV PTITTVPTTT VPTTMSIPTT TTVPTTMTVS 180
 TTTSTVPTTS IPTTTSVPVT TTVSTFVPPM FLPRQNHFPV ATSPSSPQPA ETHPTTLQGA 240
 30 IRRPTSSPL YSYTTDGNMT VTSSDGLWN NNQTQLFLEH SLLTANTTKG IYAGVCISVL 300
 VLLALLGVII AKKYFFKKEV QQLSVSFSSL QIKALQNAVE KEVQAEINLY IENSLYATD

35 Seq ID NO: 303 DNA sequence
 Nucleic Acid Accession #: NM_001044.1
 Coding sequence: 129..1991

40 1 11 21 31 41 51
 ACCGCTCCGG AGCGGGAGGG GAGGCTTCGC GGAACGCTCT CGGCGCCAGG ACTCGCGTGC 60
 AAAGCCCAAG CCGGGGCGGC CAGACCAAGA GGAAGAAGC ACAGAATTCC TCAACTCCCA 120
 GTGTGCCCAT GAGTAGAGC AAATGCTCCG TGGGACTCAT GTCTCCCGTG GTGGCCCCGG 180
 CTAAGGAGCC GAATGCCGTG GCGCCGAAGG AGGTGGAGCT CATCTTGTG AAGGAGCAGA 240
 ACGAGGTGCA GCTCACGAGC TCCACCTTCA CCAACCCGCG CAGAGCCCC GTGGAGGCC 300
 AGGATCGGGA GACCTGGGCG AAGAAGATCG ACTTCTCTCT GTCCGTCATT GGCTTTGCTG 360
 45 TGGACCTGGC CAACGCTGGG CGGTTCCTCT ACCTGTGCTA CAAAAATGGT GCGCGTGCT 420
 TCTGTGTCCC CTACCTGCTC TTCTGTGTCA TTGCTGGGAT GCCACTTTTC TACATGGAGC 480
 TGGCCCTCGG CCACTTCAAC AGGGAAGGGG CCGCTGGTGT CTGGAAGATC TGCCCCATAC 540
 TGAAAGGTGT GGCTTCAAG GTCATCTTCA TCTCACTGTA TGTGGCTTC TTCTACAACG 600
 TCAATCATCGC CTGGGCGCTG CACTATCTCT TCTCTCTCT CACCAGGAG CTCCCCGGA 660
 50 TCCACTGCAA CAACTCCTGG AACAGCCCA ACTGCTGGGA TGCCCATCTT GGTGACTCCA 720
 GTGGAGACAG CTGGGCGCTC AACGACACT TTGGGACCAC ACCTGCTGCC GAGTACTTTG 780
 AAOGTGGGT GCTGCACCTC CACCAGAGCC ATGGCATOGA CGACTGGG CCTCCGGGT 840
 GGCAGCTCAC AGCTGCTG GTGCTGTGTA TCGTGTGCT CTACTTCAGC CTCTGGAAGG 900
 CGGTGAAGAC CTGAGGGAAG GTGATATGGA TCACAGCCAC CATGCCATAC GTGGTCTCA 960
 55 CTGCCCCTCT CCGTGTGGG GTCACTCTCC CTGGAGCCAT AGAAGGATC AGAGCATACC 1020
 TGAGCGTGA CTCTACCGG CTCTGCGAGG CGTCTGTTG GATTGAACGG GCCACCCAGG 1080
 TGTGCTTCTC CCGGGCGTG GGGTTCGGG TGTGATCGC CTCTCCAGC TACAACAAAT 1140
 TCACCAACA CTGCTACAGG GACGCGATT TCACCACTC CATCACTCC CTGACGAGCT 1200
 TCTCTCGCG CTCTGCTGCT TTCTCTCTCC TGGGTATCAT GGCACAGAAG CACAGTGTGC 1260
 CCAATGGGGA CGTGGCCAA GAOGGGCCAG GGTGATCTT CATCATCTAC CCGGAAGCCA 1320
 60 TCGCCACGCT CCTCTGTCTC TCAGCTGGG CCGTGTCTT CTTCATCATG CTGCTCACC 1380
 TGGGTATCGA CAGCGCCATG GGTGATATG AGTCAGTAT CACCGGCTC ATCGATGAT 1440
 TCCAGCTGCT GCACAGACAC CGTGAGCTCT TCACGCTCT CATGTCCTG GCGACCTTCC 1500
 TCTCTCTCT GTTCTGCTC ACCAAGCGTG GCATCTAGT CTTCAGCTC CTGGACCAT 1560
 65 TTGCAGCGG CAGTCCATC CTCTTTGGAG TGCTCATCGA AGCCATCGGA GTGGCCTGGT 1620
 TCTATGTTGT TGGCAGTTT AGCGACGACA TCCAGCAGAT GACCGGCGAG CGGCCAGCC 1680
 TGTACTGGG GCTGTGCTGG AAGCTGTCTA GCCCTGCTT TCTCTGTTT GTGGTCTGTG 1740
 TCAGCATTTT GACCTTCAGA CCCCCCACT ACGGAGCCTA CATCTTCCC GACTGGGCCA 1800
 ACGCGCTGG CTGGGTCTC GCCACATCTT CCATGGCCAT GGTGCCCATC TATGCGGCT 1860
 70 ACAAGTCTG TACGCTGCTT GGTCTCTTTC GAGAGAACT GGCCTAAGCC ATTGCAACCG 1920
 AGAAGGACCG TGAGCTGGT GACAGAGGGG AGGTGCGCCA GTTCAAGCTC CGCACTGGC 1980
 TCAAGGTGTA GAGGAGCAG AGACGAAGAC CCCAGGAAGT CATCTGCAA TGGGAGAGAC 2040
 ACGAACAAAC CAAGGAATC TAAATTTGGA GAGAAAGGAG GGCACTTCT ACTCTTCAAC 2100
 CTCTACTGAA AACACAACA ACAAGCAGA AGACTCTCT CTCTGACTG TTTACACCTT 2160
 75 TCGTGCCGG GAGCGCACT GCGGTGTCT TGTGTGCTG TAATAAGGAC GTAGATCTGT 2220
 GCACGAGGT CCACCCGCTT GTTGTCTCT CAGGCGAGAA AAACGTCTAA CTTCATGCTG 2280
 TCTGTGTGAG GCTCTCTCCC TCCCTGCTCC CTGCTCCCG CTCTGAGGCT GCCCCAGGG 2340
 CACTGTGTTT TCAGGCGGG ATCAAGATCC TTGTAGAAGC ACCTGCTGAG AATCCCGTG 2400
 CTCACAGTAG CTCTTAGAC CATTACTTTT GCCATATTA AAAAGCCAA GTCTCTGCTT 2460
 80 GGTTAGCTG TGCAAGAGT GAAATGAGG AAACCAAAA TTATGCAAA GTCTTTTCCC 2520
 GATGCGTGGC TCCAGCAGA GGCCTGAAAT TGAGGTTTCA GTTGACATC TGCAACACAT 2580
 GTCTGTTCAG AGGCATTGGA GGTGAGGGGT CTGCTATGAT CTCACAGGA AATCTGTTT 2640
 ATGTTCTTGC AGCAGAGAGA AATAAACTC CTGAAACCA GCTCAGGCTA CTGCACTCA 2700
 GGCAGCTGT GGTCTCTGT GGTGTAGGA ACGGCTGAG AGGAGCTGT CCTATCCCCC 2760
 GACGATGCA GGGCCCCAC AGGAGCTGT CTTATCCCC GAGCATGCA GGGCCCCAC 2820

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10
15
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AGGAGCATGT CCTATCCCTG GACGCATGCA GGGCCCCCAG AGGAGCGTGT ACTACCCACG 2880
AACGCATGCA GGGCCCCCAG AGGAGCGTGT ACTACCCACG GACGCATGCA GGGCCCCCAG 2940
TGGAGCGTGT ACTACCCACG GACGCATGCA GGGCCCCCAG AGGAGCGTGT CCTATCCCTG 3000
GACCCGAGCG ATGCAGGGCC CCCACAGGAG CGTGTACTAC CCCAGGACGC ATGCAGGGCC 3060
CCCAAGGAG CGTGTACTAC CCCAGGATGC ATGCAGGGCC CCCACAGGAG CGTGTACTAC 3120
CCCAGGACGC ATGCAGGGCC CCCATGCAGG CAGCTGCAG ACCAACACTC TGCGTGGCCT 3180
TGAGCGGTGA CCTCCAGGAA GGGACCCAC TGGAAATTTA TTTCTCTCAG GTGCGTGCCA 3240
CATCAATAAC AACAGTTTTT ATGTTTGCGA ATGGCTTTTT AAAATCATAT TTACCTGTGA 3300
ATCAAAACAA ATTCAAGAAAT GCAGTATCCG CGAGCCTGCT TGCTGATATT GCAGTTTTTG 3360
TTTACAAGAA TAATTAGCAA TACTGAGTGA AGGATGTTGG CCAAAAGCTG CTTTCCATGG 3420
CACACTGCCC TCTGCCACTG ACAGGAAAGT GGATGCCATA GTTTGAATTC ATGCCTCAAG 3480
TCGCTGGGCC TGCCCTACGTG CTGCCCGAGG GCAGGGGCCG TGCAAGGCCA GTCATGGCTG 3540
TCGCCGTCAA GTGGAGCTGG GCTCCAGGGA CTGGAGTGTG ATGCTCGGTG GGAGCCGTCA 3600
GCCTGTGAAC TGCCAGGCAAG CTGCAGTTAG CACAGAGGAT GGCTTCCCA TTGCTTCTG 3660
GGGAGGGACA CAGAGGAAGG CTGCCCATC GCCTTCTGGC CGCTGCAGTC AGCAGAGAGA 3720
CGCGCTTCCC CATTGCCTTC TGGGAGGGA CACAGAGGAC AGTTTCCCA TGCGCTTCTG 3780
GTTGTTGAAG ACAGCAGAGA GAGCGGCTTC CCCATCGCCT TCTGGGGAGG GGCTCCGTGT 3840
AGCAACCCAG GTGTGTCCG TGCTGTGTA CCAATCTCTA TTCAGCATCG TGTGGGTCCC 3900
TAAGCAAAAT AAAAGACATC CACAATGGAA AAAAAAAG GAATTC

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Seq ID NO: 304 Protein sequence
Protein Accession #: NP_001035.1

25
30
35

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1 11 21 31 41 51
MSKSKCSVL MSSVVAPEKE PNAVGPIKEVE LILVKEQNGV QLSSTLTNP RQSPVEAQDR 60
ETWKKIDPL LSVIGFAVDL ANVWRFPYLC YKNGGAPLV PYLLFMVIAG MPLFYMELAL 120
GQFNREGAAG WMKICPILKG VGPTVILISL YVGFYFNVII AWALHYLFSS FTTELPNHL 180
NNSWNSPNCB DAHPGDSSGD SSGLNDTFGT TPAEYFERG VHLHLQSHGI DDLGPPRNQL 240
TACLVLIVIL LYPSLWKGVK TSGKVVWITA TMPVVLTLAL LLRGVTLFGA IDGIRAVLSV 300
DFYRLCBASV WIDAATQVCF SLGVGFGVLI APSSYNKPTN NCRYDAIVTT SINSITSFSS 360
GVVVFSPFLG MAQKHSVPFG DVAKDGPGLI FIIYPEAIAT LPLSSAWAVV PFIMLLTLGI 420
DSAMGMSBSV ITGLIDEFQL LHRHRELFTL FIVLATPLLS LFCVTNGGIY VPTLLDHPAA 480
GTSILFGLVI EAIGVAWFYV VGQFSDDIOQ MTGQRPSLYW RLCWKLVSFC FLLFVVVSVI 540
VTFRPPHYGA YIFEDWANAL GWVIATSSMA MVPIYAAYKF CSLPGSFREK LAYATAPEKD 600
RELVDREGEV QTLRHWLKV

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Seq ID NO: 305 DNA sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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50
55
60
65
70

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1 11 21 31 41 51
GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 60
AGCCCTGGCC TCCCTCTGTT GATCCCGGCC CTGTCTCCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCACAGAGT TGCCCCGGAT GCAGGAGGAT 180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GATCTGCCCC 240
AGTGAAGAGG ATTCAACCCAG AGAGGAGGAT CCACCCGAGG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAATTCAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTOCTG GAGATCCTCA AGAACCCAG 420
AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGOGAC 480
CGCCCTGGCC CCGGGGTGCT CCCAGCCTGC GCGGGCGGCT TCCAGTCCCC GGTGGATATC 540
CGCCCGCAGC TCGCCGCTTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG 600
CTCCCGCCGC CTCCGAGAACT GCGCCTGCGC AACAAATGCC ACAGTGTGCA ACTGACCCCTG 660
CCTCCTGGCC TAGAGATGSC TCTGGGTCCC GGGGGGAGT ACGGGCTCT GCAGCTGCAT 720
CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC 780
CTGCGCAGGA TCCAGTGCT TCACTCAGC ACCGCTTTG CCAGAGTTGA CGAGGCTTTC 840
GGGCGCCCGG GAGGCTTGGC CGTGTGCGCC GCCTTCTTGG AGGAGGGCCC GGAAGAAAAC 900
AGTGCCTATG AGCAGTTGCT GTCTGCTTGG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
CAGGTCCAGC GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCGC CTACTTCCAA 1020
TATGAGGGGT CTCTGACTAC ACGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC 1080
CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCTCT CTGACACCTT GTGGGACCT 1140
GGTGACTCTC GGCTACAGCT GAACCTCCGA GCGACGAGC CTTTGAATGG GCGAGTGATT 1200
GAGGCTCTCT TCCCTGTGGA AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGTGTCT 1320
ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAAC CAAAGGGGGT 1380
GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGAGAAA 1440
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GAGCCCGGTA ACTGTCTCTG CCTGCTCATT 1500
ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTATA AT

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Seq ID NO: 306 Protein sequence
Protein Accession #: NP_001207.1

75
80

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1 11 21 31 41 51
MAPLCPSPWL PLLIPAPAPG LTVQLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPREDPPGE EDLPGEEDLP GEEDLPVVKP KSEEEGSLKL EDLPVTEAPG 120
DPQEPQNNAH RKEGDDQSH WRYGGDPPWP RVSPACAGRF QSPVDIRPQL AAFPALRPL 180
ELLGQPLPPL PELRLRNNGH SVQLTLPPGL EMALGPGRFY RALQLHLHWG AAGRPGSEHT 240
VEGHRFPFBI HVVHLSTAPA RVDEALGRPG GLAVLAAPLE EGPEENSAYE QLSRLBEEIA 300
EEGSETQVPG LDISALLPSD PSRYFYQEGS LTPPCAQGV IWTVFNTQVM LSAQLHLTSL 360
DTLWGPDSR LQINFRATQP LNGRVIEASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
QLLFAVTSVA FLVQMRQRHR RGTGGGVSYR PAEVAETGA

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Seq ID NO: 307 DNA sequence
Nucleic Acid Accession #: NM_003039.1
Coding sequence: 76..1581

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5      1      11      21      31      41      51
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      CTCTCTCTC  CATTCACTGC  ACGCGTTACT  TTGGCTAAAA  GGAGGTGAGC  GGCACCTCTGC  60
      CCTTCCAGAG  CAAGCATGGA  GCAACAGGAT  CAGAGCATGA  AGGAAGGGAG  GCTGACGCTT  120
      GTGCTTGCCC  TGGCAACCCCT  GATAGCTGCC  TTTGGGTGAT  CCTTCCAGTA  TGGGTACAAC  180
10     GTGCTGCTG  TCAACTCCCC  AGCACTGCTC  ATGCAACAAT  TTTACAATGA  GACTTACTAT  240
      GGTAGGACCG  GTGAATTCAT  GGAAGACTTC  CCCTTGACGT  TGCTGTGGTC  TGTAAACGTC  300
      TCCATGTTTC  CATTTCGAGG  GTTTATCGGA  TCCCTCCTGG  TCGGCCCTTT  GGTGAATAAA  360
      TTTGGCAGAA  AAGGGGCCCT  GCTGTTCAAC  AACATATTTT  CTATCGTGCC  TGCATCTTA  420
      ATGGGATGCA  GCAGAGTCGC  CACATCATTT  GAGCTTATCA  TTATTTCCAG  ACTTTTGGTG  480
15     GGAATATGTG  CAGGTGTATC  TTCCAACTGC  GTCCCATGT  ACTTAGGGGA  GCTGGCCCT  540
      AAAAACTGCG  GGGGGGCTCT  CGGGGTGGTG  CCCAGCTCT  TCATCACTGT  TGGCATCCTT  600
      TGGGCCATG  TCTTTGGTCT  TCGGAATCTC  CTTGCAAAAG  TAGATGGCTG  GCCGATCCTG  660
      TCGGGGCTGA  CCGGGGTCCC  CGCGGCGCTG  CAGCTCCTTC  TGCTGCCCTT  CTTCGCCGAG  720
      AGCCCCAGGT  ACCTGCTGAT  TCAGAAGAAA  GACGAAGCGG  CGCCAAGAA  AGCCCTACAG  780
20     ACGCTGCGCG  GCTGGGACTC  TGTGGACAGG  GAGGTGGCCG  AGATCCGCA  GGAGGATGAG  840
      GCAGAGAAGG  CCGCGGGCTT  CATCTCCGTG  CTGAAGCTGT  TCCGATGCG  CTGCTGCGC  900
      TGGCAGCTGC  TGTCCATCAT  CGTCTCATG  GGCGGCCAGC  AGCTGTGGG  CGTCAACGCT  960
      ATCTACTACT  ACGCGGACCA  GATCTACCTG  AGCGCCGCG  TGCCGAGGGA  GCACGTGCAG  1020
      TACGTGACCT  CGCGACCGG  GGCCGTGAAC  GTGGTATGA  CCTTCTGCGC  CGTGTGCTG  1080
25     GTGAGCTCC  TGGGTCCGAG  GCTGCTGCTG  CTGCTGGGCT  TCTCCATCTG  CCTCATAGCC  1140
      TGCTGCGTGC  TCACTGCAGC  TCTGGCAGT  CAGGACACAG  TGTCTGGAT  GCCATACATC  1200
      AGCATGCTC  GTGTCATCTC  CTACGTGATA  GGACATGCC  TCGGCCCCAG  TCCCATACCC  1260
      GCGCTGCTCA  TCACTGAGAT  CTTCTGCGAG  TCCTCTGGG  CATCTGCCCT  CATGTTGGGG  1320
      GGCACTGTGC  ACTGCTCTC  CAACCTCAC  GTGGGCTGA  TCTTCCGCTT  CATCCAGGAG  1380
30     GGCTCGGCC  CGTACAGCTT  CATTGTCTTC  GCGGTGATCT  GCCTCCTCAC  CACCATCTAC  1440
      ATCTTCTTGA  TTGTCCCGGA  GACCAAGGCC  AAGACGTTC  TAGAGATCAA  CCAGATTTTC  1500
      ACCAAGTGA  ATAAGGTGCT  TGAAGTGATC  CCGGAAAAGG  AGGAAGTGA  AGAGCTTCCA  1560
      CCTGTCACTT  CGGAACAGTG  ACTCTGGAGA  GGAAGCCAGT  GGAGCTGGTC  TGCCAGGGGC  1620
      TTCCCACTTT  GGCTTATTTT  TCTGACTTCT  AGCTGTCTGT  GAATATCCAG  AAATAAAACA  1680
35     ACTCTGATGT  GGAATGCAGT  CCTCATCTCC  AGCCTCCCCA  CCCAGTGGG  AACTGTGCAA  1740
      AGGGCTGCCT  TGCTGTCTTT  GAAAGTGGGC  TGTCTCTCTC  CATGTTGGCC  TGTCAACAGA  1800
      CCGAGTCAA  TTAACAGCT  TTTGCTGGTT  CAGCCTTCGT  TGTGGCTCCTG  1860
      GTAAAGTGGC  TCCACCTTGA  TGGGTCAACC  TTTGTGTGGC  TCCTGGTAA  ATAACAACAA  1920
      CAGTTACTAT  AGTGGTGAGA  TGAAGGAAT  CAAATTTTGC  CAGAGAACT  AACTCGGTGG  1980
40     CCCCACAGG  TCTTCCGGGG  CCATGGGCAT  TTGTTAGAG  CCAAATTCAT  CCTCTTACCA  2040
      GATCCTTTTC  CAGAAATACC  TGTCTAGGAA  GGTGTGATGT  CAGAAACAT  GACATCCAGA  2100
      AAGCTGAGGA  ACAGGTTCTT  GTGGAGACAC  TGAGTCAGAA  TTCTTCATCC  AAATTATTTT  2160
      GTTAGTGAAA  AATGGAATTG  CTTCTGTGTA  GTCAATAAAA  TGAACCTGAT  CACTTTTC

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Seq ID NO: 308 Protein sequence
Protein Accession #: NP_003030.1

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50     1      11      21      31      41      51
      |      |      |      |      |      |
      MEQQDQSMKE  GRLTLVLALA  TLIAAFGSSP  QYGVNVAAVN  SPALLMQQFY  NETYYGRGTGE  60
      FMEFPLTLL  WSVTVSMFPF  GGFIGSLLVG  PLVNFKFRKG  ALLENNIFSI  VPAILMGCSR  120
      VATSFELIII  SRLLVGICAG  VSSNVVPMYL  GELAPKNLRG  ALGVVPLFI  TVGILVAQIF  180
      GLRNLILNVD  GWPILLGLTG  VPAALQLLLL  PFFPESPRYL  LIQKDEAAA  KKALQTLRGN  240
      DSVDREVAEI  RQDEAEKAA  GPISVLKLF  MRSLRQLLS  IIVLMGGQQL  SGVNAIYYVA  300
55     DQIYLSAGVP  EEHVQYVTAG  TGAVNVMTF  CAVFVVBLLG  RRLLLLLGFS  ICLIACCVLT  360
      AALALQDTS  WNPYISIVCV  ISYVIGHALG  PSPIPALLIT  EIFLQSSRPS  AFMVGGSVHM  420
      LSNFTVGLIF  PPIQEGLGYP  SFIVFAVICL  LTTIYIFLIV  PETKAKTFIE  INQIFTRMKN  480
      VSEVYPEKEE  LKELPFFTSE  Q

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Seq ID NO: 309 DNA sequence
Nucleic Acid Accession #: NM_001252.1
Coding sequence: 138..719

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65     1      11      21      31      41      51
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      GGCTGGTCCC  CTGACAGGTT  GAAGCAAGTA  GACGCCCCAG  AGCCCCGGA  GGGGGCTGCA  60
      GTTTCCTTCC  TTCTTCTCG  GCAGCGCTCC  GCGCCCCCAT  CGCCCCCTCT  GCGCTAGCGG  120
      AGGTGATGCG  CGCGGCGATG  CCGGAGGAGG  GTTCGGGCTG  CTGGTGCGG  CGCAGGCCCT  180
      ATGGGTGCGT  CCTGCGGGCT  GCTTTGGTCC  CATTGGTGC  GGGCTTGCTG  ATCTGCCTCG  240
      TGGTGTGCAT  CCGAGCGCTC  GCACAGGCTC  AGCAGCAGCT  GCGCTGAGG  TCACTTGGGT  300
      GGGACGTAGC  TGAGCTGCAG  CTGAATCACA  CAGGAACCTCA  GCAGGACCCC  AGGCTATACT  360
      GGCAGGGGGG  CCCAGCACTG  GGCGCTCCT  TCCTGCATGG  ACCAGAGCTG  GACAGGGGGC  420
      AGCTACGTAT  CCATCGTGAT  GGCATCTACA  TGGTACACAT  CCAGGTGACG  CTGGCCATCT  480
      GCTCTCCAC  GACGCGCTCC  AGGCACCACC  CCACCACCTT  GGCGTGGGA  ATCTGCTCTC  540
75     CCGCTCCCG  TAGCATCAGC  CTGCTGCGTC  TCAGCTTCCA  CCAAGGTTGT  ACCATTGCTT  600
      CCGAGCGCTC  GACGCGCTCG  GCCCGAGGGG  ACACACTCTG  CACCAACCTC  ACTGGGACAC  660
      TTTTGCCTTC  CCGAACAAC  GATGAGACCT  TCTTTGGAGT  GCAGTGGGTG  CGCCCTTGAC  720
      CACTGCTGCT  GATTAGGGTT  TTTTAAATTT  TATTTTATTT  TATTTAAGTT  CAAGAGAAAA  780
      AGGTACACA  CAGGGGCCAC  CCGGGGTGG  GGTGGGAGTG  TGGTGGGGG  TAGTGTGGGC  840
      AGGACAAGAG  AAGGCATTGA  GCTTTTCTT  TCATTTCTT  ATTAATAA

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Seq ID NO: 310 Protein sequence
Protein Accession #: NP_001243.1

1 11 21 31 41 51
 5 MPBEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL 60
 QLWHTGPQD PRLYWGGGA LGRSPLHGPE LDKGQLRIHR DGIYVHIQV TLAICSSTTA 120
 SRHHPITLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN 180
 TDETFPGVQW VRP

Seq ID NO: 311 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..3978

1 11 21 31 41 51
 15 ATGGTGGGTG AAGGACCTTA CCTTATCTCA GATCTGGACC AGCGAGGCGG GCGGAGATCC 60
 TTTCAGAAAA GATATGACCC CAGCCTGAAG ACCATGATCC CAGTGGGACC CTGTGCAAGG 120
 TTAGCACCAC ACCCGGTGGA TGATGCGGGG CTACTCTCCT TCGCCACATT TTCCTGGCTC 180
 ACGCCGGTGA TGGTGAAGAG CTACCGGCAA AGGCTGACCG TAGACACCCT GCCCCCATTTG 240
 TCGACATATG ACTCATCTGA CACCAATGCC AAAAGATTTC GAGTCTCTTG GGATGAAGAG 300
 GTAGCAAGGG TGGGTCTCTG GAAGGCCTCT CTGAGCCACG TGGTGTGGAA ATTCCAGAGG 360
 20 ACAGCGGTGT TGATGACAT CGTGGCCCAAC ATCCTGTGCA TCATCATGGC AGCCATAGGG 420
 CGACAGTTTC TCATTACCA AATCCTCCAG CAGACTGAGA GGACCTCTGG GAAAGTCTGG 480
 GTTGGCATTG GACTGTGACAT AGCCCTTTTT GCCACGAGT TTACCAAGT CTTCTTTTGG 540
 GCCCTTGGCT GGGCCATCAA CTACCGCAAG GCCATCGGCT TGAAGGTGGC GCTCTCCACC 600
 TTGGTTTTTG AAAACCTAGT GTCCCTCAAG ACATTGACCC ACATCTCTGT TGGCGAGGTG 660
 25 CTCAATATAC TGTCAAGTGA TAGCTATTCT TTGTTTGAAG CTGCTCTGTT TTGTCTTTTG 720
 CCAGCCACCA TCCCGATCCT AATGGTCTTT TGTGCGGCGT ACGCCTTTTT CATTCGGGG 780
 CCCACAGCTC TCATCGGGAT ATCAGTGTAT GTCATATTCA TACCGTGCCA GATGTTTATG 840
 GCCAAGCTCA ATTCACTTT CCGAAGGTCA GCAATTTTGG TGACAGACAA GCGAGTTTCA 900
 30 ACAAATGAAT AGTTTCTGAC CTGCATCAGG CTGATCAAAA TGTATGCTGT GGAGAAATCT 960
 TTTACCAACA CTATCCAAGA TATAAGAAGG AGGGAAGAA AATTACTGGA AAAAGCTGGA 1020
 TTTGTCCAAA GTGGAAGTCT TGCCCTGGCC CCCATCGTGT CCACCATAGC CATCGTGTCT 1080
 ACATTATCCCT GCCCATCTCT CCGTGAAGCG AAATCAACCG CACCGGTGGC ATTTAGTGTG 1140
 ATTGCCATGT TTAATGTAAAT GAAATTTTCC ATTGCAATCT TGCCCTTCTC CATCAAAAGCA 1200
 35 ATGGCTGAAG CGAATGTCTC TCTAAGGAGA ATGAAGAAAA TTCTCATAGA TAAAGCCCC 1260
 CCATCTTACA TCACCCAAAC AGAAGACCCA GATACTGTCT TGCTTTTAGC AAATGCCACC 1320
 TTGACATGGG AGCATGAAGC CAGCAGGAAA AGTACCCCAA AGAAATTGCA GAACCAGAAA 1380
 AGGCATTTAT GCAAGAAACA GAGGTGAGAG GCATACAGTG AGAGGAGTCC ACCAGCCAA 1440
 GGAGCCACTG GCCCAGAGGA GCAAAGTGAC AGCCTCAAAT CGGTCTGCA CAGCATAAGC 1500
 40 TTTGTGGTGA GAAATTTATC TCGTTATCCC GAAGCCACG TCCTGGCTTG GAGGTGGCCA 1560
 GCAGTGTGTT TGGGAGAAT CATCAGAGGA TACAGGCCTC ATGGATTTTC TGCTAAAGAC 1620
 AAGGATGAAT CTAGAAGGCT TCTTACTTGG CCCCAAGAAG TGGATAGGAC TCAAGGGGCA 1680
 GCCAAATATC TGGGGAAGAT CTGGGAATA TGTGGGAATG TGGGAAGTGG AAAGAGCTCC 1740
 CTCCTTGCAG CTCTCCTAGG ACAGATGCAG CTGCAGAAAG GGGTGGTGGC AGTCAATGGA 1800
 45 ACTTTGGCCT ACGTTTACAC GCAGGCATGG ATCTTTCATG GAAATGTGAG AGAAACACATA 1860
 CTCTTTGGAG AAAAGTATGA TCACCAAAGG TATCAGCACA CAGTCCGCTG CTGTGGCCTC 1920
 CAGAAGGACC TGAGCAACCT CCCCTATGGA GACCTGACTG AGATTGGGGA GCGGGGCTC 1980
 AACCTCTCTT GCGGGCAGAG GCAGAGGATT AGCCTGGGCC GCGCTGTCTA CTCGAGCTGT 2040
 CAGCTCTACC TGCTGGACGA CCCCTGTGCG GCCGTGGACG CCCACGTGGG GAAGCACGTC 2100
 50 TTTGAGGAGT GAAATTAAGA GACGCTCAGG GGAAGACAG TCGTCTGTGT GACCCACGAG 2160
 CTACAGTTCT TAGAGTCTTG TGATGAAGTT ATTTTATTAG AAGATGGAGA GATTGTGAA 2220
 AAGGGAACCC ACAAGGAGTT AATGAGGAG AGAGGGGCGT ATGCAAAACT GATTCAACAC 2280
 CTGCGAGGAT TGCAGTTCAA GGATCCTGAA CACCTTTACA ATGCAGCAAT GGTGGAAGCC 2340
 TTCAAGGAGA GCCCTGCTGA GAGAGAGGAA GATGCTGGTA TAATCGGTTA CCTCCTTTCT 2400
 55 CTCTTCACTG TGTCTCTCTT CCTCTGATG ATTGGCAGCG CTGCTTTCAG CAACTGGTGG 2460
 CTGGGTCTCT GGTGGACAA GGGCTCACGG ATGACCTGTG GGGCCACGG CAACAGGACC 2520
 ATGTGTGAGG TGGGCGCGGT GCTGGCAGAC ATCGGTGAGC ATGTGTACCA GTGGGTGTAC 2580
 ACTGCAAGCA TGGTGTTCAT GCTGGTGTAT GCGTCAACCA AAGGCTTCGT CTTCAACCA 2640
 60 ACCACACTGA TGGCATCTCT CTCTCTGATG GACACGCTGT TTGATAAGAT CTTAAAGAGC 2700
 CCAATGAGTT TCTTTGACAC GACTCCCACT GGCAGGCTAA TGAACCGTTT TTCCAAGGAT 2760
 ATGACAGAGC TGGATGTGAG GCTGCCGTTT CAGCAGAGAG ACTTTCTGCA GCAGTTTTTT 2820
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 65 GCCAGCCTTG CTGTAGGCTT CTTCAATCTG TTACGCAATT TCCACAGAGG AGTCCAGGAG 2940
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 70 TCGACCTGTG TTCCTGAAAT CACTCATCCC CTCAAAGTGG GGACCTGTCC CAAGGACTGG 3240
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 CTTGTTCTCG ACAGCCTGAA CTTGAACATA CAAAGTGGGC AGACAGTCCG GATTGTTGGA 3360
 75 AGAACAGGTT CCGGAAAGTC ATCGTTAGGA ATGGCTTTGT TTGCTCTGTT GGAGCCAGCC 3420
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Seq ID NO: 312 Protein sequence

Protein Accession #: Eos sequence

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 TRVLMDIVAN ILCIMAAIG PTVLIHQILQ QTERTSQKVN VOIGLCIALF ATEPTKVFPW 180
 ALANAINYRT AIRLKVALST LVPENLVSPK TLTHISVGEV LNILSSDSYS LFEAALFCPL 240
 PATIPILMVF CAAYAFPIIG PTALIGISVY VIFIPVQMFM AKLNSAFRRS AILVTDKRVQ 300
 10 TMNEFLTICR LIOMYAMEKS PTNTIQDIRR RERKLEKAG PVQSGNSALA PIVSTIAIVL 360
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 PSYITQPEDP DTULLLANAT LTWEHEASRK STPKKLQNKQ RELCKQRSE AYSESPPAK 480
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 15 NLSGGQRORI SLARAVYSDR QLYLLDDPLS AVDAHVGKHV FEBCIKKTLR GKTVVVLVTHQ 720
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 25 VQNTIKDAFK GCTVLTIAHR LNTVLNCDHV LVMENGKVIE FDKPEVLAEK PDSAFAMLLA 1320
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 Nucleic Acid Accession #: Z31560
 Coding sequence: 1-966

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Seq ID NO: 314 Protein sequence
 Protein Accession #: CAA83435

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 QLGYPOHPGL NARGAQMOP MERYDVSAIQ YNSMTSSQTY MNGSPITYSMS YSQQGTGMA 240
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Seq ID NO: 315 DNA sequence
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 Coding sequence: 29..541

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 75 TCCCTCTTGG AAGATGACTT TGCTAAATGT TTGAGTCTT GTAATAATT TGAACAGCCC 240
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 TCACAGCAGG GCTTTTCAAC ACTGGGAGTT AATCCAGGAA GATATTCTTG ATACTGGAAA 420
 TGACAAAAT GGAAGGAAAG AAGTCATAAA GAGAAAAATT CCTTATATTC TGAACGCGCA 480
 80 GCTGTATGAG AATAAACCCA GAAGACCTTA CATACTCAA AGAGATTCTT ACTATTACTG 540
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Seq ID NO: 316 Protein sequence
Protein Accession #: AAB50564

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LIQEDILDTG NDQNGKEEVI KRKIPYILKR QLYENKPRRP YILKRDSSYY

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Seq ID NO: 317 DNA sequence
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Coding sequence: 109..2940

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GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
ATTGCAATTA ATCTCAGGT ACCTGAGAAT CAGAACCTCA TCTCAACAT TAAGGAAATG 300
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ATTCATACCT TCGTGGGCAT TGCCAGTTTC GACAGCAAA GAGAGATCAG AGCCAGCTA 1200
CACCAATTA ACAGCAATGA TGATCGAAG TTGCTGTTT CATATCTGCC CACCACTGTA 1260
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Seq ID NO: 318 Protein sequence
Protein Accession #: NP_006527.1

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 KPFIYINGQV IKVTRCSSDI TGIFVCEKGP CPQENCIISK LPKEGCTFIY NSTQNTASI 240
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 15 AVPPATVEAF VERDSLHFPF FVMYIANVKQ GPYPILNATV TATVEPTGD PVTLLRLDDG 660
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Seq ID NO: 320 Protein sequence
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VQSPDGHRLY VTIPGLIKLQ VNTPLVGASL LRLAVKLDIT AEILAVRDKQ ERIHLVLGDC 180
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GACCCAGTCA CCTGTGATGT CCTCTATGGG CCGGACACCC CCATCATTTT CCCCCAGAC 1920
TGTCTTACC TTTGGGAGC GAACCTCAAC CTCTCTGCC ACTGGCCTC TAACCCATCC 1980
CCGCAATATT CTGGCGTAT CAATGGGATA CCGCAGCAAC ACACACAAGT TCTCTTATC 2040
GCCAAATAC GCGCAATAA TAAACGGGACC TATGCTCTGT TTGTCTCTAA CTGGCTACT 2100
GGCCGCAATA ATTCCATAGT CAAGAGCATC ACAGTCTCTG CATCTGGAAC TTCTCTGCT 2160
CTCTCAGCTG GCGCAGCTGT CGGCATCATG ATTGGAGTGC TGGTTGGGTG TGCTCTGATA 2220
TAGCAGCCCT GGTGTAGTTT CTTCATTTC GGAAGACTGA CAGTTGTTT GCTCTCTCT 2280
TAAAGCATTT GCAACAGCTA CAGTCTAAAA TTGCTTCTT ACCAAGGATA TTTACAGAAA 2340
AGACTCTGAC CAGAGATCGA GACCATCTTA GCCAACATCG TGAAACCCCA TCTCTACTAA 2400
AAATCAAAAA ATGAGCTGGG CTGTGGTGGC CGCACCTGTA GTCCAGTGA CTGGGAGGC 2460
TGAGGCAGGA GAATGCTTGG AACCCGGGAG GTGGAGATTG CAGTGAGCCC AGATGCGACC 2520
ACTGCATCTC AGTCTGGCAA CAGAGCAAGA CTCATCTCA AAAAGAAAG AAAAGAAAGAC 2580
TCTGACCTGT ACTCTTGAAT ACAAGTTTCT GATACCACTG CAGTGTCTGA GAATTTCCAA 2640
AACTTTAATG AACTAACTGA CAGCTTCTATG AAATGTCTCA CCAAGATCAA GCAGAGAAAA 2700
TAATTAATTT CATGGGACTA AATGAACATA TGAGGATTGC TGATTCTTTA AATGTCTTGT 2760
TTCCAGATT TCAGAAACT TTTTCTCTT TAAGCTATCC ACTCTACAG CAATTGATA 2820
AAATATACTT TTGTGAACAA AAATTGAGAC ATTTACATTT TCTCCCTATG TGGTGCCTCC 2880
AGACTTGGGA AACTATTCAT GAATATTAT ATTGTATGGT AATATAGTTA TTGCACAAAT 2940
TCAATAAAAA TCTGCTCTTT GTATAACAGA AAAA

Seq ID NO: 332 Protein sequence
Protein Accession #: NP_004354.1

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1 11 21 31 41 51
MESPSAPPHR WCIPWQRLLL TASLLTFWNP PTTAKLTIES TPFNVAEKGE VLLLVRNLPO 60
HLFGYSWYKG ERVDGNRQII GYVIGTQQAT PGPAYSGREI IYPNASLLIQ NIIQNDYGFY 120
TLHVHKSDLV NEEATQQPRV YPELKPSPIS SNNSKPVEDK DAVAFTEPEE TQDATYLNWV 180
NNQSLVSPFR LQLSNGNRTL TLFNVTRNDT ASYKCEQNP VSARRSDSVI LNVLYGPDAP 240
TISPLMTSYR SGENLNLSCA AASNPAPQYS WFNVTGTFQS TQELFIPNIT VNNSSGYTCQ 300
AHNSDTGLNR TTVTTITVYA EPPKPPITSN NSNPVEDEDA VALTCEPEIQ NITVLRWVNN 360
QSLPVSPLRQ LSNDRNLTL LSVTRNDVGP YECGIQNELS VDHSDFVILN VLYGPDDETI 420
SPSYTYFRFG VNLSSLCHAA SNPPAQYSWL IDGNIQHTQ ELFISNITEK NSGLYTCQAN 480
NSASGHSRRT VKTITVSAEL PKPSISSNNS KPVEDKDAVA FTCEPEAQNT TYLWVNVGQS 540
LPVSPRLQLS NGRNTLTLFN VTRNDARAYV CGIQNSVSAN RSDPVTLDVL YGPDPTIISP 600
PDSSYLSGAN LNLSSCHASN PSPQYSWRIN GIPQHTQVL FLAKITPNNN GTYACFVSNL 660
ATGRNNSIVK SITVSASGTS PGLSAGATVG IMIGVLVGVA LI

Seq ID NO: 333 DNA sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

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1 11 21 31 41 51
AATCCCGACA ATGGCGAAAG ACAACTCAAC TGTTCGTGTC TTCCAGGGCC TGCTGATTTT 60
TGGAAATGTG ATTATIGGTT GTTGGGCGAT TGCCCTGACT GCGAGTGCAC TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCCTGG ATCGGCATAT TTGTGGGCGT CTGCTCTTTC TGCCGTCTGT TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAAAT TCTCTGGCG TATTTCATTC TGATGTTTAT 300
AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACAG ACTTTTCAC 360
ACCCAACCTC TTCTGTAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAACAA 420
TGATGACCAG TGGAAAAACA ATGGAGTCAC CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GGGTAAATG GTCCATCAGA CTGGCAAAAA TACACATCTG CCTTCGGGAC 540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCTCTC AACCTGGAGG CTGTAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660
CTGCTATGAA CTGATCTCTG GTCCAAATGAA CCGACACGCC TGGGGGGTGG CCGTGTGGT 720
ATTGCCCATT TCTGCTGGA CTTTTGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA

Seq ID NO: 334 Protein sequence
Protein Accession #: NP_008883.1

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1 11 21 31 41 51
MAKINSTVRC FQGLLIFGNV IIGCCGIALT AECIPFVSDQ HSLYPLEAT DNDDIYGAAW 60
IGIFVIGICLF CLSVLGIIVGI MKSSRRKILLA YPILMPIVYA FEVASCITAA TORDFFTPNL 120
FLKQMLERYQ NNSFPNNDQ WKXNGVTKTW DRLMLQDNCC GVNGPSDNQK YTSAPRTENN 180
DADYWPFRQC CVMNNIKEPL NLEACKLGVF GPYHNQGCYE LISGPMNRHA WGVAWFGPAI 240
LCATFWVLIG TMFYWSRIEY

10
Seq ID NO: 335 DNA sequence
Nucleic Acid Accession #: NM_002638.1
Coding sequence: 120..473

15 1 11 21 31 41 51
CAATACAGCT AAGGAATTAT CCCTTGTAAT TACCACAGAC CGCCCTGGA GCCAGGCCAA 60
GCTGGACTGC ATAAAGATTG GTATGGCCTT AGCTCTTAGC CAAACACCTT CCTGACACCA 120
TGAGGGCCAG CAGCTTCTTG ATCGTGGTGG TGTTCTTCAT CGCTGGGACG CTGGTCTAG 180
AGGCAGCTGT CACGGAGATT CCTGTTAAAG GTCAAGACAC TGTCAAAGGC CGTGTTCAT 240
20 TCAATGGACA AGATCCCGTT AAAGGACAAG TTTCAGTTAA AGGTCAAGAT AAAGTCAAAG 300
CGCAAGAGCC AGTCAAGAGT CCAGTCTCCA CTAAGCCTGG CTCCTGCCCC ATTATCTTGA 360
TCCGGTGCAG CATGTTGAAT CCCCCTAACC GCTGCTTGAA AGATACTGAC TGCCGAGGAA 420
TCAAGAAGTG CTGTGAAGGC TCTTGCGGGA TGGCCTGTTT CGTTCCCCAG TGAAGGGAGC 480
CGTCCCTTGC TGCACCTGTG CCGTCCCCAG AGCTACAGGC CCCATCTGGT CCTAAGTCCC 540
25 TGCTGCCCTT CCCCTTCCCA CACTGTCCAT TCTTCTCCCC ATTCAAGATG CCCACGGCTG 600
GAGCTGCCTC TCTCATCCAC TTTCCAATAA A

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Seq ID NO: 336 Protein sequence
Protein Accession #: NP_002629.1

35 1 11 21 31 41 51
MRASSFLIVV VFLIAGTLVL EAAVTGVFVK QDQTVKGRVP FNGQDPVKQ VSVKQDKVK 60
AQEPVKGFPV TKPGSCPIIL IRCAMLNPPN RCLKQTDPCF IKKCCBSCG MACFPVQ

40
Seq ID NO: 337 DNA sequence
Nucleic Acid Accession #: NM_001793.2
Coding sequence: 71..2560

45 1 11 21 31 41 51
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGCCCGTGC GGCAGCTGCT TCACCCCCTCT 60
CTCTGCAGCC ATGGGGCTCC CTCTGGGACC TCTCGCGTCT CTCTCCCTTC TCCAGGTTTG 120
CTGGCTGCAG TGGCGGGCCT CCGAGCCGTG CCGGGGGGTC TTCAGGGAGG CTGAAGTGAC 180
45 CTTGAGGCGG GGAGGCGGGG AGCAGGAGCC CGGCCAGGGG CTGGGGAAGG TATTCATGGG 240
CTGCCCTGGG CAGAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCAGAGCA GTCCAGGAAA GAAGGTCACT GAAGGAAAAG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
50 TGAANAATGC AAGGTCCTCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCCC CTGAGGGTGT 540
CTTGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTACAGG AATGGTGCCCT CAGTGGAGGA 660
CCCATGAAAC ATCTCCATCA TGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
55 GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTTCTG TGAATGAGGT 780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
CCATAGCCAA GAACCAAGAG ACCCACACGA CCTCATGTTT ACCATTCAAC GGAGCACAGG 900
CACATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAGAA GTCCCTGAGT ACACTAGAC 960
CATCCAGGCC ACAGACATGG ATGGGAGCGG CTCACCAACC ACGGCAGTGG CAGTAGTGA 1020
60 GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
GCCTGAGAAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
CAACTCACC ACGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
TACCATCACC ACCACCCCTG AGAGCAACCA GGGCATCTGT ACAACGAGGA AGGGTTTGA 1260
65 TTTTAGGGCC AAAAACGAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGAGGATG TGAATGAGGC 1380
ACCTGTGTTT GTCCACCCCT CCAAGTCTGT TGAAGTCCAG GAGGGCATCC CCACTGGGGA 1440
GCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAGA TCAGTACCG 1500
CATCTTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
TGTGGGCACC CTGACCGGTG AGGATGAGCA GTTTGTGAGG AACACATCT ATGAATCAT 1620
70 GGTCTTGGCC ATGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680
ACTGATTGAT GTCAATGACC ATGGCCAGT COCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGGGCCAGG TGCTGAACAT CACGGAACAG GACCTGTCTC CCCACACCTC 1800
CCCTTCCAG GCCACGCTCA CAGATGACTC AGACATCTAC TGGAGGGCAG AGGTCAAAGA 1860
GGAAGGTGAC ACAGTGTCTT TGTCCCTGAA GAAGTCTCTG AAGCAGGATA CATATGACGT 1920
75 GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
GTGCGACTGC CATGGCCATG TGGAAACCTG CCTTGGACCC TGGAAAGGAG GTTTCATCCT 2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTGTC TTTTGTGGT 2100
GAGAAAGAG CGGAAGATCA AGGAGCCCTT CTAATCTCCA GAAGATGACA CCGTGAACA 2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
80 GCTCCACCGA GGTCTGGAGG CCAGGCCCGA GGTGGTTCTC CGCAATGAGG TGGACCAAC 2280
CATCATCCCG ACACCATGTG ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCAAC GCCCGCCCTC ACACACCCCT 2400
CTGGTGTTCT GACTATGAGG GCAGCGGCTC OGACGCGCGG TCCTGAGCTC CCTCACTC 2460
CTCCGCTCTC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCGCTTCAA 2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GACGACTAG GCGGCTGCC TGCAGGGCTG 2580

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GGGACCAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
GACTTCGGAG CTGTGCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCCTCAG AGGCCAAGTT TCCAGAAAGCC 2820
TCTTACCTCG CGTAAATATG TCAACCTGT GTCTGGGCC TGGGCTGTCT GTGACTGACC 2880
TACAGTGGAC TTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
TTTTTTTAAAT GCTATCTTCA AAACGTTAGA GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCCGTCC TGCAATTCTG GTTTCAGAC CCCAATGCCT CCCATTGCGA 3060
TGGATCTCTG CGTTTATATA CTGAGTGTGC CTAGGTTGCC CTTATTTTT TATTTTCCT 3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAAACT TTCCAGAA AAAAA

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Seq ID NO: 338 Protein sequence
Protein Accession #: NP_001784.2

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1 11 21 31 41 51
MGLPRGPLAS LLLQLQCNLQ CAASEPCRAV PREAEVTLEA GGAEQEPGQA LGKVPMGCPG 60
QEPALPSTDN DDPTVRNGST VQERRSLKER NFLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPPFPRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREBIK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTP RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAVSIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TDMGDSGTT TAVAVSEILD ANDNAPMFDQ QKYEAFVFN AVGHVQRLT VTDLDPNSP 360
AWRATYLIMG GDDGDHPTIT THPESNQIIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
DPAGWLAMPD DSGQVTAAGT LDREDEQFVR NNIEVMVLA MDNGSPPTTG TGTLTLTLID 540
VNDHGPVPEP RQITICNPSQ VRQVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDQ HGHVETCPGP WKGSPILPVL 660
GAVLALLFL LVLVLLVRKK RKIKEPLLLP EDDTRDNVEY YGEGGGEED QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVP 780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKLA DMYGGGEDD

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Seq ID NO: 339 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

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1 11 21 31 41 51
ATGAGGCTCC AAAGACCCCG ACAGGCCCGG CGGGGTGGGA GGCGCGCGCC CCGGGGCGGG 60
CGGGGCTCCC CTACCCGCGC AGACCCGCGG AGAGGCGCGC GGAGGCTCGC AAGGTTCCAG 120
AAGGGCGGGG AGGGGCGGCC GCGCGCTGAC CCTCCCTGGG CACCGCTGGG GAGCATGGCG 180
CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
GCGAGACAA CAGATCCAGA GGAATCCAG CAAACGAGAC AGGCTGACAA TAGAGTGTGG 300
TGTCATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAATGG 360
ACAGAGCCAT ACTGCTTAT AGCGGCGGTG AAAATATTTC CACGTTTTTT CATGGTTCGG 420
AAGCAGTGCT CGCTGCTGTG TGCAGCATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
CTCTGGGAAG AGCCCATGSC CTTCTTTTAC CTCAAGTGT GTAAAAATCG CTACTGCAAT 540
TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAGAAT ATGCTGGGAG CATGGGTGAG 600
AGCTGTGGTG GGCTGTGGCT GGCCATCTTC CTGCTGCTGG CCTCCATTGC AGCCGCGCTC 660
AGCTGTCTT GA

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Seq ID NO: 340 Protein sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
MRLQRPRQAP AGGRRAPRGG RGSFYRPDPQ RGARRLRRFQ KGGGAPRAD PFWAPLGTMA 60
LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVN CHVCERENTP EQCNPRRCKW 120
TEPYCVIAAV KIFPRFFMVA KQCSAGCAAM ERPKEEKRFP LLEBPMPPFY LKCKIRYCN 180
LEGPPINSSV FKEYAGSMGE SCGGLMLAIL LLLASIAAGL SLS

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Seq ID NO: 341 DNA sequence
Nucleic Acid Accession #: XM_035292.2
Coding sequence: 53..1576

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1 11 21 31 41 51
GCTCGCTGGG CCGCGGCTCC CGGGTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGCGGCC GAGGAGAAAG AAGAGGCGCG 120
GGAGAAGATG CTGGCGGCCA AGAGCGCGGA CGGCTCGCG CCGGCAGGCG AGGGCGAGGG 180
CGTGACCCCTG CAGCGGAACA TCAAGCTGCT CAAAGCGCTG GCCATCATCG TGGGGACCAT 240
TATCGGCTCG GGCATCTTGG TGAAGCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCGGG 300
GCTGGCGCTG GTGGTGTGGG CGCGTGTGCG GTCTCTTCTC ATCGTGGGCG CGCTCTGCTA 360
CGCGAGCTCG GGCACCAACA TCTCCTCAAT GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420
CTAAGGCTCG CTGCGCGCCT TCTCCTCAAG CTGATCGAG CTGCTCATCA TCGGCCTTTC 480
ATCGCAGTAC ATCGTGGGCC TGGTCTTCTG CACCTACCTG CTCAAGCGCG TCTTCCCCAC 540
CTGCGCGCTG CCGGAGGAGG CAGCCAAGCT CGTGGCCTGC CTCTGCGTGC TGCTGCTCAC 600
GGCGGTGAAC TGCTACAGCG TGAAGGCGCG CACCGCGGTC CAGGATGCCT TTGCGCGCGC 660
CAAGCTCCTG GCCCTGGCCC TGATCATCCT GCTGGGCTTC GTCCAGATCG GAAAGGCTGA 720
TGTGTCCAAT CTAGATCCCA ACTTCTCATT TGAAGGCACC AAACCTGGATG TGGGGAACAT 780
TGTGCTGGCA TTATACAGCG GCTCTTTTGC CTATGAGGGA TGGAAATTA TGAATTTCTG 840
CACAGAGGAA ATGATCAACC CCTACAGAAA CCGCGCCCTG GCCATCATCA TCTCCCTGCG 900
CATCGTGACG CTGGTGTACG TGCTGACCAA CCGGCGCTAC TTCACACACC TGTCACCGGA 960
GCAGATGCTG TGTGCGAGG CCGTGGCGGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020

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GTCTGGATC ATCCCGGTCT TGGTGGGCTT GTCTGCTTC GGCTCCGTCA ATGGGTCCCT 1080
GTTCCATATC TCCAGGCTCT TCTTCGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
CTCCATGATC CACCACAGC TCTCACCCTC CGTCCGTCC CTGTGTGATC CGTGTGTGAT 1200
GACGCTGCTC TACGCTTCT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
CAACTGGCTC TGGTGGGCTC TGGCCATCAT CGGCATGATC TGGCTGGGCTC ACAGAAAGCC 1320
TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCCTGCCT GTGTCTTCA TCCTGGGCTG 1380
CCTCTCTCTG ATCCCGGTCT CCTTCTGGAA GACACCGCTG GAGTGTGGCA TCGGCTTCAC 1440
CATCATCTCT AGCGGGCTGC CCGTCTACTT CTTCGGGGTC TGGTGGAAAA ACAAGCCCAA 1500
GTGGCTCTCT CAGGGCATCT TCTCCACGAC CGTCTGTGT CAGAAGCTCA TGCAGGTGTT 1560
CCCCAGGAG ACATAGCCAG GAGGCGGAGT GGCTGCCGA GGAGCATGC

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Seq ID NO: 342 Protein sequence
Protein Accession #: XP_035292.2

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1 11 21 31 41 51
MAGAGPKRRA LAAPAAEKEE EAREKMLAAK SADGSAPAGE GSGVTLQRNI TLLNGVAIIV 60
GTIIGSGIFV TPTGVLKEAG SPGLALVVAW ACGVPSIVGA LCYAELOTTI SKSGGDYAYM 120
LEVYGSIPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPBEA AKLVACLCLV 180
LLTAVNCYSV KAATRVQDAF AAAKLALAL ILLGFVQIG KGDVSNLDPN PSFEGTKLDV 240
GNIVLALYSG LPAYCGWNYL NFVTEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
STEQMLSEEA VAVDFGNVHL GVMSWIIIPV VGLSCFGSVN GSLFTSSRLF FVGSREGLHP 360
SILSMIHQPL LTPVPVSLVPT CVMTLIYAFS KDIPSVINFF SFENWLCVAL AIGMINLHRH 420
RKPELRPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GPTIILSGLP VYFFGVWWMK 480
KPKWLQGIIF STTLCQKLM QVVPQET

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Seq ID NO: 343 DNA sequence
Nucleic Acid Accession #: NM_005268.1
Coding sequence: 168..989

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1 11 21 31 41 51
TAAAAAGCAA AAGAATTGCG GGCCGGCTCG ACACGGGCTT CCCCAGAAAC CTTCCTCCGCT 60
TCTGGATATG AAATTCACAG TGCTTGCTGA GTCTTATTGC CGGCTGCTGG GAGCCAGGAG 120
AGCCCTGAGG AGTAGTCACT CAGTAGCAGC TGACGGGTGG GTCCACCATG AACTGGAGTA 180
CTTTTACGCG ACTCTGAGT GGGGTCAACA AGTACTCCAC AGCCTTTGGG CGCATCTGGC 240
TGTCTCTGGT CTTCATCTTC CGGTGCTGG TGTACCTGGT GACGCGCGAG CGTGTGTGGA 300
GTGATGACCA CAGGACTTTC GACTGCAATA CTGCCAGCC CGGCTGCTCC AACGTCTGCT 360
TTGATGAGTT CTTCCTCTGT TCCCATGTGC GCCTCTGGGC CCTGCAGCTT ATCCTGGTGA 420
CATGCCCTCT ACTGCTCTGT GTCATGCACG TGGCCTACCG GGAGGTTTCA GAGAAGAGGC 480
ACCGAGAAGC CCATGGGGAG AACAGTGGGC GCCTCTACCT GAACCCCGGC AAGAAGCGGG 540
GTGGGCTCTG GTGGACATAT GTCTGCAGCC TAGTGTTCAA GGCGAGCGTG GACATCGCCT 600
TTCTCTATGT GTTCCACTCA TTCTACCCCA AATATATCCT CCTCTCTGTG GTCAAGTGCC 660
ACGAGATGCC ATGTCCCAAT ATAGTGGACT GCTTCATCTC CAAGCCCTCA GAGAAGAAC 720
TTTTCACCTC CTTCATGGTG GCCACAGCTG CCATCTGCAT CCTGCTCAAC CTGTGGAGG 780
TCATCTACCT GGTGAGCAAG AGATGCCACG AGTGCTGGC AGCAAGGAAA GCTCAAGCCA 840
TGTGCACAGG TCATCACCCC CACGGTACCA CCTCTCTCTG CAAACAAGAC GACCTCCTTT 900
CGGGTGACCT CATCTTTCTG GGCTCAGACA GTCATCTCTC TCTCTTACCA GACCGCCCCC 960
GAGACCATGT GAAGAAAACC ATCTTGTGAG GGGCTGCTGG GACTGGTCTG GCAGGTTGGG 1020
CCTGGATGGG GAGGCTCTAG CATCTCTCAT AGGTGCAACC TGAGAGTGGG GGAGCTAAGC 1080
CATGAGGTAG GGCAGGCAAG GAGAGAGGAT TCAGACGCTC TGGGAGCCAG TTCCTAGTCC 1140
TCACTCCAGC CCACCTGCCC CAGCTCGACG GCACTGGGCC AGTTCCTCCCT CTGCTCTGCA 1200
GCTCGGTTTC CTTTCTAGA ATGGAATAG TGAGGGCCAA TGC

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Seq ID NO: 344 Protein sequence
Protein Accession #: NP_005259.1

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1 11 21 31 41 51
MNWSIFEGLL SGVNKYSTAF GRIWLSLVFI FRVLVYLVT A ERVWSDHDKD FDCNTRQPGC 60
SNVCFDEFPP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKREERBAH ENSGRLYLNP 120
GKKRGGWLWT YVCSLVFKAS VDIAPLYVPH SPYPKYILPP VVKCHADPCP NIVDCPISKP 180
SEKNIPTLFM VATAAICILL NLVELIYLVH KRCHECLEAAR KAQAMCTGHE PHGTTSSCKQ 240
DILLSGDLIF LGSDSHPPLL PDRPRDHVKK TIL

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Seq ID NO: 345 DNA sequence
Nucleic Acid Accession #: NM_002391.1
Coding sequence: 26..457

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1 11 21 31 41 51
CGGGCGAAGC AGCGCGGGCA GCGAGATGCA GCACCGAGGC TTCTCTCTCTC TCACCTCTCT 60
CGCCTGCTGT GCGCTCACCT CGCGGTGCTG CAAAAAGAAA GATAAGGTGA AGAAGGGCGG 120
CCCGGGGAGC GAGTGGGCTG AGTGGGCTGC GGGGCGCTGC ACCCCAGCA GCAAGGATTG 180
CGGCGTGGGT TTCCGCGAGG GCACCTGCGG GGCCAGAGCC CAGCGCATCC GGTGCAAGGT 240
GCCCTGCAAC TGGAGAGAGG AGTTTGGAGC GCACTGCAAG TACAAGTTTG AGAAGTGGG 300
TGCGTGTGAT GGGGGCACAG GCACCAAGT CCGCAAGGC ACCCTGAAGA AGCGCGCTA 360
CAATGTCTAG TGCCAGGAGA CCATCCGCT CACCAAGCCC TGACCCCTCA AGACCAAGC 420
AAAGGCCAAA GCCAGAAAAG GGAAGGGAAA GCACTAGACG CCAAGCCTGG ATGCCAAGA 480
GCCCTGGTGT TCACATGGGG CCTGGCCACG CCTCTCTCTC CCGAGGCGCG AGATGTGACC 540
CACCAGTGGC TTCTGTCTGC TGGTTAGCTT TAATCAATCA TGCCCTGCTC TGTCTCTCTC 600
ACTCCCGAGC CCCACCCCTA AGTGCCCAA GTGGGAGGG ACAAGGATT TTGGGAAGCT 660
TGAGCCTCCC CCAAGCAAT GTGAGTCCCA GAGCCCGCTT TTGTCTTCC CCACATTC 720
ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAGC TCTTCTTTT 780

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TAATAT

Seq ID NO: 346 Protein sequence
 Protein Accession #: NP_002382.1

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1      11      21      31      41      51
|      |      |      |      |      |
MQHRGFLLLT LLALLALISA VAKKKDKVKK GPGSECAEW AMGPCTPSSK DCGVGFREGT 60
CGAQTQRIKC RVPCNWKKEF GADCKYKPEW WGACDGGTGT KVRQSTLKKK RYNAQCQETI 120
RVTKPCTPPT KAKAKAKKGG GKD

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Seq ID NO: 347 DNA sequence
 Nucleic Acid Accession #: NM_006783.1
 Coding sequence: 1..786

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGATTGGG GGACGCTGCA CACTTTCATC GGCGGTGTCA ACAACACTC CACCAGCATC 60
GGGAAGGTGT GGATCACAGT CATCTTTATT TTCGAGTCA TGATCCTAGT GGTGGCTGCC 120
CAGGAAGTGT GGGGTGACGA GCAAGAGGAC TTGCTGTGCA ACACACTGCA ACCGGGATGC 180
AAAAATGTGT GCTATGACCA CTTTTCCTCC GTGTCCACA TCCGCTGTG GGCCCTCCAG 240
CTGATCTTCT TCTCCACCCC AGCGCTGCTG GTGGCCATGC ATGTGGCCTA CTACAGGCAC 300
GAAACCACTC GCAAGTTCAG GCGAGGAGAG AAGAGGAATG ATTCAAAGA CATAGAGGAC 360
ATTAAAAAGC ACAAGTTTCC GATAGAGGGG TCGCTGTGGT GGACGTACAC CAGCAGATC 420
TTTTTCGAA TCATCTTTGA AGCAGCCTTT ATGTATGTGT TTTACTTCTT TTAACAATGGG 480
TACCACCTGT CTTGGGTGTT GAAATGTGGG ATTGACCCCT GCCCAACCT TGTGACTGTC 540
TTTATTCTTA GGCCACAGA GAAGACCGTG TTTACCATTT TTATGATTC TGCCTCTGTG 600
ATTTCATGTC TGCTTAACGT GGCAGAGTTG TGCTACCTGC TGCTGAAAGT GTGTTTATGG 660
AGATCAAAAG GAGCACAGAG GCAAAAAAAT CACCCCAATC ATGCCCTAAA GGAGAGTAAG 720
CAGAAAGAAA TGAATGAGCT GATTTCAGAT AGTGGTCAAA ATGCAATCAC AGGTTTCCCA 780
AGCTAA

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Seq ID NO: 348 Protein sequence
 Protein Accession #: NP_006774.1

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1      11      21      31      41      51
|      |      |      |      |      |
MDWGLHTFI GGVNKHSTSI GKWITVIPI FRVMILVVA QEVWGEDEQED FVCNTLQPGC 60
KNVCYDHFFP VSHIRLWALQ LIFVSTPALL VAMHVAYYRH ETTRKFRGGE KRNDFKDIED 120
IKKHVRIGES SLWWTYTSSI FFRIFPEAAP MYVFYFLYNG YHLPWVLKCG IDPCPNLVDC 180
FISRPTEKTV FTIFMISASV ICMLLNVAEL CYLLLVKVCPR RSKRAQTQKN HPNHALKBSK 240
QNMENELISD SQQNAITGFP S

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Seq ID NO: 349 DNA sequence
 Nucleic Acid Accession #: NM_002571.1
 Coding sequence: 99..587

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1      11      21      31      41      51
|      |      |      |      |      |
CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCTGGG CBTGGCCCTG GTCTGTGGTG TCCCGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGGACA CTGAAGGCCC CTCGTAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCGGA GGACAACTCG GAGATCGTTC TGACAGATG GGAGAAACAC AGCTGTGTTG 300
AGAAGAAGGT CCTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGGAAGCGA GGCCACGCTG CTGATACTG ACTACGACAA TTTCTGTTT CTCTGCTAC 420
AGGACACCAC CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGTGTGG 480
AGGACGATGA GATCATGCAG GATTCATCA GGGCTTTCAG GCCCTGCCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCTT 600
CCAGGAAGAC CAGACTCCCA CCTTCCACA CCTCCAGAGC AGTGGGACTT CCTCTGCCCC 660
TTTCAAGAAA TAACACAGC TCAGAAGACG ATGACGTGGT CATCTGTGTC GCCATCCCCT 720
TCCTGCTGCA CACCTGCACC ATTGCCATGG GGAGGCTGCT CCTTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAACC CTTGAGCAT G

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Seq ID NO: 350 Protein sequence
 Protein Accession #: NP_002562.1

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1      11      21      31      41      51
|      |      |      |      |      |
MDIPQTKQDL BLPKLAGTWH SMAMATNNIS LMATLKAPLR VHITSLLPTP EDNLEIVLHR 60
WENNSCVEKK VLGETGNPK KFKINYTVAN EATLLDIDYD NFLFLCLQDT TPIQSMQCQ 120
YLARVLVEDD EIMQGFIRAF RPLPRHLWYL LDLQKMEEPK RF

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Seq ID NO: 351 DNA sequence
 Nucleic Acid Accession #: NM_006500.1
 Coding sequence: 27..1967

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1      11      21      31      41      51
|      |      |      |      |      |
ACTTGCTCTT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
TCGCGGCTGT CTGCTGCTGT CCTCGGCTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG 120
CGCTTGAAGT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
AGTCCCAAGG CAACCTCAGC CATGTGCACT GGTTTTCTGT CCACAAGGAG AAGCGGAGCG 240
TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300

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TCTACAAAGC TCCGAGGAGG CCAAAATATCC AGGTCAACCC CCTGGGCATC CCTGTGAACA 480
GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCTCAAG 540
TCATCTGGTA CAAGAATGGC CGGCCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCACT 600
CGTCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
TGGTTAAAGA AGACAAGAT GCCAGTTTT ACTGTGAGCT CAACTACCGG CTGCCAGTG 720
GGAAACACAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTTCTACCGG ACAGAAAAG 780
TGTGGCTCGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840
GTTTGGCTGA TGGCAACCTT CCACCACTCT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900
GGGAGGACAG GAAGAGGACA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CCTGCCCGGA 960
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TGAGTGAACC ACAGGAACCTA CTGGTGAATC ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080
CCCTGAGAG ACAGGAAGGC AGCAGCCTCA CCTGTACCTG TGAGGCAGAG AGTAGCCAGG 1140
ACCTCGAGT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAGG GGGCCTGTGC 1200
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GCTCAGGAAA GCAGGAGATC ACGCTGCCCC CGTCTCGTAA GACCGAAGCT GTAGTTGAAG 1860
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GGGCTCCGGG AGACCAAGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT 1980
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TCCCGGTGTT CACTGTCTCC CATAGCCCTC TTGATGGATC ACCTAAAACT GAAAGGCAGC 3000
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CTGTGTGAT CATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTGCAAA 3240
TTGTTTCCTT TATATATATA TGTATATATA TATATGAAAA TATGAAAAAT 3300
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AACCTGGGGG CCTGTGAAGC TACAACCAA AGGCACACAA AACCTTTCC AGTGTGCAGC 3420
AGAGATCAGG GGTATCCTCT GCTTCTGAGC AATAGGCTCA AGCTCTACCA GAGCAGACAG 3480
CTACCTACTT TTTACAGAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC 3540
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Seq ID NO: 352 Protein sequence
Protein Accession #: NP_006491.1

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1 11 21 31 41 51
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WFSVHEKEKRT LIPRVQGGQ QSRPGEYZQR LSLQDRGATL ALTQVTPQDE RIFLCQKGRP 120
RSQRYRIQLR VYKAPEEPNI QVNPLGIPVN SKEPEEVATC VGRNGYPIQ VIWYKNGRPL 180
KEEKNRVHIQ SSQTVESSGL YTLQSILKAQ LVKEDKDAQF YCBLYRLPS GNHMKESREV 240
TVPVFYPTKE VNLVEFVPM LKEGDREVEIR CLADGNPPPH FSIKQNPST REAEETND 300
NGVLVLEPAR KEHSGRYEQ AWWLDTMISL LSEPQELLVN YSDVRVSPA APERQEGSSL 360
TLTCEABSSQ DLEFQWLRZ TDQVLERGPV LQLHDLKREA GGGYRCVASV PSIPGLNRTQ 420
LVKLAIFGPP WMAFKERKVN VKENMVLNLS CEASGHPRPT ISWNVNGTAS EQDQDPQRLV 480
STLVNIVTPE LLETGVECTA SNDLGKNTSI LFLVLNLT LTPTDNTTGT LSTSTASPH 540
RANSTYTERK LPPEPESRGV IVAVIVCILV LAVLGAVLYP LYKKGKLPFR RSGKQIEITLP 600
PSRTELVEVE VKSDKLPEEM GLQGSAGDK RAPGDQGEKY IDLRH

Seq ID NO: 353 DNA sequence
Nucleic Acid Accession #: NM_003183.3
Coding sequence: 165..2639

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1 11 21 31 41 51
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CGAAGGCTGC CCAGAGAGGT GGAGTGGGTA GCGGGGCGGG GAACATGAGG CAGTCTCTCC 180
TATTCTGTAC CAGCGTGGTT CCTTCTGTGC TGGGCGCGCG ACCTCCGGAT GACCCGGGCT 240
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5 CTTTATCTAA TATCCAGCAG CATTCCGGTAA GAAAAAGAGA TCTACAGACT TCAACACATG 360
 TAGAAACACT ACTAATTTTT TCAGCTTTTGA AAAGGCATT TAAATTATAC CTGACATCAA 420
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 AATATAACAT AGAGCCACTT TGGAGATTG TTAATGATAC CAAAGACAAA AGAATGTTAG 660
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 ATTTAAAGT GGATAATGAA GAGTTGCTCC CAAAAGGGTT AGTAGACAGA GAACCACTG 780
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 10 AATTATTGGT GGTACAGAT CATCGCTTCT ACAGATACAT GGGCAGAGGG GAAGAGAGTA 900
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 15 ATGAAGAAA GGAATGCTGG GATGTGAAGA TGTGCTAGA GCAATTTAGC TTTGATATAG 1140
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 20 ATGAGGACCA GGGAGGGAAA TATGTCATGT ATCCCATAGC TGTGAGTGGC GATCAGGAGA 1500
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 25 GCACGTTGAA GGAAGGTGTC CAGTGCAGTG ACAGGAACAG TCCCTGTCTG AAAAAGCTGT 1740
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 55 CGCCACTACA CTCAGCCTG GGTGACAGAG TGAGATCTGC CTC

Seq ID NO: 354 Protein sequence
 Protein Accession #: NP_003174.2

60 1 11 21 31 41 51
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 QTSHTVELL TFSALKRHF LYLTSSTERF SQNFVIVVD GKNESEYTA WQDPFTGHV 120
 GEPDSRVLAH IRDDVIRI NTDGAENIE PLWRFVNDTK DKRMLVYKE DIKNVRLQS 180
 PKVGYLKV NELLPKGLV DREPPEELVH RVKRRADPD MONTCKLLV ADHRFPYR 240
 65 RGEESTTNY LIELIDRVDD IYRNTSWDNA GEKGYGQIE QIRILKSPQE VRPGKHYNM 300
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 Coding sequence: 164..2248

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Seq ID NO: 356 Protein sequence
Protein Accession #: NP_068604.1

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Protein Accession #: NP_004985.1

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45	FDGKDLLLAH	AFPPGPGIQQ	DAHFDDELW	SLGKGVVPT	RFGNADGAAC	HPPFPEGRS	240
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	ACTTDGRSDG	YRWCAATTANY	DRDKLPGFCP	TRADSTVMGG	NSAGELCVFP	FTPLGKEYST	360
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GGCCTGTAT CCAGTTCCT TGGGAGGCTG AGCGGGGAGA ATTGCTTGAA CCGGGGAGC 780
GAGGTGCGA TGAACCGAGA TCGCACTGCT GTACCCAGCC TGGGCCACAG TGCAAGACTC 840
CATCTCAAAA AAAAAAAGC AAAAAAAGC CTGTTTAATG CACAGGTGTG AGTGGATTGC 900
TTATGGCTAT GAGATAGGTT GATCTCGCCC TTACCCCGGG GTCTGGTGTG TGCTGTGCTT 960
TCCTCAGCAG TATGGCTCTG ACATCTCTTA GATGTCCCAA CTTGAGCTGT TGGAGATGG 1020
TGATATTTTC AACCTACTT CCTAAACATC TGTCTGGGTG TCCTTTAGTC TTGAATGTCT 1080
TATGCTCAAT TATTGTGTTG TGAGCCTCTC TTCCACAAGA GCTCCTCCAT GTTGTGATAG 1140
CAGTTGAAGA GGTGTGTGTT GTGGGCTGTT GGGAGTGAGG ATGGAGTGT CAGTGCCCAT 1200
TTCCTATTTT ACATTTTAAA GTCGTTCTTC CAACATAGTG TGTATTGGTC TGAAGGGGTT 1260
GGTGGGATGC CAAAGCCTGC TCAGTTATG GACATTGTGG CCACCATGTG GCTTAAATGA 1320
TTTTTCTTAA CTAATAAAGT GGAATATATA TTTCAAAAAA AAAAAAAAAA AA

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Seq ID NO: 362 Protein sequence
Protein Accession #: NP_037464.1

60

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1 11 21 31 41 51
MKHVLNLYLL GVVLTLISIF VRVMESLEGL LESPSPTSW TTRSQLANTE PTKGLPDHPS 60
RSM

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Seq ID NO: 363 DNA sequence
Nucleic Acid Accession #: NM_023915.1
Coding sequence: 250..1326

70
75
80

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1 11 21 31 41 51
GGCAGGAGGG TTTGTTTTTC ATGCTTTACC AGAAAAATCCA CTTCCCTGCC GACCTTAGTT 60
TCAAGCTTGA TTCTTAATTA GAGACAAGAA ACCTGTTTCA ACTTGAAGAC ACCGTATGAG 120
GTGAATGGAC AGCCAGCCAC CACAATGAAA GAATCAAAAC CAGGAATAAC CTATGCTGAA 180
CCACGCTCTC AATCGTCCCTC AAGTGTTTCC TGACACGCAT CTTTGCTTAC AGTGATCAC 240
AACTGAAGAA TGGGGTTCAA CTTGACGCTT GCAAAATTAC CAAATAACGA GGTGACGGC 300
CAGAGAGTGC TGAATTCAGG CAACAGGAGC GACGGGCCAG GAAAGAACAC CACCCCTCAC 360
AATGAATTG ACACAAATGT CTTGCCGGTG CTTTATCTCA TTATATTGT GGCAGCATC 420
TTGCTGAATG GTTTAGCAGT GTGGATCTTC TTCCACATTA GGAATAAAC CAGCTTCATA 480
TTCTATCTCA AAAACATAGT GGTTCGACAG CTCATAATGA CGCTGACATT TCATTTCGA 540
ATAGTCCATG ATCAGGAGTT TGGACCTTGG TACTTCAAGT TTATTCTCTG CAGATACACT 600
TCAGTTTGTG TTTATGCAAA CATGTATACT TCCATCGTGT TCCTTGGGCT GATAAGCATT 660
GATCGCTATC TGAAGGTGGT CAAGCCATTT GGGGACTCTC GGATGTACAG CATAACCTTC 720
ACGAAGGTTT TATCTGTTTG TGTTTGGGTG ATCATGGCTG TTTTGTCTTT GCCAAACATC 780
ATCCTGACAA ATGGTCAGCC AACAGAGGAC AATATCCATG ACTGCTCAAA ACTTAAAGT 840
CCTTTGGGGG TCAAAATGCA TACGGCAGTC ACCTATGTGA ACAGCTGCTT GTTTGTGGCC 900
GTGCTGGTGA TTCTGATCGG ATGTTACATA GCCATATCCA GGTACATCCA CAAATCCAGC 960

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5 AGGCAATTCA TAAGTCAGTC AAGCGAAAG CGAAAACATA ACCAGAGCAT CAGGGTTGTT 1020
 GTGGCTGTGT TTTTACCTG CTITCTACCA TATCACTTGT GCAGAATTC TTTTACTTTT 1080
 AGTCACCTAG ACAGGCTTTT AGATGAATCT GCACAAAAAA TCCTATATTA CTGCAAGAA 1140
 ATTACACTTT TCTGTCTGCG GTGTAATGTT TGCCCTGGATC CAATAATTTA CTTTTCATG 1200
 TGTAGGTGAT TTTCAAGAAG GCTGTTCAAA AAATCAAATA TCAGAACCA GAGTGAAGC 1260
 ATCAGATCAC TGCAGAGTGT GAGAAGATCG GAAGTTCGCA TATATTATGA TTCACTGAT 1320
 GTGTAGGCCT TTTATTGTTT GTTGAATCG ATATGTACAA AGTGTAAATA AATGTTTCTT 1380
 TTCATTATCC TTAATAAAAA AA

10 Seq ID NO: 364 Protein sequence
 Protein Accession #: NP_076404

15 1 11 21 31 41 51
 MGFNLTLAKL PNNELHQQES HNSGNRSDGP GQNTTLHNEF DTIVLPVLYL IIFVASILLN 60
 GLAVWIFPHI RNKTSFIPYL KNIIVVADLIM TLTFFPRIVH DAGFGPWYFK PILCRYTSVL 120
 FYAMMTTSIV FLGLISIDRY LKVVKPFQDS RMYSTPTKV LSVCVWVIMA VLSLPNIILT 180
 NGQPTEDNIH DCSKLKSPGL VKWHTAVTYV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQF 240
 ISQSSRRKRX NQSRIRVVAV PFTCFPLVHL CRIPFTPSHL DRLLDESAQK ILYCKEITL 300
 20 FLSACNVCLD PIIFYFMCRS PSRRLFKKSN ITRSESIRS LQSVRRSEVR IYYDYTDV

25 Seq ID NO: 365 DNA sequence
 Nucleic Acid Accession #: NM_005365.1
 Coding sequence: 1..948

25 1 11 21 31 41 51
 ATGTCTCTCG AGCAGAGGAG TCCGCACTGC AAGCCTGATG AAGACCTTGA AGCCCAAGGA 60
 GAGGACTTGG GCCTGATGGG TGCACAGGAA CCCACAGGCG AGGAGGAGGA GACTACCTCC 120
 30 TCTCTGACA GCAAGGAGGA GGAGGTGTCT GCTGCTGGGT CATCAAGTCC TCCCAGAGT
 CTTCAAGGAG GCGCTTCTCT CTCCATTTCC GTCTACTACA CTTTATGGAG CCAATTGAT 240
 GAGGGCTCCA GCAGTCAAGA AGAGGAAGAG CCAAGCTCCT CGGTGACACC AGCTCAGCTG 300
 GAGTTCATGT TCCAAGAAGC ACTGAAATTG AAGGTGGCTG AGTTGGTTCA TTTCTGCTC 360
 CACAAATATC GAGTCAAGGA GCCGTCACA AAGGCAGAAA TGCTGGAGAG CGTCATCAA 420
 35 AATTACAAGC GCTACTTTCC TGTGATCTTC GGCAGAGCCT CCGAGTTCAT GCAGGTGATC 480
 TTTGGCACTG ATGTGAAGGA GGTGGACCCC GCCGGCCACT CCTACATCCT TGTCACTGCT 540
 CTTGGCCTCT CGTGGGATAG CATGCTGGGT GATGGTCATA GCATGCCCAA GGCCGCCCTC 600
 CTGATCATTG TCTCGGTGT GATCCTAACC AAAGACAAC GCGCCCTGA AGAGTTATC 660
 40 TGGGAAGCGT TGAGTGTGAT GGGGGTGTAT GTTGGGAAG AGCACATGTT CTACGGGAG 720
 CCCAGGAAGC TGCTCACCCA AGATTGGGTG CAGGAAAAC ACCTGGAGTA CCGGCAGGTG 780
 CCGGCAGGTG ATCTGCGGCA CTACGAGTTC CTGTGGGTT CCAAGGCCCA CGCTGAAACC 840
 AGCTATGAGA AGTGCATAAA TTATTGGTTC ATGCTCAATG CAAGAGAGCC CATCTGTAC 900
 CCATCCCTTT ATGAAGAGGT TTTGGGAGAG GAGCAAGAGG GAGTCTGA

45 Seq ID NO: 366 Protein sequence
 Protein Accession #: NP_005356.1

50 1 11 21 31 41 51
 MSLEQRSPHC KPDEDLBAQD EDLGLMGAQE PTGEEEBETS SSDSKEREVS AAGSSPPQES 60
 PQGASSSIS VYITLWSQFD EGSSSQEEEE PSSSVDPAQL EFMFQEAALK KVAELVHFL 120
 HKYRVKEPVT KAEMLESVIK NYKRYFPVIF GKASEFMQVI FQTDVKEVDP AGHSYILVTA 180
 LGLSCDSMLG DGHSMPKAAL LIIVLGVILT KDNCAPEEVI WEALSVMGVY VGKERMFYGE 240
 55 PRKLLTQDNV QENYLEYRQV PGSDPAHYEF LWGSKAHAET SYEKVINYL MLNAREPICY 300
 PSLYEELVGE EQEGV

60 Seq ID NO: 367 DNA sequence
 Nucleic Acid Accession #: NM_014400
 Coding sequence: 86..1126

60 1 11 21 31 41 51
 GGTACTCAT CCTGGGCTCA GGTAAAGAGG CCCGAGCTCG GAGGCGGCAC ACCCAGGGGG 60
 GAGCCCAAGG GAGCAGGACG GAGCCATGGA CCCCAGCAGG AAAGCAGGTG CCCCAGCCAT 120
 65 GATCTGGACT GCAGGCTGGC TGCTGCTGCT GCTGCTTGGC GGAGGAGGCG AGGCCCTGGA
 GTGCTACAGC TGCGTGCAGA AAGCAGATGA CGGATGCTCC CGAACAAGA TGAAGACAGT 240
 GAAGTGGCGC CCGGGCGTGG ACCTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
 CGGACAATTC TCGCTGGCAG TGCGGGGTG CGGTTCGGGA CTCGCCGCA AGAATGACCG 360
 70 CGGCTGGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
 CTGCAACGCC AAGCTCAACC TCACTCTGCG GCGCTGCGAC CCGCAGGTA ATGAGAGTGC 480
 ATACCCGCCC AACGGCGTGG AGTGTACAG CTGTGTGGGC CTGAGCCGGG AGGCGTGCCA 540
 GGGTACATCG CCGCCGCTCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
 CTTGACGGCG AACGTCACTT TGACGGCAGC TAATGTGACT GTGTCTTGC CTGTCCGGGG 660
 75 CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCAGGGT TCACGCTCAG 720
 TGGCTCTGTT TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CTTACTTCTC 780
 CCTGTGAATC CCACCCCTTG TCGGCTGCC CCTCCAGAG CCAAGGACTG TGGCTCAAC 840
 CACATCTGTC ACCACTTCTA CCTCGGCCCC AGTGAGACCC ACATCCACCA CCAACCCCAT 900
 GCGAGCGCCA ACCAGTCAGA CTCGAGACA GGGAGTAGAA CAGAGGCCT CCGGATGA 960
 80 GAGGCCAGG TTGACTGGAG GCGCGCTGG CCACCCAGGAC CGCAGCAATT CAGGCGAGTA 1020
 TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCT CTTCTGTTGG CGGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCACCTGG 1140
 AAATTTCCCT CTCACCTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
 CCCACCACTG GACTGGGCTG GCCCAGCCCC TGTTTTTCCA ACATTCCCA GTATCCCCAG 1260
 CTTCTGCTGC GCTGTTTGGG GGCTTTGGGA AATAAAATAC CGTTGTATAT ATTCTGGCAG 1320

5
GGGTGTTCTA GCTTTTGTAG GACAGCTCCT GTATCCTTCT CATCCTGTG TCTCCGCTTG 1380
TCTCTTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
AGGATGCTAA GCTTCTTACT CACTTTCTCC TAGCCAGCCT GGACTTTGGA GCGTGGGGTG 1500
GGTGGGACAA TGGCTCCCCA CTCTAAGCAC TGCTCCCTC ACTCCCGCA TCTTTGGGGA 1560
ATCGGTTCOC CATATGTCTT CTTTACTAGA CTGTGAGCTC CTGAGGGGA GGGACCGTGC 1620
CTTAGTCTG TGTGTGATCA GTTCTGGCA CATAAATGCC TCAATAAAGA TTTAATTACT 1680
TTGTATAGTG AAAAAAAA

Seq ID NO: 368 Protein sequence
Protein Accession #: NP_055215

10
1 11 21 31 41 51
MDPARKAGAQ AMINTAGWLL LLLLRGGAQA LECYSCVQKA DDGCSFNKMK TVKCAPGVDV 60
15 CTEAVGAVET IHGQFSLAVX GCGSGLPGKN DRGLDLHGLL AFIQLQQCAQ DRCNAKLNLT 120
SRALDPAGNE SAYPPNGVEE YSCVGLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVTLT 180
AANVTVSLPV RGCVCQDEFCT RDGVTGPGFT LSGSCCQGSR CNSDLRNKTY PFPRIPLVR 240
LPPPEPTTVA STTSVTITST APVVRTSTTK PMPAPTSQTP RQGVHEASR DEEPRLTGGA 300
20 AGHQDRSNSG QYPAKGGPQQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 369 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

25 1 11 21 31 41 51
ATGCCGGTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAGA 120
30 CACTACCTGT CTTTCCGCTT GTACGGCGCC ATCCTGGGCC TGCACTGCTT CATTGAGAGC 180
CTTTTGGCTT TCTTGGAGCA CCGGCGCATG CGACGTGCGC GCCAGGCCCT GAAGCTGCCC 240
TCCCGCGCGC GGGGCTCGGT GGCACGTGTC ATTGCGCAT ACCAGGAGGA CCCTGACTAC 300
TTGGGCAAGT GCCTGCGCTC GCGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
GTGGTGGATG GCAACCGCCA GGAGGACGCC TACATGTCTG ACATCTTCCA CGAGGTGCTG 420
GGCGGACCG AGCAGGCGCG CTTCTTTGTG TGGCGCAGCA ACTTCCATGA GGCAGGCGAG 480
35 GGTGAGACGG AGGCCAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC 540
AGCACTTCTT CGTGATCATAT GCAGAAAGTG GGAGGCAAGC GCGAGGTGAT GTACACGGCC 600
TTCAAGGCCC TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
GATCCAGCCT GCACCATCGA GATGCTTGA GTCTGGAGG AGGATCCCA AGTAGGGGA 720
40 GTCCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCTTT CTTGAGCAGC 780
GTGCGGTACT GGATGGCCTT CAACGTGGAG CCGGCCCTGCC AGTCTACTT TGGCTGTGTG 840
CAGTGATATTA GTGGGCCCTT GGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900
GACTGGTACC ATCAGAAGTT OCTAGGCAGC AAGTGACAGT TCGGGGATGA CCGGACCTTC 960
ACCAACCGAG TCTGAGCCTT TGGTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCCTC 1020
45 ACAGAGACCC CCACTAAGTA CCTCCGGTGG CTCAACAGC AAACCCGCTG GAGCAAGTCT 1080
TACTTCCGGG AGTGCTCTA CAACTCTCTG TGGTTCCTA AGCACCACCT CTGGATGACC 1140
TACAGTACAG TGGTCAOCSG TTTCTTCCCC TTCTTCTCTA TTGCCACGGT TATACAGCTT 1200
TTCTACCGGG GCGCATCTG GAACATTCTC CTCTTCTCTG TGACCGTGCA GCTGGTGGGC 1260
ATTATCAAGG CCACCTACGC CTGCTTCTT CCGGGCAATG CAGAGATGAT CTTTATGTCC 1320
50 CTCTACTCCC TCTCTATAT GTCCAGCCTT CTGCGGCGCA AGATCTTTGC CATGTCTACC 1380
ATCAACAAAT CTGGCTGGGG CACCTCTGGC GGAACAAACA TTGTGGTGAA CTTTATTGGC 1440
CTCATCTCTG TGTCCACTG GGTGGCAGTT CTCTGGAGG GGCTGGCTA CACAGCTTAT 1500
TGCCAGGACC TGTTCAGTGA GACAGAGCTA GCCTTCTCTG TCTCTGGGCG TATACTGTAT 1560
GGCTGCTACT GGTGGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620
55 AAGAAGCCGG AGCAGTACAG CTTGGCTTTT CTGAGGTGT GA

Seq ID NO: 370 Protein sequence
Protein Accession #: NP_005320.1

60 1 11 21 31 41 51
MPVQLTTLAL VVGTSFLPALA VLGGILAAYV TGYQFIHTEK HYLSEFLYGA ILGLHLIIQS 60
LPAPLEHRRM RRAGQALKLP SPRRGSAVAL IAAYQEDPDY LRKCLRSAQR ISFPDLKVV 120
VVDGNRQEDA YMLDIFHEVL GGTGQAGFPV WRNPFHEAGE GETEASLQEG MDRVRDVVRA 180
65 STFCIMQKRW GKKREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
VGGDVQILNK YDSWISFLSS VRYWMAFVNE RACQSYFGCV QCISGPIGMY RNSLLQGFLE 300
DWHYKQFLQS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLRL LNQQTRNRSK 360
YFREWLINSL WPHKHLWMT YESVVTGFFP PFLLIATVIQL PYRGRWNIIL LPLLTVQLVG 420
70 IIKATYACFL RGNABMIFMS LYSLLYMSSL LPAKIFAIAT INKSGWGTSG RKTIVVNF 480
LIPVSIWVAV LLEGLAYTAY CQDLFSETEL AFLVSGAILY GCYVWALLML YLAIIARRCG 540
KKPEQSLAP AEV

Seq ID NO: 371 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 148-7095

75 1 11 21 31 41 51
CACACATACG CACGCACGAT CTCACCTTGA TCTATACACT GGAGGATTAA AACAAACAAA 60
80 CAAAAAAGAC ATTTCTCTTG CTCCCTCTCC CTCTCCACTC TGAGAAAGCAG AGGAGCGSCA 120
CGGCGAGGGG CCGCAGACCG TCTGSAATG CGAATCTTAA AGCGTTTCTT CGCTTGCAAT 180
CAGCTCCTCT GTGTTTGGCG CCTGGATTGG GCTAATGGAT ACTACAGACA ACAGAGAAAA 240
CTTGTGGAAG AGATTGGCTG GTCCATATACA GGAGCACTGA ATCAAAAAA TTGGGGAAG 300
AAATATCCAA CATGTAATAG CCAAAACAA TCTCTATCA ATATTGATGA AGATCTTACA 360
CAAGTAAATG TGAATCTTAA GAAACTTAAA TTTCAGGGTT GGGATAAAAC ATCATTGGAA 420

	AACACATTCA	TTCATAACAC	TGGGAAAACA	GTGGAAATTA	ATCTCACTAA	TGACTACCGT	480
	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTIT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAA	ATTTCACCTT	600
5	GAGATGCAAA	TCTACTGCTT	TGATGCGGAC	CGATTTTCAA	GTTTTGAGGA	AGCAGTCAAA	660
	GGAAAAGGGA	AGTTAAGAGC	TTTATCCATT	TTGTTTGAGG	TTGGGACAGA	AGAAAATTTG	720
	GATTTTCAAG	CGATTATTGA	TGGAGTCGAA	AGTGTIAGTC	GTTTTGGGAA	GCAGGCTGCT	780
	TTAGATCCAT	TCATACTGTT	GAACTTCTG	CCAACTCAA	CTGACAAGTA	TTACATTTAC	840
	AATGGCTCAT	TGACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
10	ACAGTTAGCA	TCTCTGAAAG	CCAGTTGGCT	GTTTTTTGTG	AAGTCTTAC	AATGCAACAA	960
	TCTGTGTATG	TCATGCTGAT	GGACTACTTA	CAAAACAATT	TTGAGAGCA	ACAGTACAG	1020
	TCTCTAGAG	AGGTGTTTTT	CTCATACACT	GGAAAGGAAG	AGATTCTAGA	AGCAGTTTGT	1080
	AGTTCAGAAC	CAGAAAATGT	TCAGGCTGAC	CCAGAGAATT	ATACCAAGCT	TCTTGTGTACA	1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
15	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTG	TCAATAATTT	GCTACCCAAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCATAAATG	GCTTCAATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACCT	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGTCTACA	1500
20	AACCAATATCA	GGAAAAGGGA	ACCCAGATT	TCTACACAA	CACACTACAA	TCGCATAGGG	1560
	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTAAAG	GCTTCAATAT	ATCTTTAAAT	TCCACTTCCC	AACCACTCAC	TAAATTAGCC	1680
	ACAGAAAAG	ATATTTCCCT	GACTTCTCAG	ACTGTGACTG	AACCTGCCAC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
25	AACCTGTGCG	GGACTGCGA	ATCCTTAAAT	ACAGTTTCTA	TAACAGAATA	TGAGGAGGAG	1860
	AGTTTATTGA	CCAGTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
	GCACCTTCTG	CTATCCCAT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCTCTC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAAG	TCACATAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
30	GTGTGTTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
	AGCTTCTCTC	AGACTAATTA	CACGTAGATA	CGTGTGTATG	AATCTGAGAA	GACAAACCAAG	2220
	TCCTTTTCTG	CAGGCCCATG	GATGTACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CTTTGCTCTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
	TCCAGACAAC	AGGATTGGT	CTCCACGGTC	AACGTGGTAT	ACTCCGAGAC	AACCCAAACG	2400
35	GTATACAATG	GTGAGACACC	TCTTCAACCT	TCTTACAGTA	GTGAAGTCTT	TCTCTAGTCT	2460
	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
	TCGGCTTTGC	ATGCTACGCC	TGTATTTCCC	AGTGTGATG	TGTCAATTGA	ATCCATCCTG	2580
	TCTTCTATG	ATGCTGACCC	TTTGCTTCCA	TTTTCTCTG	CTTCTTCAG	TAGTGAATTG	2640
	TTTCTCTATG	TGCTATACAGT	TTCTCAAATC	CTTCCACAAG	TTACTTTCAG	TACCGAGAGT	2700
40	TTTCTCTATG	TGCTATACAGT	TTCTCAAATC	CTTCCACAAG	TTACTTTCAG	TACCGAGAGT	2760
	GATAAGGTGC	CCTTGCATGC	TTCTCTGCCA	GTGGCTGGGG	GTGATTGTCT	ATTAGAGCCC	2820
	AGCCTTGCTC	AGTATTCTGA	TGTGCTGTCC	ACTACTCATG	CTGCTTCAGA	GACGCTGGAA	2880
	TTTGTAGTGT	AATCTGGTGT	TCTTTATAAA	ACGCTTATGT	TTTCTCAAGT	TGAACCAACC	2940
	AGCAGTGATG	CCATGATGCA	TGCAAGTCTT	TCAGGCGCTG	AACCTTCTTA	TGCCTTGTCT	3000
45	GATAATGAGG	GCTCCCAACA	CATCTTCACT	GTTCCTTACA	GTTCGCAAT	ACCTGTGCTAT	3060
	GATTCTGATG	GTGTAACCTTA	TCAGGCTTCC	TTAATTAGCG	GCCTTAGCCA	TATACCAATA	3120
	CCTAAGTCTT	CGTTAATAAC	CCCAACTGCA	TCATTACTGC	AGCCTACTCA	TGCCCCCTCT	3180
	GGTGATGGGG	AATGGTCTGG	AGCCTCTTCT	GATAGTGAAT	TTCTTTTACC	TGACACAGAT	3240
	GGGCTGACAG	CCCTTAACAT	TTCTTCACTT	GTTCCTGTAG	CTGAATTTAC	ATATACAACA	3300
50	TCTGTGTTTG	GTGATGATAA	TAAGGCGCTT	TCTAAAAGTG	AAATAATATA	TGGAATAGAG	3360
	ACTGAGATTG	GTGTAACCTT	TTTCAATGAG	ATGGTTTACC	CTTCTGAAAG	CACAGTCTAG	3420
	CCCAACATGT	ATGATAATGT	AAATAAGTTG	AATGCGTCTT	TACAAGAAAC	CTCTGTTTCC	3480
	ATTCTTAGCA	CCAAGGGCAT	GTTCACAGG	TCCCTTGTCT	ATACCAACAC	TAAGGTTTTT	3540
	GATCATGAGA	TTAGTCAAGT	TCCAGAAAAT	AACCTTTTCA	TTCAACCTAC	ACATACTGTC	3600
55	TCTCAAGCAT	CTGGTGACAC	TTGCTTTAAA	CCTGTGCTTA	GTGCAAACTC	AGAGCCAGCA	3660
	TCTCTGACCC	CTGCTTCTAG	TGAAATGTTA	TCTCCTTCAA	CTCAGCTCTT	ATTTTATGAG	3720
	AOCTCAGCTT	CTTTTAGTAC	TGAAGTATTG	CTACAACCTT	CCTTTCAGGC	TTCTGATGTT	3780
	GACACCTTGC	TTAAAACCTG	TCTTCCAGCT	GTGCCAGTG	ATCCAATATT	GGTTGAAACC	3840
	CCCAAGTTTG	ATAAAATTAG	TTCTACAATG	TTGCACTCTA	TTGTATCAAA	TTCTGCTTCA	3900
60	AGTGAAGAAC	TGCTGCACTC	TACATCTGTA	CCAGTTTGTG	ATGTTGTCGC	TACTTCTCAT	3960
	ATGCACTCTG	CTTCACTTCA	AGGTTTGACC	ATTTCTATG	CAAGTGAGAA	ATATGAACCA	4020
	GTTTTGTATA	AAAGTGAAAG	TTCCACCAA	GTGTAACCTT	CTTTGTACAG	TAATGATGAG	4080
	TTGTTCCCAA	CGGCCAATTT	GGAGATTAA	CAGGCCATC	CCCCAAAAGG	AAGGCATGTA	4140
	TTTGCTACAC	CTGTTTATC	AATTGATGAA	CCATTAAATA	CACATAATAA	TAAGCTTATA	4200
65	CATTCCGATG	AAATTTTAA	CTCCACCAA	AGTCTGTGTA	CTGTTAAGGT	ATTGCTGGT	4260
	ATTCCAACAG	TTGCTTCTGA	TACATTGTA	TCTACTGATC	ATTCTGTTC	TATAGGAAAT	4320
	GGGCAATGTT	CCATTACAGC	TGTTCTTCCC	CACAGAGATG	GTCTGTAAAC	CTCAACAAAG	4380
	TTGCTGTTTC	CTTCTAAGGC	AACCTCTGAG	CTGAGTCATA	GTGCCAAATC	TGATGCGGT	4440
	TTAGTGGGTG	GTGGTGAAGA	TGGTGACACT	GATGATGATG	GTGATGATGA	TGATGATGAC	4500
70	AGAGGTAGTG	ATGGCTTATC	CATTCTAAG	TGTATGTCTAT	GCTCATCTTA	TAGAGAATCA	4560
	CAGGAAAAGG	TAATGAATGA	TTTCAACACC	CAAGAAAACA	GTCTTATGGA	TCAGAATAAT	4620
	CCAATCTCAT	ACTCACTATC	TGAGAATTCT	GAAGAAGATA	ATAGAGTCA	AAGTGTATCC	4680
	TCAGACAGTC	AAACTGGTAT	GGACAGAAGT	CCTGGTAAAT	CACCATCAGC	AAATGGGCTA	4740
75	TCCAAAAGC	ACAAATGATG	AAAAGAGGAA	AATGACATTC	AGACTGGTAG	TGCTCTGCTT	4800
	CCTCTCAGCC	CTGAATCTAA	AGCATGGGCA	GTCTGACAA	GTGATGAAGA	AAGTGGATCA	4860
	GGGCAAGGTA	TGCTGAGATG	CCTTAATGAG	AATGAGACTT	CCACAGATTT	CAGTTTGTGA	4920
	GACACTAATG	AAAAGATGTC	TGATGGGATC	CTGGCAGCAG	GTGACTCAGA	AATAACTCCT	4980
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 Protein Accession #: built from XP_031379

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Seq ID NO: 380 Protein sequence:
Protein Accession #: EOS sequence

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	EVIVMITNLV	EKGRRKCDQY	WPADGSSEYG	NFLVTQKSVQ	VLAYYTVRNP	TLRNTKIKKG	1020
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	INCESFKVTL	MAEBHKCLSN	EKLIIQDFI	LEATQDDYVL	EVRRHFQCEKW	PNFDPISIKT	1380
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Seq ID NO: 381 DNA sequence
Nucleic Acid Accession #: NM_002851.1
Coding sequence: 148..7092

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Seq ID NO: 382 Protein sequence
 Protein Accession #: NP_002842.1

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Seq ID NO: 383 DNA sequence

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Coding sequence: 126..4439

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 Protein Accession #: NP_005679.1

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Seq ID NO: 386 Protein sequence
Protein Accession #: NP_001318.1

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Seq ID NO: 388 Protein sequence
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Seq ID NO: 389 DNA sequence
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	KRLGEGAGFG	KVFLAECAPL	CPEDOKILVA	AKRDPFHREAS	LLTNLOHEHI	600	

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 AAGMVLASQ HPVHRDLATR NCLVGENLLV KIGDFGMSRD VYSTDYRVG QHTMLPIRWM 720
 PFESIMYRKF TTESDVWSLG VVLWEIFTYG KQFWYQLSNN EVIECTQGR VLQRPRTCPQ 780
 EVYELMLGCW QREPHMRKNI KGIHTLLQNL ARASPVYLDI LG

5

Seq ID NO: 395 DNA sequence
 Nucleic Acid Accession #: AF410899
 Coding sequence: 483..2999

10 1 11 21 31 41 51
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 15 CCGCCGCTCG GTGCCCGGCG CGCCCGG3CCA TGCAGCGAGC GCGCCGCGCG AGCTCCGAGC 240
 AGCGGTAGCG CCCCCTCTGA AAGCGGTTCG CTATGCCGGG ACCACTGTGA ACCCTGCGCG 300
 CTGCCGGAAC ACTCTTCGCT CGGACCAAGC TCAGCTCTG ATAAGCTTGA CTCCGCAAGC 360
 CCGCAACAAG CACCGAGGAG TTAAGAGAGC CGCAAGCGCA GGAAGGCTC CCGCGCAGG 420
 GTGGGGGAAA GCGGCGGGTG CAGCGCGGGG ACAGGCACTC GGGCTGGCAC TGGCTGCTAG 480
 20 GGATGTCTGC CTGGATAAGG TGGCATGAGC CCGCCATGGC GCGGCTCTGG GGCTTCTGCT 540
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 25 AAATCATCAA CGAAGATGAT GTTGAAGCTT ATGTGGGACT GAGAAATCTG ACAATTGTGG 780
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 30 GCAGCAAGAA TATTTCCCTG GCAAACTGTC AGATACCCAA TTGTGGTTTG CCATCTGCAA 1080
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 40 GCTGCGCTGG AATTGACGAT GGTGCAAAAC CAAATTATCC TGATGTAATT TATGAAGATT 1680
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 45 GTGTGCGCCC AGCCTCCGTT ATCAGCAATG ATGATGACTC TGCCAGCCCA CTCCATCACA 1980
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 TCAAGCCAGA CACATTTGTT CAGCACATCA AGCGACATAA CATTTGTTCTG AAAAGGGAGC 2160
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 50 AGGACAAGAT CTGTGTGCA GTGAAGACCC TGAAGGATGC CAGTGACAA TGCACGAAGG 2280
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 ACCTCAACAA GTTCTCTCAG GCACACGGCC CTGATGCCGT GCTGATGGCT GAGGCGCAAC 2460
 CGCCCAAGGA ACTGACGAGC TCGCAGATGC TGCATATAGC CCAGCAGATC GCGGCGGGCA 2520
 55 TGGTCTACCT GCGGTCCCA CACTTGTGTC ACCGCGATT TGCACACAGG AACTGCGCTG 2580
 TCGGGGAGAA CTGTCTGTGT AAAATOGGGG ACTTTGGGAT GTCCCGGGAC GTGTACAGCA 2640
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 GCATCATGTA CAGGAATTC ACGACGAAA GCGACGTCG GAGCCTGGGG GTCTGTGTGT 2760
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 AGCTGATGCT GGGGTGCTG CAGCGAGAGC CCCACATGAG GAAGAATATC AAGGGCATCC 2940
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 GCCCTTTTCC CCAGACCGAT CCTTCCCAAC GTACTCTCTA GACGGGCTGA GAGGATGAAC 3060
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 65 TCAAAAGACT CGAAGAAGCT TCGAGGGAAG CAGTGTGTAC TTCTTCTACC ATAGACACAG 3180
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 70 TTAACAAACG TAATTTGTGA TATCAGCAGA CACTCCAGTT TGCCCAACC AACTAACAT 3420
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 75 TTTATTATGA ACCGCAATAT GGGAGGAACA AAGACAACCA CTGGGATCAG CTGGTGTGAG 3720
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 CTGAGGACCT TTCTGAGGAG TAAAAAGACT ACTGGCTCT GTGCCATGGA TGATTTCTTT 3840
 CCCATCACCA GAAATGATAG CGTGCAATAG AGAGCAAGA TGGCTTCCGT GAGACACAAG 3900
 ATGGGCGATA GTGTGCTCGG ACACAGTTTT GTCTTCTGAG GTTGTGATGA TAGCACTGGT 3960
 80 TTGTTCTCTA AGCGCTATCC ACAGAACCTT TGTCAACTTC AGTTGAAAA AGGTGGATT 4020
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Seq ID NO: 396 Protein sequence
 Protein Accession #: AAL67965.1

1 11 21 31 41 51

	MSSWIRMHGP	AMARLWGFPCW	LVVGFWRAAF	ACPTSCKCSA	SRINCSDPSP	GIVAFPRLEP	60
	NSVDPENITE	IFIANQKRLE	IINEDDVEAY	VGLRNLITVD	SGLKPVAKHA	PLKNSNLQHI	120
5	NFTRNKLTSL	SRKHFRHLDL	SELILVGNPF	TCSCDIMWIK	TLQBAKSSPD	TQDLYCLNES	180
	SKNIPLANLQ	IPNCGPLPSAN	LAAPNLTVES	GKSITLSCSV	AGDPVPNMYW	DVGNLVSKHM	240
	NETSHTQSL	RITNISDDSD	GKQISCVAEN	LVGEDQDSVN	LTVHFAPTIT	FLESPTSDRH	300
	WCIPPTVKGN	PKPALQWFYN	GAILNESKYI	CTKIHVTNHT	EVHGCLQLDN	PTHMNGDYT	360
	LIARNEYGKD	EKQISAHFMG	WPGIDDGANP	NYPDVIYEDY	GTAANDIGDT	TNRSNEIPST	420
10	DVTDKTRGHE	LSVYAVVVIA	SVVGFCLLMV	LFLKLARHS	KFGMKDFSWP	GPGKVKSRQG	480
	VGPASVISND	DDSGAPLHHI	SNGSNTFSSS	EGGPDVAIIG	MTKIPVIEINP	QYFGITNSQL	540
	KPDTFVQHIK	RHINIVLKREL	GEGAFGKVFL	ABCYNLCPAQ	DKILVAVKTL	KDASDNARKD	600
	FHREAELLTN	LQHEHIVKPY	GVCVEGDPLI	MVPEYMKHGD	LNKPLRAHGP	DAVLMAEGNP	660
	PTBLTQSQML	HIAQQIAAGM	VYLASQHFVH	RDLATRNCLV	GENLLVKIGD	FGMSRDVYST	720
15	DYIRVGGHTM	LPIRNMPPEP	IMYRKPTTES	DVWSLGVVLW	EIFTYKQPPW	YQLSNNEVIE	780
	CITQGRVLQR	PRTCPQEVYE	LMLGCNQREP	HMRKNIRGIH	TLLQNLAKAS	PVYLDILG	

Seq ID NO: 397 DNA sequence
Nucleic Acid Accession #: AB052906
Coding sequence: 74..814

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	CTCTGGGTCC	TTAATGGCAG	CAGCCGCCGC	TACCAAGATC	CTTCTGTGCC	TCCCGCTTCT	120
25	GCTCCTGCTG	TCCGGCTGGT	CCCGGGCTGG	GCGAGCCGAC	CCTCACTCTC	TTTGCTATGA	180
	CATCACCGTC	ATCCCTAAGT	TCAGACCTGG	ACCACGGTGG	TGTGGGTTTC	AAGGCCAGGT	240
	GGATGAAAAG	ACTTTTCTTC	ACTATGACTG	TGGCAACAAG	ACAGTCACAC	CTGTCACTCC	300
	CCTGGGAAG	AAACTAAATG	TCACAACGGC	CTGGAAGACA	CAGAACCAG	TACTGAGAGA	360
	GGTGGTGGAC	ATACTTACAG	AGCAACTGCG	TGACATTCAG	CTGGAGAATT	ACACACCCAA	420
30	GGAAACCCCTC	ACCTGTCAGG	CCAGGATGTC	TTGTAGCAG	AAAGCTGAAG	GACACAGCAG	480
	TGGATCTTGG	CAGTTCAGTT	TCGATGGGCA	GATCTTCCTC	CTCTTTGACT	CAGAGAAGAG	540
	AATGTGGACA	ACGGTTCATC	CTGGAGCCAG	AAAGATGAAA	GAAGAGTGGG	AGAATGACAA	600
	GGTGTGGGCC	ATGTCCCTCC	ATTACTTCTC	AATGGGAGAC	TGTATAGGAT	GGCTTGAGGA	660
	CTTCTTGATG	GGCATGGACA	GCACCTGGGA	GCCAAGTGCA	GGAGCACCAC	TGCCCATGTC	720
35	CTCAGGCACA	ACCCAATCA	GGGCCACAGC	CACCACCCCTC	ATCCTTTGCT	GCCTCCTCAT	780
	CATCCTCCCC	TGCTTCATCC	TCCCTGGCAT	CTGAGGAGAG	TCCTTTAGAG	TGACAGGTTA	840
	AAGCTGATAC	CAAAAGGCTC	CTGTGAGCAC	GGTCTTGATC	AAACTCGCCC	TTCTGTCTGG	900
	CCAGCTGCCC	ACGACCTACG	GTGTATGTCC	AGTGGCCTCC	AGCAGATCAT	GATGACATCA	960
	TGGACCCAAT	AGCTCATCA	CTGCCCTGAT	TCCTTTTGCC	AACAATTITA	CCAGCAGTTA	1020
40	TACCTAACAT	ATTATGCAAT	TTTCTCTTGG	TGCTACCTGA	TGGAATTCTC	GCACCTAAAG	1080
	TTCTGGCTGA	CTAAACAAGA	TATATCATTT	TCTTTCTTCT	CTTTTGTGTT	GGAAAAATCA	1140
	GTACTTCTTT	GAATGATGAT	CTCTTTCTTG	CAATGATAT	TGTCAGTAAA	ATAATCACGT	1200
	TAGACTTCAG	ACCTCTGGGG	ATTCTTCCCG	TGTCCTGAAA	GAGAATTTT	AAATTATTTA	1260
45	ATAAGAAAAA	ATTATATTTA	ATGATTGTTT	CCTTTAGTAA	TTTATTGTTC	TGTACTGATA	1320
	TTTAAATAAA	GAGTTCATTT	TCCCAAAAAA	AAAAAAAAAA	AA		

Seq ID NO: 398 Protein sequence
Protein Accession #: BAB61048.1

50	1	11	21	31	41	51	
	MAAAAATKIL	LCLPLLLLLS	GWSRAGRADP	HSLCYDITVI	PKFRPGPRNC	AVQGQVDEKT	60
	FLHYDCGNKT	VTEVSLGKHK	LNVTAWKAQ	NPVLREVVDI	LTEQLRDIQL	ENYTPKEPLT	120
55	LQARMSCEQK	ABGHSSGSQ	FSFDGQIFLL	FDSEKRMWTT	VHPGARKMKE	KWENDKVAM	180
	SPHYPSMGDC	IGWLEDFLMG	MDSTLEPSAG	APLAMSSGTT	QLRATATTLI	LCCLLILLPC	240
	PILPGI						

Seq ID NO: 399 DNA sequence
Nucleic Acid Accession #: NM_001898.1
Coding sequence: 57..482

60	1	11	21	31	41	51	
	GGCTCTCACC	CTCCTCTCCT	GCAGCTCCAG	CTTTGTGCTC	TGCCTCTGAG	GAGACCATGG	60
65	CCCAGTATCT	GAGTACCCCTG	CTGCTCCTGC	TGGCCACCCT	AGCTGTGGCC	CTGGCCTGGA	120
	CGCCCAAGGA	GGAGGATAGG	ATAATCCCGG	GTGGCATCTA	TAACGCAGAC	CTCAATGATG	180
	AGTGGGTACA	CGGTGCCCTT	CACCTCGCCA	TCAGCGAGTA	TAACAAGGCC	ACCAAAGATG	240
	ACTACTACAG	ACGTCCGCTG	CGGGTACTAA	GAGCCAGGCA	ACAGACCGTT	GGGGGGGTGA	300
	ATTACTTCTT	CGAGCTAGAG	GTGGGCCGCA	CCATATGTAC	CAAGTCCCAG	CCCAACTTGG	360
70	ACACCTGTGC	CTTCCATGAA	CAGCCAGAAC	TGCAGAAAGAA	ACAGTTGTGC	TCTTTCGAGA	420
	TCTACGAAGT	TCCCTGGGAG	AACAGAAGGT	CCCTGGTGAA	ATCCAGGTGT	CAAGAATCCT	480
	AGGGATCTGT	GCCAGGCCAT	TCGCACCAGC	CACCACCCAC	TCCACCCCC	TGTAGTGCTC	540
	CCACCCCTGG	ACTGGTGGCC	CCACCCCTGC	GGGAGGCCCTC	CCCATGTGCC	TGCGCCAAGA	600
75	GACAGACAGA	GAAAGCTGCA	GGAGTCTTTT	GTGTCTCAGC	AGGGCGCTCT	GCCTCCCTC	660
	CTTCTCTTCT	GCTTCTAATA	GCCTGGGTAC	ATGGTACACA	CCCCCCCCACC	TCTTGCAATT	720
	AAACAGTAGC	ATCGCC					

Seq ID NO: 400 Protein sequence
Protein Accession #: NP_001889.1

80	1	11	21	31	41	51	
	MAQYLSTLLL	LLATLAVALA	WSPKEEDRII	PGGIYNADLN	DEWVQALHP	AISEYNKATK	60
	DDYRRRLRV	LRARQQTGG	VNYFFDVEVG	RTICTKSQPN	LDTCAFHEQP	ELQKKQLCSP	120

BIYEVFWENR RSLVKSRCQE S

Seq ID NO: 401 DNA sequence

Nucleic Acid Accession #: NM_003976.2

Coding sequence: 299..961

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1      11      21      31      41      51
|      |      |      |      |      |
CTCTGAGCTT CTCTGAGCCT TGTTTGCTCA TCTGGAAAAA GGGGATTAAA CCAITTTACCT 60
CATGGAGTTG TGAAAGAATA GCTGCAAAGC ACCTAACACA TAGTAAGGTT CCCAGTGCAG 120
CTACTTCTGC TGGGTTGAGT CTAGCTGTGT AGGCCCTTGG TTCCTCACCT GGAGAAACTG 180
GGGTGGCAGG CCGGTCCTCC ACAAAGATA ACTCATCTCT TAATTTCGAA GCTGCCTCAA 240
CAGGAGGGTG GGGGAACAGC TCACAAATGG CTGATGGGCG CTCTCTGGTG TGATAGAGAT 300
GGAACTTGGA CTGGAGAGCC TCTCCACGCT GTCCCACTGC CCCTGGCCTA GCGGCGAGCC 360
TGCCCTGTGG CCCACCTGG CCGCTCTGGC TCTGCTGAGC AGCGTCGAG AGGCCTCCCT 420
GGGCTCCGCG CCGCGCAGCC CTGCCCCCGG GGAAGGCCCG CCGCTGTGCC TGGGTCCCC 480
CGCCGCGCAC CTGCGCGGGG GACGCACGCG CCGCTGGTGC AGTGAAGAG CCCGCGCGCC 540
GCGCGCGCAG CCTTCTGGGC CCGCGCCCCG GCGGCTGCA CCCCATCTG CTCTTCCCCG 600
CGGGGCGCGC GCGGCGCGGG CTGGGGGCCC GGCAGCGCG GCTCGGCGAG CGGGGCGCG 660
GGGCTGCGCG CTGCGCTGCG AGCTGGTGCC GGTGCGCGCG CTGCGCCTGG GCCACGCTC 720
CGACGAGCTG GTGCGTTTCC GCTTCTGCAG CGGCTCCTGC CGCGCGCGCG GCTCTCCACA 780
GACCTCAGC CTGGCCAGCC TACTGGGCGC CGGGGCCCTG CGACCGCCCC CGGGCTCCCC 840
GCCGCTCAGC CAGCCCTGCT GCGCAACCCG GCGCTACGAA GCGGTCTCCT TCATGGACGT 900
CAACAGCACC TGGAGAACCG TGGACCGCCT CTCGCGCACC GCGTGGGCTG GCGTGGGCTG 960
AGGGCTCGCT CCGAGGCTTT GCAGACTGGA CCTTACCGG TGGCTCTTCC TGCCCTGGAC 1020
CCTCCGCGAG AGTCCCACTA GCCAGCGGCC TCAGCCAGGG ACGAAGCGCT CAAAGCTGAG 1080
AGGCCCTTAC CGGTGGGTGA TGGATATCAT CCCCGAACAG GTGAAGGGAC AACTGACTAG 1140
CAGCCCGAGA GCCCTCACCC TCGGATCCCC AGCCTAAAG ACACAGAGA CCTCAGCTAT 1200
GGAGCCCTTC GCGCCCACTT CTCACAGACT CTGGCAGCTG CCAGGCGCTG AACCTGGGAG 1260
CCCTCTCTG ATGAACAATA CAGTGGCTGA GGCATCAGCC CCGGCCCAGG CCTGTAGGG 1320
ACAGCATTG AAGACACAT ATTGCACTG CTGGTTGAA AGTGCTGTG CTGGAAGTGG 1380
CTGTACTCA CTCATGGAG CTGGCCCC

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Seq ID NO: 402 Protein sequence

Protein Accession #: NP_003967.1

35
40

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1      11      21      31      41      51
|      |      |      |      |      |
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PAGHLPGGRT ARWCSGRARR PFPQPSRPAP PPPAPPSALP RGRRAARAGG PGSRARAAGA 120
RGCRRLSQLV FVRALGLGHR SDELVRFRPC SGSCRRARSP HDLSLASLLO AGALRPPPGS 180
RPVQPCCRP TRYEAVSFMD VNSTWRTVDR LSATACGLG

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Seq ID NO: 403 DNA sequence

Nucleic Acid Accession #: NM_057091.1

Coding sequence: 783..1445

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|      |      |      |      |      |
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GGACCCCAAA ATCTGCAAGT ACCAGCAGTC AGCCGCCCCA CGCAGGAGCC GGCTTACCCC 120
TCGCTTCCCG CCTCTACTCA CTCTCTCCCG CCTCGGCCCG GGCCTCCAGC CTCTCTACTT 180
CGCGTGTCTA CAAACTCAAC TCCCGGTTTC CGTGCCTCTC CACCGCTGGA GTTCTCTACT 240
CTCCATATCC GAGGGGCCCC TCCAGCATC TACCCCTCTC CCAACCTCGG GGGACCTAGC 300
CAGCTAGGG GGGACTGGAT CCGACGSGTG GAGCAGCCAG GTGAGCCCGG AAAGGTGGGG 360
CGGGGCGAGG GCGCTCCAG CCACCCCGCG GATCTGGTG ACCTGTGGGG TGGAATTGGA 420
CACCGGACGG CTGCGGCGCG GGGCAGGAGG CTGCTGAGGG ATGGAGTTGG GCCCGGCCCG 480
CAGACAAGGC CCGGGGCGTC CGCCAGCAGC AGGTCCCTCG GGCCTCAGCC CTGCTGCCCA 540
CCCGGGCGCT GAGCCCCACA CCGAGGGGTG CAGACTGGCT GCCAAGGCCA CACTTTTGGC 600
TAAAGAGGC ACTGCCAGGT GTACAGTCTT GGCATGCGC TGTTTGAGCT TCGGGGAGA 660
GCCAGCACT GGTCCCCGGA AAGGTGCTTA GAAGAACAG GTGCAGGACC CCGTGTCTCC 720
TCAACAGGAG GGTGGGGGAA CAGCTCAACA ATGGCTGATG GCGCTCCTG GTGTTGATAG 780
AGATGGAAT TGAATTTGGA GGCCTCTCCA CGCTGTCCCA CTGCCCCCTG CCTAGGCGCG 840
AGCCTGCCCT GTGGCCACC CTGGCGCTC TGGCTCTGCT GAGCAGGCTC GCAGAGGCTC 900
CCCTGGGCTC CGCGCCCCCG AGCCCTGCCG CCGCGAAGG CCCCCCGCT GTCTGGGCT 960
CCCCCGCGCG CCACCTGCGG GGGGAGCGCA CGGCCCGCTG GTGCAGTGA AGACCCCGCG 1020
GGCCGCGCGG CGAGCTTCTT CGGCCCGGCG CCGCGCGCG TGCACCCCA TCTGCTCTT 1080
CCCGCGGGGG CCGCGCGCGG CGGCTGGGG GCGCGGCGAG CCGGCTCGG GCAGCGGGGG 1140
CGCGGGGCTG CCGCTTGGCG TCGCAGCTGG TCGCGGTGCG CGGCTCGGC CTGGGCCACC 1200
GCTCGAGA GCTGGTGGT TTCCGCTTCT GCAGCGGCTC CTGCGCGCG GCGGCTCTC 1260
CACACAGCT CAGCTTGGCC AGCCTACTGG GCGCGGGGCG CCTGCGAGCG CCCCCGGGCT 1320
CCCGCGCGGT CAGAGCCCTT TGCTGCGGAC CCAAGCGCTA CGAAGCGGCT TCCTTATGG 1380
AGCTCAACAG CAGCTGGAGA ACCGTGGACC GCCTCTCCCG CACCGCTGCG GGCTGCCTGG 1440
CTGAGGGCT CGCTCAGGG CTTTGCAGAC TGAACCTTA CCGGTGGCTC TTCTGCTG 1500
GGACCTTCCC GCAGATCCC ACTAGCCAGC GGCCTCAGCC AGGAGCGAAG GCCTCAAAGC 1560
TGAGAGGCC CTACCGGTGG GTGATGGATA TCATCCCGGA ACAGGTGAAG GGACAACTGA 1620
CTAGCAGCCC CAGAGCCCTT ACCCTGCGGA TCCAGCCTA AAAGACACCA GAGACCTCAG 1680
CTATGAGGCC CTTCGAGACC ACTTCTCACA GACTCTGGCA CTGGCCAGGC CTGGAACCTG 1740
GGAACCCCTC TCTGATGAAC ACTACAGTGG CTGAGGCATC AGCCCCCGCG CAGGCCCTGT 1800
AGGGACAGCA TTTGAAGGAC ACATATTGCA GTTGCTTGGT TGAAAGTGCC TGTGCTGGAA 1860
CTGGCTGTA CTCACCTATG GGAGCTGGCC CC

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Seq ID NO: 404 Protein sequence

Protein Accession #: NP_003967.1

1 11 21 31 41 51
 5 MELGLGLST LSHCPWPRRQ PALWPTLAAL ALLSSVAEAS LGSAPRSPAP REGPPFVLAS 60
 PAGHLPGGRT ARWCSGRARR PPPQSPRPAP PPPAPPSALP RGGRAARAGG PGSRARAAGA 120
 RGCRLRSQLV FVRALGLGHR SDELVRFRFC SGSCRRARSP HDLSLASLLG AGALRPPPGS 180
 RPSVQPCCRP TRYAVSPMD VNSTWRTVDR LSATACGCLG

10 Seq ID NO: 405 DNA sequence
 Nucleic Acid Accession #: NM_057160.1
 Coding sequence: 1..714

1 11 21 31 41 51
 15 ATGCCCGGCC TGATCTCAGC CCGAGGACAG CCCCTCCTTG AGGTCCTTCC TCCCCAAGCC 60
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 TGGCCACACC TGGCCGCTCT GGCTCTGCTG AGCAGCGTCG CAGAGGCCCT CCTGGGCTCC 180
 20 GCGCCCGCA GCGCTGCCCC CCGGAAGGC CCCCCTGCTG TCTTGGCTGC CCCGCGCGGC 240
 CACCTGCGGG GGGGACGACG GCGCGCTGG TGCACTGGAA GAGCCCGGCG CGCGCGCGCG 300
 CAGCCTTCTC GCGCCGCGCC CCGCGCGCT GCACCCCAT CTGCTCTTCC CCGCGGGGGC 360
 CGCGCGCGGC GGGCTGGGG CCCGCGCAGC CGCGCTCGGG CAGCGGGGCG GCGGGGCTGC 420
 CGCTCGCTCG CAGAGCTGGT GCGGTGCGC GCGCTCGGCT TGGGCCACCG CTCGACGAG 480
 25 CTGGTGCGTT TCGCTTCTG CAGCGCTCC TGCGCGCGCG CGCGCTCTCC ACAAGACCTC 540
 AGCCTGGACA GCTACTTGGG CGCGCGGCGC CTGCGACCGC CCGCGGCTCC CCGCGCGCTC 600
 AGCCAGCCCT GCTGCGGACC CACGCGCTAC GAAGCGGTCT CTTTCAATGA CGTCAACAGC 660
 ACCTGAGAGG CCGTGGACCG CCTCTCGGCC ACCGCGCTCG GCTGCTGGG CTGAGGGCTC 720
 GCTCCAGGGC TTTCAGAGCT GGACCTTAC CGTGCGCTCT TCCTGCCCTG GACCTCTCCG 780
 30 CAGAGTCCCA CTAGCCAGCG GCCTCAGCCA GGGACGAAGG CCTCAAGCTC GAGAGGCCCC 840
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 AGAGCCCTCA CCTGCGGAT CCGAGCTAA AAGACACAG AGACCTCAGC TATGGAGCCC 960
 TTCGAGACCA CTCTCAGAG ACTCTGGCAC TGGCCAGGCC TCGAAGCTGG GACCCCTCCT 1020
 CTGATGAACA CTACAGTGGC TGAGGCATCA GCGCCCGGCC AGGCCCTGTA GGGACAGCAT 1080
 35 TTGAAGGACA CATATTGCAG TTGCTTGTT GAAAGTGCT GTGCTGGAAC TGGCTGTGAC 1140
 TCACTCATGG GAGCTGGCCC C

Seq ID NO: 406 Protein sequence
 Protein Accession #: NP_476501.1

1 11 21 31 41 51
 40 MPGLISARGQ PLLEVLPPQA HLGALFLPEA PLGLSAQPAL WPTLAALALL SSVAEASLGS 60
 APRSPAPREG PPPVLASPAQ HLPGGRTARW CSGRARRPPP QPSRPAPPPP APPSALPRGG 120
 45 RAARAGGPGS RARAGARGC RLRSQLVFVR ALGLGHRSD LVRFRFCSGS CRRARSPHDL 180
 SLASLLGAGA LRPPPGSRPV SQPCCRPTRY EAVSFMDVNS TWRTVDRLSA TACGCLG

50 Seq ID NO: 407 DNA sequence
 Nucleic Acid Accession #: NM_057090.1
 Coding sequence: 29..715

1 11 21 31 41 51
 55 CTGATGGGCG CTCCTGGTGT TGATAGAGAT GGAACCTGGA CTGGAGGCC TCTCCACGCT 60
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 60 CCGCGCGGCG CCGGCTGGGG GCGCGGCGAG CCGCGCTCGG GCAGCGGGGG CCGCGGGCTG 420
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Seq ID NO: 408 Protein sequence
 Protein Accession #: NP_476431.1

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 SRARAAGARG CRLRSQLVFV RALGLGHRSD ELVRFRFCSG SCRRARSPHD LSLASLLGAG 180
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Seq ID NO: 409 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1746

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Seq ID NO: 410 Protein sequence
Protein Accession #: BAB84587.1

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FQGLDSLIESL LLSNNQLLQI QPAHFSQCSN LKELQLHGNH LEYIPDGAFD HLVGLTKLNL 180
GKNSLTHISP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQRLALQQ NQIGLLSPGL 240
PHNNHNLQRL YLSNNHISQL PPSIFMQLPQ LNRLLTFGNS LKELSLGIFG PMPNLRRLWL 300
YDNHISLQPD NVFNSNLRLQ VLILSRNQIS FISPGAFNGL TELRELSLHT NALQDLQDNV 360
FEMLANLQNI SLQNNRLRQL PGNIPANVNG LMAIQLQNNQ LENLPLGIFD HLGKLCRLRL 420
YDNPHRCDSD ILPLRNLALL NQPRLGTDIV PVPSPANVR GQSLIINVN VAVPSVHVPE 480
VPSYPTFPY PDPSPYDPT SVSSTELTS FVEDYDILT IQVTDPRSVM GMTQAQSGLA 540
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Seq ID NO: 411 DNA sequence
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Coding sequence: 1..447

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Seq ID NO: 412 Protein sequence
Protein Accession #: XP_098151

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Seq ID NO: 413 DNA sequence
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Coding sequence: 77..1372

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Seq ID NO: 414 Protein sequence
Protein Accession #: NP_002649.1

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GSEPTTIENQ PWFRAIYRRH RGSVTVVCG GSLISPCWVI SATHCFIDYP KKEYIYVILG 240
RSRLNSNTQG EMKFEVENLI LHKDYSADTL AHINDIALLK IRSKEGRCAQ PSRTIQTICL 300
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Seq ID NO: 415 DNA sequence
Nucleic Acid Accession #: NM_024422.1
Coding sequence: 202..2907

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 ACGGAGGTGG ACAACTGCGAG ATACACTTAC TCGGAGTGGC ACAGTTTAC TCAGCCCGCT 2700
 CTGTGTGAAA AAGTGTATCT GTGTAATCAA GATGAAAATC ACAAGCATGC CCAAGACTAT 2760
 GTCTGTGACAT ATAACTATGA AGGAAGAGGA TCGGTGGCTG GGTCTGTAGG TTGTTGCAGT 2820
 GAACGACAG AAGAAGATGG GCTTGAATTT TTGGATAATT TGGAGCCCAA ATTTAGGACA 2880
 CTAGCAGAG CATGCATGAA GAGATGAGTG TGTCTAATA AGTCTCTGAA AGCCAGTGGC 2940
 TTTATGACTT TTAACAAAAA TTACAAACCA AGAATTTTIT AAAGCAGAAG ATGCTATTG 3000
 TGGGGGTTT TCTCTCATT TTTGGATGGA ATCTCTTTGG TCAATGCAC ATTTACAGAG 3060
 10 AGACACTATA AACAACTACA CAAATTTTTC AATTTTACA TATTTTAAA TTACTTATCT 3120
 TCTATCCAG GAGGTCTACA GAGAAATTA AGTCTGCCCT ATTTGTACA TTTGGGTATA 3180
 ATGACAACAG CCAATTATA GTGCAATAAA ATGTAATTA TTCAAGTCTT TATTATAGAC 3240
 TATTTGAAGC ACAACCTAAT GGAATAATGT AGAGACCTTG CTTAACATT ATCTCCAGTT 3300
 15 AATTAAAGTG TCATGTGGTG CTTGGAAACT GTTGTITTC TGAACATCTA AAGTGTGTAG 3360
 ACTGCATTCT TGCTATTATT TTATTCTTGT AATGTGACCT TTTCACTGTG CAAAGGGAGA 3420
 TTTCTAGCCA GGCATTGACT ATTACAATTT CATT

Seq ID NO: 416 Protein sequence
 Protein Accession #: NP_077740.1

20 1 11 21 31 41 51
 MEAARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLEVP SKLDAEKLVG RVNLKECFCTA 60
 ANLIHSSDPD PQILEDGSVY TINTILLSSE KRSPTILLSN TENQEKKKIP VFLEHQTKVL 120
 25 KKRHTKEKVL RRAIKRWAPI PCSMLENSLG PPFLFLQQVQ SDTAQNYTIY YSIRGPGVDQ 180
 EPRNLFYVER DTGNLYCTRP VDREQYBSFE IIAFATTPDG YTFELPLPLI IKIEDENDNY 240
 PIFTEBTYTF TIFENCVRGT TVGQVCATDK DEPTDMITRL KYSIIQVPP SPTLFMSHPT 300
 TGVITTTSSQ LDRELIDKYQ LKIKVQDMOG QYFGLQTTST CIINIDVDND HLPFTPTTSY 360
 30 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKONE NGNFKIVTDA KINRGVLCVV 420
 KPLNYEKKQQ MIIIGVUNE APPSREASPR SAMSTATVTV NVEDQDEGPE CNPPIQTVM 480
 KENAEVTKG NGYKAYDPRT RSSSGIRYKK LTDPTGWVTI DENTGSIKVF RSLDREAETI 540
 KNGIYNITVL ASDQGRSTCT GTLGIILODV NDNSPPIPKK TVIICKPTMS SAEIVAVDFD 600
 EPIHGPPDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPPGSYVVP I TVRDLGMSS 660
 35 VTSLDVTLCD CITENDCTHR VDPRIGGGGV QLQKMAILAI LLGIALLFPI LFTLVCGASG 720
 TSKQPKVIPD DLAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAGQVCG TVSGIKINGG 780
 QETIEMVKGG HQTSESCRGA GHHTLDSCR GHTEVDNCR YTYSEHNSFT QPRLGEKVYL 840
 CNQDENHKA QDYVLTYNVE GRGSVAGSVG CCSERQEBDG LEFLDNLEPK FRTLAEACMK 900
 R

40 Seq ID NO: 417 DNA sequence
 Nucleic Acid Accession #: NM_004949.1
 Coding sequence: 202..2745

45 1 11 21 31 41 51
 CGCCAAAGGA AAAGCCCTT GGATGAGAGG CAGGCGCTTC AGAGAAGCTA AGAAAAGCAC 60
 CTCTCCGGGC GCCCCACCTC CTCGCGCTCG CGCTCCTCCT GAGCAGCGGG CCCAGACTGC 120
 GCTCCGGCGC CGGCGCTCGC CCGCGGAGC CCTCCTACCC CGGCCGACG CTCGGCCCGC 180
 50 GACCTGCCCC GAGCCCTCTC CATGAGGCA GCCCGCCCT CGGCTCCTG GAACGAGAGC 240
 CTCTGCCGGC TGCTCTCTCT GACCCTCGCG ATCTTAATAT TTGCCAGTGA TGCCGTGAAA 300
 AATGTGACAT TGACGTCTCC CTCCAACTA GATGCCGAGA AACTGTGTGG TAGAGTTAAC 360
 CTGAAAGAGT GCTTTAAGC TGCAAACTCA ATTCAATCAA GTGATCTGA CTTCCAAATT 420
 TTGAGGATG GTTCAGTCTA TACAACAAAT ACTATTCTAT TGTCCTCGGA GAAGAGAAGT 480
 55 TTTACCATAT TACTTTCCAA CACTGAGAAC CAAGAAAAGA AGAAAATATT TGTCTTTTGG 540
 GAGCATCAAA CAAAGTCTCT AAAGAAAAGA CATACTAAAG AAAAAGTTCT AAGGCGCGCC 600
 AAGAGAAGAT GGGCTCCAAT TCCTGTGTCG ATGTAGAAA ACTCCTTGGG TCCTTTTCCA 660
 CTTTCTCTTC AACAGGTTCA ATCTGACACG GCCCAAACT ATACCATATA CTATTCCATA 720
 AGAGGTCTCG GAGTGTACCA AGAACCTCGG AATTATTITT ATGTGGAGAG AGACACTGGA 780
 60 AACTGTATT GTACTGCTCC GTTAGATCGT GAGCAGTATG AATCTTTTGA GATAATTGCC 840
 TTGCAACAA CTCAGATGG GTATACTCCA GAACCTCCAC TGCCCTCAAT AATCAAAATA 900
 GAGGATGAAA ATGATAACTA CCCAATTTT ACAGAAGAAA CTTATACTTT TACAATTTT 960
 GAAAATTGCA GAGTGGGCAC TACTGTGGGA CAAGTGTGTG CTACTGACAA AGATGAGCCT 1020
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 65 CTATTTTCTA TGATCCCAAC TACAGGCGTG ATCACCACAA CATCATCTCA GCTAGACAGA 1140
 GAGTTAATTG ACAGTACCA GTTGAAAATA AAAGTACAAG ACATGATGGG TCAGTATTTT 1200
 GGTCTACAGA CAACCTCAAC TTGTATCATT AACATTGATG ATGTAAATGA CCACTTGCCA 1260
 ACATTTACTC GTACTTCTTA TGTGACATCA GTGGAAGAAA ATACAGTTGA TGTGGAATC 1320
 TTACGAGTTA CTGTTGAGGA TAAGGACTTA GTGAATACTG CTAAGTGGAG AGCTAATTAT 1380
 70 ACCATTTTAA AGGGCAATGA AAATGGCAAT TTTAAATTG TAACAGATGC CAAAACCAAT 1440
 GAAGGAGTTC TTTGTGTAGT TAAGCCTTTG AATTATGAAG AAAAGCAACA GATGATCTTG 1500
 CAAATTTGGT TAGTTAATGA AGCTCCATT TCCAGAGAGG CTAGTCCAAG ATCAGCCATG 1560
 AGCACAGCAA CAGTTACTGT TAATGTAGAA GATCAGGATG AGGGCCCTGA GTGTAACCTT 1620
 CCAATACAGA CTGTTGCGAT GAAAGAAAAT GCAGAAGTGG GAACAACAAG CAATGGATAT 1680
 75 AAAGCATATG ACCCAGAAAC AAGAAGTAGC AGTGGCATAA GGTATAAGAA ATTAAGTAT 1740
 CCAACAGGGT GGGTCACCAT TGATGAAAAT ACAGGATCAA TCAAGTTTT CAGAAGCCTG 1800
 GATAGAGAGG CAGAGACCAT CAAAAATGGC ATATATAATA TTACAGTCTT TGCATCAGAC 1860
 CAAGGAGGGA GAACATGTAC GGGGACACTG GGCATTATAC TTCAAGAGCT GAATGATAAC 1920
 AGCCCATCTA TACCTAAAAA GACAGTGATC ATCTGCAAAC CCACCATGTC ATCTGCGGAG 1980
 80 ATGTTGCGG TTGATCTCTG TGAGCCTATC CATGGCCAC CCTTTGACTT TAGTCTGGAG 2040
 AGTTCTACTT CAGAAGTACA GAGAATGTGG AGACTGAAAG CAAATTAATGA TACAGCAGCA 2100
 CGTCTTCTCT ATCAGAATGA TCCTCCATT GGCTCATATG TAGTACCTAT AACAGTGA 2160
 GATAGACTTG GCATGTCTAG TGTCACTTCA TTGGATGTTA CACTGTGTGA CTGCATTACC 2220
 GAAAATGACT GCACACATCG TGTAGATCCA AGGATTGGCG GTGGAGGAGT ACAACTTGA 2280
 AAGTGGGCCA TCCTTGCAAT ATTGTTGGC ATAGCAATTG TCTTTTGAT CCGTTTACG 2340

5 CTGGTCTGTG GGGCTTCTGG GACGTCTAAA CAACCAAAAG TAATTCCTGA TGATTAGGCC 2400
 CAGCAGAACC TAATTGTATC AAACACAGAA GCTCCTGGAG ATGACAAAGT GTATTCTGGG 2460
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 10 TCGGAATCCT GCGCGGGGGC TGGCCACCAT CACACCTGG ACTCCTGCAG GGGAGGACAC 2640
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 CTTGGTGAAG AATCCATTAG AGGACACACT CTGATTAAAA ATTAACAAT GAAAGAAAGT 2760
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 CTATGAAGGA AGAGGATCGG TGGCTGGGTC TGTAGGTGTG TGCAGTGAAC GACAAGAAGA 2880
 AGATGGGCTT GAATTTTGG ATAATTGGA GCCCAAAATT AGGACACTAG CAGAAGCATG 2940
 CATGAAGAGA TGAGTGTGTT CTAATAAGTC TCTGAAAGCC AGTGGCTTTA TGACTTTTAA 3000
 AAAAAATTAC AAACCAAGAA TTTTAAAG CAGAAGATGC TATTTGTGGG GGTTTTCTC 3060
 TCATTATTGG GATGGAATCT CTTTGGTCAA ATGCACATT ACAGAGAGAC ACTATAAACA 3120
 15 AGTACACAAA TTTTCAATT TTTACATATT TTTAAATTAC TTATCTCTA TCCAAGGAGG 3180
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 TTTATAGTGC AATAAAATGT AATTAATTCA AGTCCTTATT ATAGACTATT TSAAGCACAA 3300
 CCTAATGGAA AATTGTAGAG ACCTTGCTTT AACATTATCT CCAGTTAATT AAGTGTTCAT 3360
 GTGGTGCTTG GAAACTGTGG TTTTCTGAA CATCTAAAGT GTGTAGACTG CATTCTTGCT 3420
 20 ATTATTTTAT TCTGTAAAG TGACCTTTTC ACTGTGCAAA GGGAGATTTC TAGCCAGGCA 3480
 TTGACTATTA CAATTCATT

Seq ID NO: 418 Protein sequence
 Protein Accession #: NP_004940.1

25 1 11 21 31 41 51
 MEARPSGSW NGALCRLLLL TLAILIFASD ACKNVTLHVP SKLDASKLVG RVNLKECPTA 60
 ANLIHSSDPD FQILEDGSVY TINTILLSSE KRSPTILLSN TENQEKKKIF VFLEHQTKVL 120
 30 KKRHTKEKVL RRAKRRWAPI PCSMLENSLG PFPLFLQQVQ SDTAQNYTII YSIRGPGVDQ 180
 EPRNLVFER DTGNLYCTRP VDREQYESFE ILAPATTPDG YTEPLPLPLI IKIEDENDNY 240
 PIPTEETYP TIFENCVRGT TVGQVCATDK DEPDIMHTRL KYSIIGQVPP SPTLFSMHPT 300
 TGVITTTSSQ LDRBLIDKYG LKIKVQDMDG QYFGLQTTST CIINIDDVND HLPTPTRTSY 360
 VTSVEENTVD VEILRVTVED KDLVNTANWR ANYTILKGNB NGNFKIVTDA KTNBGLVLCV 420
 35 KPLNYEEKQ MILQIGVNE APFSREASPR SAMSTATTV NVBDQDEGPE CNPPIQTVRM 480
 KENAEVGTTS NQYKAYDPET RSSSGIRYKK LTDPTGWTI DENTGSIKVF RSLDREASTI 540
 KNGIYNITVL ASDQGGRTCT GTLGIILQDV NDNSPFIPKK TVIICKPTMS SAEIVAVDFD 600
 EPIHGPPDF SLESSTSEVQ RMWRLKAIND TAARLSYQND PPFSGYVVPV TVRDLGMSS 660
 VTSLDVTLCD CITENDCTHR VDPRIGGGGV QLGKWLAI LGLIALLPCI LPTLVCGASG 720
 40 TSKQPKVIPD DIAQNLIVS NTEAPGDDKV YSANGFTTQT VGASAQGVCG TVSGGIKNGG 780
 QETIEMVKGQ HQTSESCRGA GHHTLDSCR GHTEVDNCR YTYSEHNSPT QPRLGESIR 840
 GHTLLKN

Seq ID NO: 419 DNA sequence
 Nucleic Acid Accession #: NM_002722.1
 Coding sequence: 14..301

45 1 11 21 31 41 51
 ACTCTGGACT CCGGATGGCT GCGGCACGCC TCTGCCTCTC CTGCTGCTC CTGTCCACCT 60
 50 GGGTGGCTCT GTTACTACAG CCACTGCTGG GTGCCAGGG AGCCCACTG GAGCCAGTGT 120
 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCACGTA TGCAGCTGAT CTCCTAGAT 180
 ACATCAACAT GCTGACCAAG CCTAGGTATG GGAAAAGACA CAAAGAGGAC ACGCTGGCCT 240
 TCTCGGAGTG GGGGTCCCG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300
 55 AATGCCACT CTGTCTCTCT ACGACTCCAT GAGCAGCGCC AGCCCACTC TCCCTCTGC 360
 ACCCTTGGCT CTGGCCAAAG CTGTCTCCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420
 AAGCC

Seq ID NO: 420 Protein sequence
 Protein Accession #: NP_002713.1

60 1 11 21 31 41 51
 MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPQMAQYA ADLRRYINML 60
 65 TRPRYGRHK EDLAFSEWG SPHAAPREL SPLDL

Seq ID NO: 421 DNA sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 46..718

70 1 11 21 31 41 51
 AAATGATCT TCAATGCAT AAGAGAAGGA GACTCTCAA CCAAAAATGA CTTGGAGGCA 60
 CCATGTCAGG CTCTCTGTTA CGGTCACTTT GGCATTACAG ATCATCAATT TGGGAAACAG 120
 75 CTATCAAGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGTTG CCACTCAGAA 180
 GCACCGACAG TCACCGCTCA ACTGACCTC CAGTCAATTC GAGAGAGTGA CTGGAGCGC 240
 CGAGGGCTGG GGGCGGAGG AGCGCTCCC CTACTCCCG GCTTTCGGAG AGGGTGCCTG 300
 OGCGCGCCG CGCTGCTGCA GGAACGGCGG TACCTGGGTG CTGGCGAGCT TCTGGGTGTG 360
 CCGGGCCCA TACACCGGCC GCTACTGCGA GCATGACCA AGGCGCAGTG AATGCGGCGC 420
 80 CCTGGAGCAC GAGGCTGGGA CCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTCGGGGC 480
 CCTGCACTGC CTCCCCCTCC AGACGCTGA CCGCTGTGAC CCGAAAGACT TCCTGGCCTC 540
 CCACGCTCAC GGGCGAGCG CGGGGGGCGC GCCAGGCTG CTACTCTTGC TGCCCTGGCG 600
 ACTCCTGCAC GCGCTCTGCG GCCCGGATGC GCCCGGCGAC CCTCGGTCCT TGTCTCCCTC 660
 CGTCTCCAG CGGAGCGCGC GCCCTGCGG AAGGCGGGA CTTGGGCATC GCCTTTAATT 720
 TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780

TTTTTATTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
AAAAAA

5 Seq ID NO: 422 Protein sequence
Protein Accession #: NP_115934.1

1 11 21 31 41 51
10 MTWRHVRLL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRQSP LNWTSSEHGE 60
VTGSAEAGWGP EEPLPYSRAP GEGASARPRC CRNGGTCTVLG SFCVCPAHT GRYCEHDQRR 120
SBCGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAHGP SAGGAPSLLL 180
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRPCGRPLGL HRL

15 Seq ID NO: 423 DNA sequence
Nucleic Acid Accession #: NM_006533.1
Coding sequence: 72..467

1 11 21 31 41 51
20 AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60
CACAGTCCAC GATGCCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGCTCGCCT 120
TCTCCGGACC TGGTGTTCAG GGTGGTCCCTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
CGACTGCGG ATTCCCTGACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
25 AGGGCCGTGG GCGGCTCTTC TGGGAGGACA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360
CTGCTCGCCT GGGCTATTTC CCCAGTAGCA TTGTCCGAGA GGACCAGACC CTGAACCTG 420
GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCACTGAGCT CAGCCTACCG 480
CTGGCCCTGC CGTTTCCCTC CTCTGGGTTT ATGCAATAC AATCAGCCCA GTGCAAAC

30 Seq ID NO: 424 Protein sequence
Protein Accession #: NP_006524.1

1 11 21 31 41 51
35 MARSLVCLGV IILLSAFSGP GVRGQPHPKL ADRKLCADQE CSHPISMAVA LDYMAPDCR 60
FLTIHRQVQV YVPSKLGKRG RLFWGGSVQG DYVGDLAARL GYFPSSIVRE DQTLKPGKVD 120
VKTDKWDFFC Q

40 Seq ID NO: 425 DNA sequence
Nucleic Acid Accession #: NM_080870.1
Coding sequence: 3..710

1 11 21 31 41 51
45 AGATGACACA AGTCACAGAA AAGTCCACAG AACACCCAGA AAAGACCACG TCAACCACAG 60
AGAAAAACCA AAGAACCCCA GAAAAGCCTA CGCTATATCT AGAGAAGACC ATATGCACCA 120
AAGGGAAAAA CACACCAATC CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCCACTGA 180
CCACTGAGAC CATAAAAGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240
TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300
50 CTCTCATCT AAATAAAACT GAAGTTACTC ATCAGGTGCC CACTGGTCTT TTCAACCTCA 360
TTACATCTAG AACGAAGCTG AGTTCTATCA CATCAGAGC CACAGGAAC GAGAGCCATC 420
CATACCTCAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GGAGAGAATG 480
ATTCAATCCC TGCAATGGGC ATAGTTATTG TGGTCTCTGT GGTCTGTATT CTCTCTCTGG 540
55 TGTCTCTTGG CCGTATCTTC TTGGTCTCCT ATATGATGCG GACACGCGCG ACCTAACCCT 600
AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAATTCCTAC CCGGTCTACC 660
TGATGGAGCA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA 720
GGGCGCCAGC CCTGGCTCTT CCATGCTCTG CCCCCTTCTC GATGAGGAAA CCGGACTCAC 780
AATTTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAAAC 840
60 CTTCATCTGT TCTTGAACCT GTTGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT 900
AGGGGACAAA GAAGAAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT 960
CTGAGAAATGA AAGGTGTGTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020
TGAGTCTCTAA AGGAAGGACA GGAGCCTTAT AGGCAATGCC CCAGACTGAC TTGTGAGTGG 1080
GGTTTATGGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140
65 TTATTTCCAT TCACTATTAC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTTCTC 1200
AGGACCCCTG CCCCCACCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AAACGGATCC 1260
AAGAAGAAAA GAGAAATTTAT TTCTTTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320
CCAGAAGAAA TCATAAATAT CTCTCATCTA CATGGTTGCT TCCTCTTCTC CCCAAATCCC 1380
TTAGTTTCCC TAAATGTCTA CAGTGGAGCG CCTGTGGTGT TGGCTTGCTG GGTGTGGGT 1440
70 GGACACGCAA GGAGGGGATT TTTATTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500
GACCTTCCCT GATTGGTGTG TCAGCATTTA TTTTCTGTCT TCTTCCACCA AAAGCCAGCT 1560
GTAGCTTTAT CTCGTAAAAG TTACCCATCT TCTCTACTGT CCCCATCTCT TCTCTCTCCA 1620
CCTTCAACCC AGATTCAAGT TTTCTCTCTT GTAGGCATTT CATCTGTGTG TGTTTTCTGG 1680
ATTTCTCTCT TCTCTCTCTA TGGCCATTTC ACCTTATTAC TGATTGGGTA GAGGGGGAAA 1740
75 AGGAGAAATGA TGATGATAGT TTCCTTCTGT CTATTGACCT TTTTATAAT AAAGTATAAC 1800
ATGTT

Seq ID NO: 426 Protein sequence
Protein Accession #: NP_543146.1

80 1 11 21 31 41 51
MTQVTEKSTE HPEKTTSTTE KTRTPKPKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60
TEIKAPVKV TENPEKTAIV TKTIKPSVKV TGDKSLITTS SHLNKTEVTH QVPTGSFTLI 120
TSRTKLSSIT SEATGNESH P YLNKDGSKG IHAGQMGEND SPPAWAIVIV VLVAIVILLV 180

PLGLIPLVSY MMRTRRLTQ NTQYNDAEDS GSPNSYPVYL MEQQNLGNGQ IPSPR

Seq ID NO: 427 DNA sequence
Nucleic Acid Accession #: XM_069480.1
Coding sequence: 1..4383

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1 11 21 31 41 51

ATGGACACTG TGCTGGTGCT GCTCCTGGGC CTGCAGGCTT TGGCCGGACC CAGTCCGAAG 60
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GCAATTGTCA GCCTAATGTA CGGTATCAAG AAGGCTGCC AGTTCGGAG GGAGATGAGT 180
CTGGGGTGTG GCTGTGGCTC TGTGACCCCT TACAGCAGCC ACCATGAGGG GGAGGCTGCC 240
AGCCAGCGCT ACTCTGTCA AATGAAAGCT TCTTGGGGGG CAGGTGTCTAC TACATTCCAA 300
GAATATCAGA AAAGTGGGA ACTCTCAACA TCGATCACA TATTTCCCT CACTCCAGGC 360
CTTGTATTATA GTATCCCTTT TGATCACAAT GTTCTGCATT CAGGACAAAG ACCTCCAGAG 420
CTCCCTAAAT CTACAGAAAT CCATGAGCAA AAACGCCACT GCAACACCAC ACGCATTCT 480
AAGCCAACCT ACAAGCCTAC AGGCAACTCC AAAACTATAG ACCACAAAAG CTCTACAGAT 540
AATCATGAGG CTCTCCCCAC TTCTGAAGAA AACTCCAGCA ACCAAGGGAA AGACCCAAATG 600
ATCCGGAACC AGCGCTCTGT TGATCCTGCT GACTCCACTA CCACACATAA AGAATCCGCT 660
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GGCAATCAA CGGTAAACAG AAAATCAGAT AAACTGGAA GACCTTTGGA AAAGTCCATG 780
AGTACTTTGG ATAAGACAAG TACCAGCTCA CATAAGACTA CAACTTCTCT CCACAACTCA 840
GGCAATTAC AGACCAAGCA AAAAGACACA TCTTTTCCAG AAAAATACAC AGCAGCCTCA 900
AAAAACAAC CATTCCGAG AGGAACCCCA GAAGAGTCAG AAAAAGTCA AGATTCCAGA 960
ACAACAGTTG CCTCAGACAA GCTCCTGACA AAACTACAA AAAACATACA AGAGACCATA 1020
TCAGCAATG AGCTCAGACA ATCTCTAGCA GAGCCTACAG AACATGGAGG AAGGACAGCC 1080
AATGAGAAAC ACACACCATC CCCAGCAGAG CCTACAGAAA ATAGAGAAAG GACAGCCAAT 1140
GAGAACAACA CACTATCCCC AGCAGAGCCT ACAGAAAATA GAGAAAGGAC AGCCAAATGAG 1200
AACACGACAC CATTCCGAG AGGCGCTACA GAAAATAGAG AAATGACAGC CAATGAGAAT 1260
ACCACACTAT TCCAGCAGA GCCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAACACC 1320
ACACCATCCC CAGCAGAGCC TACAGAACAT GCAGAAAGGA CAGCCAATGA GAACACTACA 1380
CCATCCCCAG CAGAGCCTAC AGAACATGGA GAAAGGACCC CATTTGCCAA TGACAAAACC 1440
ACATCATCCT CAGCAGAGTC TACAGAACAT GGAGAAAGGA CCCCCTGGC CAAAGAGAAC 1500
ACCACACAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA GGACAGCCAA TGAGAACACC 1560
ACACCATCCC CAGCAGGCC TACAGAAAAC AGAGAAACGA CAGCAAACGA GAAGAACACA 1620
CTATCCCCAG TAGAGCCTAC AGAAAATAGA GAAACAACAG CCAATGAGAA GACCAACCA 1680
TCCCCAGCAG AGCCTACAGA AAATGGACAA AGGACCCCAT TTGCCAATGA GAAAACACA 1740
TCATCCTCAG CAGAGCCTAC AGAACACGGA GAAAGGACCC CACTGGCCAA TGAGAACACC 1800
ACACCATCCC CCCCAGCAGA TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAAGAACACA 1860
CCATCCCCAG CAGAGCCTAC AGAAAATGGA GACAGGACTC CTTTGGCCAA TGAGAACACC 1920
AAGCCATCTC TAGCAGAGCC TACAGAAAAT GGACAAAGGA CCCCATTTCG CAATGAGAAG 1980
ACCACATCAT CCTCAGCAGA GCCTACAGAA CACGAAAGAA GGACTCCACT GGCCAATGAG 2040
AACACCAAC CACTCCCGGC AGAGCCTACA GAAAATAGAG AAAGGACAGC CAATGAGAAC 2100
ACCACACAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA TGACAGCCAA CGAGAACACC 2160
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TCATCCCCAG CAGAGCCTAC AGAAAATGGA CAAAGGACCC CATTTGCCAA TGAGAAAACC 2280
ACATCATCCC CAGCAGAGCC TACAGAACAC GGAGAAAGGA CCCCCTGGC CAATGAGAAC 2340
ACCACATCAT CCCCAGCAGA GCCTACAGAA AATAGAGAAA GGACAGCCAA TGAGAACACC 2400
ACACCATCCC CAGCAGAGCC TACAGAAAAT AGAGAAAGGA CAGCCAATGA GAACACCA 2460
CCATCCCCAG CACAGCCTAC AGAAAATGGA GACAGGACTC CATTGGCCAA TGAGAACACC 2520
ACACCATCTC TAGCAGAGCC TACAGAAAAT GGAAAAGGA CCCCATTTCG CAATGAGAAG 2580
AGCACAATCC CCTCAGCAGA GCCTACAGAA CACGAGAAA GGACTCCACT GGCCAATGAG 2640
AACACCAAT CACTCCCGC AGAGCCTACA GAAAATAGAG AAAGGACAGC CAATGAGAAG 2700
ACCACAAAT TCCAGCAGA GCCTACAGAA AATAGAGAAA GCACAGCCAA TGAGAACACC 2760
ACACCATCCC CAGCAGAGCC TACAGAAAAT AGAGAAATGGA CAGCCAATGA GAACACCA 2820
CTATCCCCAG CAGAGCCTAC AGAACATGAA GAAATGACCC CATTGGCCAA TGAGAACACC 2880
ACACTATCCC CAGCAGAGCC TACAGAAAAT GGAGAAAGGA CCCCATTTCG CAATGAGAAG 2940
ACCACACCAT CCTCAGCAGA GCCTACAGAA CATGGAGAAA GGACCCCTCT GGCCAATGAG 3000
ATCACCAAC CATCCCGAGC AGAGCCTACA GAACATGGAG AAAGGATAGC CAATGAGAAG 3060
GCCACACCAT CCCCAGCAAA GCCTACAGAA CATGGAGAAA CGACAGTCAA TGAGAACACC 3120
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ACCACAACAT CCCCAGCAGA GTCTACAGAA CATGGAGAAA GGACAGCCAA TGAGAACACC 3240
ACACCATCCC CAGCAGAGCC TACAGAACAT GGAGAAAGGA CACCATCAGC CAATGAGAAG 3300
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Seq ID NO: 428 Protein sequence
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Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..390

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40 CAGTGTCTGT ACAATGACGC CATGCTGTCC CTGAGCGAGA CCCGCCAATG TGGTCCCCCC 240
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45 Seq ID NO: 432 Protein sequence
Protein Accession #: FGENESH predicted

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SKCERGRIC

55 Seq ID NO: 433 DNA sequence
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Coding sequence: 89..2017

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Seq ID NO: 434 Protein sequence
Protein Accession #: NP_009162.1

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Nucleic Acid Accession #: M18728.1
Coding sequence: 51..1085

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 AACAAAGATC CTCATCATGA TAAAGGCTCTT ACCCCCTTTT AATTTGTCTT TGCTTATGCC 1440
 TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
 GGGTAACCTA ACAGAGTGTC AGATCTATCT GTCAATCCC AACGTTTAC ATAAAAAAG 1560
 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTAAACACAG CCGTGTGTTC 1620
 AAATGTACAG TGGTCTTTT CAGAGTTGGA CTCTAGACT CACCTGTCTT CACTCCCTGT 1680
 TTTAATTCAA CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGACACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAATAGG CTACACTCAT 1860

5 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCTCCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAAGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACGTAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 10 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCA TGTATTTATT TCTGTGGTTC 2400
 TGTTTCTTGG TTCCAATTTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
 CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

15 Seq ID NO: 438 Protein sequence
 Protein Accession #: AAA59908.1

1 11 21 31 41 51
 20 MDSPSQDVKT RLLIMIRLLP PFNLSLLMPA SFANQDDAVI SISQEVASEG NLTECQIYLV 60
 NPNVLHKIRD PLVHPVTDIS SIFNTAVCSN VQWSFSELD

25 Seq ID NO: 439 DNA sequence
 Nucleic Acid Accession #: M18728.1
 Coding sequence: 2370..2501

1 11 21 31 41 51
 30 GGAGCTCAAG CTCCTCTACA AAGAGGTGGA CAGAGAAGAC AGCAGAGACC ATGGGACCCC 60
 CCTCAGCCCC TCCCTGCAGA TTGCATGTCC CCTGGAAGGA GGTCTGTCTC ACAGCCTCAC 120
 TTCTAACCTT CTGGAACCCA CCCACCCTG CCAAGCTCAC TATTGAATCC ACGCCATTCA 180
 ATGTGCGAGA GGGGAAGGAG GTTCTTTCTAC TCGCCCAACA CCTGCCCCAG AATCGTATTG 240
 GTTACAGCTG GTACAAAGGC GAAAGAGTGG ATGGCAACAG TCTAATTGTA GGATATGTAA 300
 TAGGAACCTA ACAAGCTACC CCAGGCCCCG CATAAGTGG TOGAGAGACA ATATACCCCA 360
 35 ATGCATCCCT GCTGATCCAG AACGTCAACC AGAATGACAC AGGATTCTAT ACCCTACRAG 420
 TCATAAAGTC AGATCTTGTG AATGAAGAAG CAACCGGACA GTTCCATGTA TACCCGGAGC 480
 TGCCCAAGCC CTCCATCTCC AGCAACCACT CCAACCCCGT GGAGGACAAG GATGCTGTGG 540
 CCTTCACTGT TGAACCTGAG GTTCAGAAC CAACCTACCT GTGGTGGGTA AATGGTCAGA 600
 GCCTCCCGGT CAGTCCGAGG CTGCAGCTGT CCAATGGCAA CATGACCCCT ACTCTACTCA 660
 40 GCGTCAAAAG GAACGATGCA GGATCCTATG AATGTGAAT ACAGAACCCA GCGAGTGCCA 720
 ACCGCACTGA CCCAGTCACC CTGAATGTCC TCTATGGCCC AGATGTCCCC ACCATTTCCT 780
 CCTCAAGGC CAATTACCGT CCAGGGGAAA ATCTGAACCT CTCTGCCACG GCAGCCTCTA 840
 ACCCACTCCA ACAGTACTCT TGGTTTATCA ATGGGACGTT CCAGCAATCC ACACAAGAGC 900
 TCTTTATCCC CAACATCACT GTGAATAATA GCGGATCCTA TATGTGCCAA GCCCAACT 960
 45 CAGCCACTGG CCTCAATAGG ACCACAGTCA CGATGATCAC AGTCTCTGGA AGTGCTCTG 1020
 TCCTTCTCAG TGTGGCCACC GTGCGCATCA CGATTGGAGT GCTGGCCAGG GTGGCTCTGA 1080
 TATAGCAGCC CTGGTGTATT TTGATATTT CAGGAAGACT GGCAGATTGG ACCAGACCCT 1140
 GAATTTCTCT AGCTCTCTCA ATCCCATTTT ATCCCATGGA ACCACTAAAA ACAAGGTCTG 1200
 CTCTGCTCCT GAAGCCCTAT ATGCTGGAGA TGGACAACTC AATGAAAAAT TAAAGGGAAA 1260
 50 ACCCTCAGGC CTGAGGTGTG TGCCACTCAG AGACTTCACC TAACTAGAGA CAGTCAAACT 1320
 GCAACCACTG GTGAGAAATT GACGACTTCA CACTATGGAC AGCTTTTCCC AAGATGTCAA 1380
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 TGCTCTTTTC GCTTGGCAGG ATGATGCTGT CATTAGTATT TCACAAGAAG TAGCTTCAGA 1500
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 55 AGATCCTTTA GTGCACCCAG TGACTGACAT TAGCAGCATC TTTAACACAG CGGTGTGTTT 1620
 AAATGTACAG TGGTCTCTTT CAGAGTTGGA CTCTAGACT CACCTGTTCT CACTCCCTGT 1680
 TTTAATTCAG CCCAGCCATG CAATGCCAAA TAATAGAATT GCTCCCTACC AGCTGAACAG 1740
 GGAGGAGTCT GTGCAGTTTC TGCACTTGT TGTGAACAT GGCTAAATAC AATGGGTATC 1800
 GCTGAGACTA AGTTGTAGAA ATTAACAAAT GTGCTGCTTG GTTAAAAATG CTACACTCAT 1860
 60 CTGACTCATT CTTTATTCTA TTTTAGTTGG TTTGTATCTT GCCTAAGGTG CGTAGTCCAA 1920
 CTCTTGGTAT TACCTCCTTA ATAGTCATAC TAGTAGTCAT ACTCCCTGGT GTAGTGTATT 1980
 CTCTAAAAGC TTTAAATGTC TGCAATGCAGC CAGCCATCAA ATAGTGAATG GTCTCTCTTT 2040
 GGCTGGAATT ACAAAACCTCA GAGAAATGTG TCATCAGGAG AACATCATAA CCCATGAAGG 2100
 ATAAAAGCCC CAAATGGTGG TAACTGATAA TAGCACTAAT GCTTTAAGAT TTGGTCACAC 2160
 65 TCTCACCTAG GTGAGCGCAT TGAGCCAGTG GTGCTAAATG CTACATACTC CAACGTAAAT 2220
 GTTAAGGAAG AAGATAGATC CAATTAAAAA AAATTAAAC CAATTAAAAA AAAAAAAGA 2280
 ACACAGGAGA TTCCAGTCTA CTTGAGTTAG CATAATACAG AAGTCCCTC TACTTTAACT 2340
 TTTACAAAAA AGTAACCTGA ACTAATCTGA TGTAAACCA TGTATTTATT TCTGTGGTTC 2400
 TGTTTCTTGG TTCCAATTTG ACAAACCCA CTGTTCTTGT ATTGTATTGC CCAGGGGGAG 2460
 70 CTATCACTGT ACTGTAGAG TGGTGTGCT TTAATTCATA AATCACAAAT AAAAGCCAAT 2520
 TAGCTCTATA ACT

75 Seq ID NO: 440 Protein sequence
 Protein Accession #: AAA59909.1

1 11 21 31 41 51
 80 MLTNVPIISV LPPCSNLTKP TVLVLYCPGG AITVLVEWCC FNS

Seq ID NO: 441 DNA sequence
 Nucleic Acid Accession #: NM_002381.2
 Coding sequence: 64..1524

1 11 21 31 41 51

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5	CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG	180
	GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCCGCCCTT	CTCCTGCGCG	TCCCGACGGC	240
	GGCGCCGCTT	CGGGAGCCAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC	300
	AGACCCCTTG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GGTACGGCC	CCTGGAATTC	360
	ACCAAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC	420
10	AGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TGGAGTTCCA	ACTCCAGGCC	480
	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGAA	TACACCCCTT	GTCAACAGGC	540
	ACCATGTCAG	GCTAGCCAT	CCAGACAGCA	ATGGACGAAG	CCTTCACAGT	GGAGGCAGGG	600
	GCTGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTACAGA	TGGGAGGCC	660
	CAGGACCAGC	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT	720
15	GTGGGCGTGG	ACCGGGCAGA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTAGAG	780
	GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCTTGAAGA	AACTTTCTCT	TAGATTCCAG	840
	GAAACCTCTT	GTGGCGTGG	CCCTCTGTGT	CTTGGAAAC	ACCAAGTGCA	GCAAGCTGCG	900
	ATCAGTGATG	GGGAAGGCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC	960
20	GACAAGAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC	1020
	ATCTGTGTGA	ATGACAGAA	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG	1080
	AATGAAGACA	GGAAAACCTG	TTCACTGCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT	1140
	CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCATCATT	GTGAATGCTA	TGAGGGCTAC	1200
	ACTCTGAATG	CAGATAAAAA	AAATGTTTCA	GTCCGTGACA	AGTGTGCCCT	AGGCTCTCAT	1260
25	GGTTGCCAGC	ACATTTGTGT	GAGTGTGTTG	GCGCATCCT	ACCACTGTGA	TTGCTATCCT	1320
	GGCTACACCT	TAAATGAGGA	CAAGAAAACA	TGTTCAAGCA	CTGAGGAAGC	ACGAAGACTT	1380
	GTTTCCACTG	AAAGTGTCTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTGAGC	1440
	TGATATCTTC	AAAGACTGAA	CACATAAATT	GATGACATT	TGGAGAAAGT	GAAATAAAT	1500
	GAATATGAGC	AAATACATCG	TTAAATGTCT	CCAATTTCTC	ACCTGAAAT	GTGGACAGCT	1560
	TGGTGCATCT	AATATCTAGT	CATTCTTTTG	CACACTGTT	ATTGCCAATG	TTCTGCTAA	1620
30	TAAATTGCCA	TTATCTGAT	TAATGCTTGA	ATATTACTGG	ATAAATTGTA	TGAAGATCTT	1680
	CTGCAGATTC	AGCATGATTT	TTCCAAAGAA	ATACATATGC	AGATACTTAT	TAAGAGCAAA	1740
	CTTTAGTCTC	TCTAAGTTGA	GACTGTGAAA	TGATTGGTAG	GAAATAGAA	GAAAGATTTA	1800
	GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AAATTTTAAA	TGTTTATATT	AGATAACCAT	1860
	ATTCACAATG	GAAACTTTAG	GTCTAGTTTC	TTTTGATAGT	ATTATAATA	TAAATCAATC	1920
35	TTATTACTGA	GAGTGCAAT	TGTACAAGGT	ATTTACACAT	ACAACCTCAT	ATAACTGAGA	1980
	TGAATGTAA	TTTGAACGT	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGATTAA	2040
	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG	2100
	TGAACATTAC	ATTCGCATTT	TTAATTCATT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG	2160
40	AGCACTAGTT	GTGAATTTAG	GGTGTTAAAC	TTTTTACCAA	GTACAAAAT	CCCAATTTCA	2220
	CTTTATTATT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATAAA	ATTGCTATAA	2280
	ATCGACAAA	TCTAATGTTG	TCTTTTTAAT	GTGATGATC	CACCTGCCCT	AGCCTCCCAA	2340
	ATGCTGGGA	TACAGGCTT	GAAAGTCTAA	CTTTTTTTTA	CTTATATATT	TGATACATAT	2400
	AATTTCTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCTCTTA	AATTTTGCAC	2460
45	TGCTCAATTC	TGTTTTTGTG	TTGCAATGTC	TTTAATATAA	TAAAGTTAT	TACCTTTACA	2520
	TATTATCATG	TCTATTTTGG	ATGACTCATC	AATTTTGTCT	ATTAAGATA	TTTCTTTAAA	2580
	TTAAAAAAA	AAAAAAA					

Seq ID NO: 442 Protein sequence
Protein Accession #: NP_002372.1

50	1	11	21	31	41	51	
	MPRPAPARRL	PGLLLLLLWPL	LLLPSAAPP	VARPGFRRL	TRPGGSPGR	RPSFAAPDGA	60
	PASOTSEPR	ARGAVCKSR	PLDLVFIIDS	SRSVRPLSPT	KVKTFVSRII	DTLDIGPADT	120
55	RVAVVNYAST	VKIEPQLQAV	TDKSLKQAV	GRITPLSTGT	MSGLAIQTAM	DEAPTVBAGA	180
	REPSSNIPKV	AIIVTDGRPQ	DQVNEVAAA	QASGIELYAV	GVDRADMAEL	KMMASEPLEE	240
	HVFYVETVYG	IEKLSRFPQE	TFCALDPCVL	GTHQCQHVCI	SDGEGKHCE	CSQGYTLNAD	300
	KKTCSALDRC	ALNTHGCEHI	CVNDRSGSYH	CECYEGYTLN	EDRKTCSAGD	KCALGTHGCO	360
	HICVNDRTGS	HHCECYEGYT	LNADKKTCSV	RDKCALGSHG	CQHICVSDGA	ASYHCDCYPG	420
60	YTLNEDKKTIC	SATEARRLV	STEDACGCEA	TLAPQDKVSS	YLQRLNTKLD	DILEKLINE	480
	YQGIHR						

Seq ID NO: 443 DNA sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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	GCGGGGGGGG	CAGACAGCGG	CGGGGCGAGG	ACGTGCACTA	TGGCTCGGGG	CTGCTGCGGC	60
	CGGTTGCTGC	GGCTCTCTGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCCGGG	120
70	GAGCAAGCGC	CAGGCACCGC	CCCTGCTCC	CGCGGACGCT	CCTGGAGCGC	GGACCTGGAC	180
	AAGTGCATGG	ACTGCGCGTC	TTGCAGGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC	240
	GCTGCAGCAC	CTCCTGCCCC	CTTCCGCGTG	CITTTGCCCA	TCCTTGGGGG	CGCTCTGAGC	300
	CTGACCTTGG	TGCTGGGGCT	GCTTTCTGGC	TTTTTGGTCT	GGAGACGATG	CCGACGGAGA	360
	GAGAAGTTCA	CCACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCACG	TGTGGCGCTG	420
75	ATCCAGTGAC	AATGTGCCCC	CTGCCAGCGG	GGGCTCGCCC	ACTCATCATT	CATTATCCCA	480
	TTCTAGAGCC	AGTCTCTGCC	TCCAGACGCG	GGCGGAGGCC	AAGCTCTCTC	AACCAAGG	540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTACGGG	GAACCTTCCA	600
	AGGTGTCTGG	TTGCCCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC	660
80	ACAAACACAG	TGACACTGAC	TAAGGAAGTG	CAGCATTTGC	ACAGGGGAGG	GGGGTCCCTC	720
	CCTTCCCTAG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGCGA	GACTTGACAC	TAGGCCCCAC	780
	TCACTCAGAT	GCTCTGAAAT	TCCACCAAGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT	840
	TTAACACTAG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCACTC	900
	CCCAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT	960

AATAAAGAA TCTTTAACTT TAAAAAATAA AAAAAA

Seq ID NO: 444 Protein sequence
 Protein Accession #: NP_057723.1

5
 10
 11 21 31 41 51
 MARGSLRRL RLLVLGLWLA LRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
 SDPCLGCAAA PPAPFRLLWP ILGGALSLTF VLGLLSGFLV WRCRRRREKP TPIETGGGE 120
 GCPAVALIQ

Seq ID NO: 445 DNA sequence
 Nucleic Acid Accession #: AF322916.1
 Coding sequence: 50..4300

15
 20
 25
 30
 35
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 45
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 55
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 1
 11 21 31 41 51
 GCACTCCGCA GCCTTTAAGG TTCGCGCGGG GGCCAGGCAA GAGTTAGCCA TGAAGAGCCT 60
 CAAGTCCCGC CTGAGGAGGC AGGACGTGCC CGGCCCGCG TCGTCTGGCG CGCGCGCGGC 120
 CAGCGCGCAT GCAGCAGATT GGAATAAATA TGATGACCGA TTGATGAAAG CAGCAGAAAG 180
 GGGGGATGTA GAAAAGTGA CCTCAATCCT TGCTAAAAAG GGGGTCAATC CAGGCAAACT 240
 AGATGTGGAA GGCAGATCTG TCTTCCATGT TGTGACCTCA AAGGGGAATC TTGAGTGTIT 300
 GAATGCCATC CTTATACATG GAGTTGATAT TACAACCACT GACACTGCAG GGAGAAATGC 360
 TCTTCACTGT GCTGCTAAGT ATGGACATGC ATTGTGCCCTA CAAAACTTC TACAGTACAA 420
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 AGATTGTCTT TCTAGCATAC AGCTGCTTGT TGACCATGGG GCCTCTGTGA ATGCCAAAGA 540
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 CATGCTAGGT TCGCATATAT GTTGACAGAG TGCAAGTAGAA GTCTTAATTA AAAATGGTGC 720
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 ACCTCTGAAA CTATCTTTAC CCACTCAAAAC GTCATACTCT GAAATGAAA TTTTAAAGAA 1380
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 CCTGGCAGAG CACGAGGCAA AGATGAGCTC GCTAAGTCAG AGCATGAGAA AGGTGCAGGA 2880
 TAGTAATGCT GAAATCTTGG CCAACTACAG AAAAGGCCAA GAAGAGATTG TGACACTGCA 2940
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 ATATGCCCCA ATTGTCAGCT TTGAGGAGTG CGAGAGAAAA TTTAAGCAA CAGAGAAAGA 3060
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5 GCTTAATGAT GTGGAAAGAT TAAACAGGC ACTCAATGGC CTTTCCCAAC TCACCTACAC 4080
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 TCGGACACAC CTTCTTAGTG CTGCACAGGG TCACATGGAT GAAGATGTTT AGGAGGCTCT 4260
 GCTCCAGATC ATACAAATGC GGCAGGGGCT TGTGTGCTAG CGGTAGGCAC TGACTGCCAG 4320
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 CTTACTGTGC TGTGTATAATT AAAATAAAAT ATATTTTGTG CTGGGTGT

10 Seq ID NO: 446 Protein sequence
 Protein Accession #: AAG49577.1

1 11 21 31 41 51
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 LQYNCPTEHA DLQGRALQK KAMADCPSSI QLLCDHGASV NAKDVKGRTF LVLATQMSRP 180
 TIQQLLIDRG ADVNSRDQKN RTALMLGCEY GCRDAVEVLI KNGADISLLD ALGHDSYYA 240
 RIGDNLIDLT LLKTASENTN KRELWKKGP SLQQRNLTHM QDEVNVKSHQ REHQNIQDLE 300
 20 IENEDLKERL RKIQQBQRI LDKVNLGLQ LNEEVMVADD LSEEREKLS LLAKEKQHE 360
 ESRLTIEALK NRPKYFESDH LGSSEHFSNR KEDMLLKQGG MYMADSQCTS FGI PAHMQSR 420
 SMRLPLELSL PSQTSYSENE ILKKELEAMR TFCESAKQDR LKLQNELAHK VAECKALALE 480
 CERVKEDSDE QIKQLEDALK DVQKRMYSSE GKVKQMTHP LALKEHLTSE AASGNHRLTE 540
 ELKDQLKDLK VKYEGASAEV GKLRNQIKQN EMIVVEPKRD EGKLEENKR LQKELSMCEM 600
 25 EREKGRKVT EMEGQAKELS AKLALSIPAE KFNEMKSSLS NEVNEKAKKL VEMEREHEKS 660
 LSEIRQLKRE LENVKAKLAQ HVKPEHEQV KSRLEQKSGE LGKKITBLTL KNQTLQKEIE 720
 KVVLDNKLK BQAHNLTIEM KNHYVPLKVS EDMKSHDAI IDDLNRKLLD VTQKYTEKKL 780
 EMEKLLLEND SLKQDVSRLE TVFVPEKHE KEIITALKSNV VELKQLSEL KKKCGEDQEK 840
 IHALTSENIN LKQMSNQIV PVKTHEEVRM TLNDTLAKTN RELLDVKKGF EDINQEPVKI 900
 30 KDNELKRN LENTQNIKA EYISLABHEA KMSLSQSMR KVQDSNABIL ANYRKQBEI 960
 VTLHAIKKAQ KKELDITQEC IKVYAPIVS FEECERKPKA TEKELKDQLS EQTKYSVSE 1020
 BEVKQKQEN DKLKKEIPTL QKDLRDKTVL IEKSEHERA LSRKTDENLK QLKDLQKYT 1080
 EVNVRKEIV EENAKQTSBI LAVQNLQKQ HVPLSQVEAL KKSNGTIEY LKEELKSMQR 1140
 CYEKEQQTVT KLHQLLENQK NSSVPLAEHL QIKAFEKEV GIIKASLREK EESQNMKEE 1200
 35 VSKLQSEVQN TQALKKLET REVVDLSKYK ATKSDLETQI SSLNEKLANL NRKYEEVCEE 1260
 VLHAKKKSIS AKDKKELLHP STEQEIKDQK ERCDKSLTTI TELQRRIQES AKQIEAKDNK 1320
 ITELNDVER LKQALNGLSQ LTYTSGNPTK RQSQLIDTLQ HQVKSLEQQL ADADRQHQEV 1380
 IAYRTHLLS AAQHMDMDV QEALLQIIQM RQGLVC

40 Seq ID NO: 447 DNA sequence
 Nucleic Acid Accession #: NM_003020.1
 Coding sequence: 29..664

1 11 21 31 41 51
 45 CGCTCCTCGG GCTGCCCTCT GGTGACAAT GGTCTCCAGG ATGGTCTCTA CCATGCTATC 60
 TGGCCTACTG TTTTGGCTGG CATCTGGATG GACTCCAGCA TTTGCTTACA GCCCCCGGAC 120
 CCTTGACCGG GTCTCAGAAG CAGATATCCA GAGGCTGCTT CATGGTGTTA TGGAGCAATT 180
 GGGCATTGCC AGGCCCGGAG TGGATATCC AGCTCACCAG GCCATGAATC TTGTGGGCCC 240
 50 CCAGAGCATT GAAGGTGGAG CTCATGAAG ACTTCAGCAT TTGGGTCTTT TTGGCAACAT 300
 CCCCACATC GTGCAGAGT TGACTGGAGA CAACATTCCT AAGGACTTTA GTGAGGATCA 360
 GGGGTACCCA GACCTCCAA ATCCCTGTCC TGTGGAAAA ACAGATGATG GATGTCTAGA 420
 AAACACCCCT GACACTGCAG AGTTCACTCG AGAGTTCAG TTGCACCGAC ATCTCTTTGA 480
 TCGGAAACAT GACTATCCAG GCTTGGGCAA GTGGAACAAG AAACCTCTTT ACAGAGAAGT 540
 55 GAAGGGAGGA GAGGACGAA AGCGGAGGAG TGTCAATCCA TATCTACAAG GACAGAGACT 600
 GGATAATGTT GTTGCAAAGA AGTCTGTCCC CCATTTTTCA GATGAGGATA AGGATCCAGA 660
 GTAAAGAGAA GATGCTAGAC GAAAACCCAC ATTACCTGTT AGGCCCTCAGC ATGGCTTATG 720
 TGACCGTGA TATGGAGTCC CTGTGAATGA CAGCATGTTT CTTACATAGA TAATTATGGA 780
 TACAAAGCAG CTGTATGTAG ATAGTGTATT GTCTTCACAC CGATGATTCT GCTTTTGTCT 840
 60 AAATTAGAA TAAAGCTTTT TTGTTTCTTG GGTTTTAAAA ATGTGAATCT GCAATGATCA 900
 TAAAAATTA AATGTGAATG TCAACAATAA AAGCAGAGC TATGAAGGC TCAGATTCTT 960
 TGCAGTTTAA AATGGTGTCT GAGGTGTGAT TATTTTGGCC AAGTCTGTAG AAAGCTGTCA 1020
 TTTGATTTTG ATTATGTAGT TCATCCAGCC CTGGGCATT GTTATACACC AGTAAAGAAG 1080
 GCTGTACTCA AGAGGAGGAG CTGACACATT TCACCTTGCT GGTCTTAAAT AAACATGAAT 1140
 GCAAGCATTG GC

65 Seq ID NO: 448 Protein sequence
 Protein Accession #: NP_003011.1

1 11 21 31 41 51
 70 MVSRLVSTML SGLLFWLASG WTPAPAYSPP TPDRVSEADI QRLHGVMBQ LGIARPRVEY 60
 PAHQAMNLVG PQSIEGGAHE GLQHLGPPGN IPNIVAEITG DNIPKDFSED QGYDPFPNFC 120
 PVGKTDDGCL ENTPTAEFS REFQLHQHFL DPEHDYPGLG KWNKKLLYEK MKGGERRRKR 180
 75 SVNPLYQQQR LDNVVAKRSV PHPSDEKDP E

80 Seq ID NO: 449 DNA sequence
 Nucleic Acid Accession #: NM_003816.1
 Coding sequence: 79..2538

1 11 21 31 41 51
 CGGCAGGGTT GAAAAATGAT GGAAGAGGCG GAGGTGGAGG CGACCGAGTG CTGAGAGGAA 60
 CCTGCGGAAT CGGCCGAGAT GGGGTCTGGC GCGGCTTTC CCTCGGGGAC CCTTCGTGTC 120
 CGGTGGTTCG TTTTGTCTTG CCTGGTGGGC CCACTCCTCG GTGCGGCGCG GCCAGGCTTT 180

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CAACAGACCT CACATCTTTC TTCTTATGAA ATTATAACTC CTTGGAGATT AACTAGAGAA 240
 AGAAGAGAAG CCCCTAGGCC CTATTCAAAA CAAGTATCTT ATGTTATTCA GGCTGAAGGA 300
 AAAGAGCATA TTATTCACTT GGAAAGGAAC AAAGACCTTT TGCGTGAAGA TTTTGTGTTT 360
 TATACTTACA ACAAGGAAGG GACTTTAATC ACTGACCATC CCAATATACA GAATCATTGT 420
 CATTATCGGG GCTATGTGGA GGGAGTTCAT AATTCAATCA TTGCTCTTAG CGACTGTTTT 480
 GGACTCAGAG GATTGCTGCA TTTAGAGAAT GCGAGTTATG GGATTGAACC CCTGCAGAAC 540
 AGCTCTCATT TTGAGCACAT CATTATCGA ATGGATGATG TCTACAAAGA GCCTCTGAAA 600
 TGTGGAGTTT CCAACAAGGA TATAGAGAAA GAAACTGCAA AGGATGAAGA GGAAGAGCCT 660
 CCGAGCATGA CTCAGCTACT TCGAAGAAGA AGAGCTGTCT TGCCACAGAC CCGTATGTG 720
 GAGCTGTTC TTTGCTAGA CAAGGAAAGG TATGACATGA TGGGAAGAAA TCAGACTGCT 780
 GTGAGAGAAG AGATGATTCT CCTGGCAAAC TACTTGGATA GTATGTATAT TATGTTAAAT 840
 ATTGCAATTG TGCTAGTTGG ACTGGAGATT TGGACCAATG GAAACCTGAT CAACATAGTT 900
 GGGGGTGTCT GTGATGTGCT GGGGAACTTC GTGCAGTGGC GGGAAAAGTT TCTTATCA 960
 CGTCGGAGAC ATGACAGTGC ACAGCTAGTT CTAAAGAAAG GTTTTGGTGG AACTGCAGGA 1020
 ATGGCATTG TGGGAACAGT GTGTTCAAGG AGCCACGAG GCGGGATTAA TGTGTTTGA 1080
 CAAATCACTG TGGAGACATT TGCTTCCATT GTTGCTCATG AATTGGGTCA TAACTTTGA 1140
 ATGAATCAG AGATGGGAG AGATTGTTCC TGTGGAGCAA AGAGCTGCAT CATGAATTCA 1200
 GGAGCATCGG GTTCCAGAAA CTTTAGCAGT TGCAGTGCA AGGACTTTGA GAAGTTAACT 1260
 TTAATAAAG GAGGAACTG CCTTCTAAT ATTCCAAAGC CTGATGAAGC CTATAGTGCT 1320
 CCTCTCTGT GTAATAAGTT GGTGGACGCT GGGGAAGAGT GTGACTGTG TACTCCAAAG 1380
 GAATGTGAAT TGGACCTTGT CTGCGAAGGA AGTACCTGTA AGCTTAAATC ATTTGCTGAG 1440
 TGTGCAATG TGCTAGTTGG TAAAGACTGT CGGTTCCCTC CAGGAGGTAC TTTATGCGA 1500
 GGAAGAACCA GTGAGTGTGA TGTTCAGAG TACTGCAATG GTTCTTCTCA GTTCTGTGAG 1560
 CCAGATGTTT TTATTAGAAA TGGATATCCT TGCCAGAAAT ACAAAGCCTA TTGCTCAAC 1620
 GGCATGTGCC AGTATTATGA TGCTCAATGT CAAGTCACTT TTGGCTCAAA AGCCAAAGCT 1680
 GCCCCCAAG ATTGTTTCAAT TGAAGTGAAT TCTAAAGGTG ACAGATTGGG CAATTGTGGT 1740
 TTCTGTGGA ATGAATACAA GAAAGTGTGC ACTGGGAATG CTTTGTGTGG AAAGCTTCAG 1800
 TGTGAGAAAT TACAAGAGAT ACCTGTATTT GGAATGTGTC CTGCTATTAT TCAACGCTC 1860
 AGTCAGGAG CCAAAATGTT GGGTGTGGAT TTCCAGCTAG GATCAGATGT TCCAGATCCT 1920
 GGGATGTTA ACGAAGGCAC AAAATGTGGT GCTGGAAGA TCTGTAGAAA CTTCCAGTGT 1980
 GTAGATGCTT CTGTCTGTA TTAGTACTGT GATGTTGAGA AAAAGTGTCA TGGACATGGG 2040
 GTATGTAATA GCAATAAGAA TTGTCACTGT GAAATGGCT GGGCTCCCC AAATGTGAG 2100
 ACTAAAGGAT ACGGAGGAAG TGTGGACAGT GGAACCTCAT ACAAAGAAAT GAATCTGCA 2160
 TTGAGGGAG CACTTCTGCT CTTCTCTTC CTAATTTGTT CCGTTATTGT CTGTGCTATT 2220
 TTTATCTTCA TCAAGAGGGA TCACTGTGG AGAAGCTACT TCAGAAAGAA GAGATCACA 2280
 ACATATGAGT CAGATGGCAA AAATCAAGCA AACCTTCTA GACAGCCGGG GAGTGTCTCT 2340
 CGACATGTTT CTCCAGTGAC ACCTCCAGCA GAAAGTTCTA TATATGCAAA CAGATTGCA 2400
 GTACCAACCT ATGCAGCCAA GCAACCTCAG CAGTTCCCAT CAAGGCCACC TCCACCACA 2460
 CCGAAAGTAT CATCTCAGGG AAACCTAATT CCTGCCGCTC CTGCTCCTGC ACCTCCCTTA 2520
 TATAGTTCCC TCACTGATT TTTTAACTT TCTTTTGTCA AATGCTTCA GGGAACTGAG 2580
 CTAATCTTTT TTTTCTTCT TGTGTTTTC TTGAAAAGCC TTCTGTGTGC AACTATGAAT 2640
 GAAAACAAA CACACAAAA CAGACTTCAC TAACACAGAA AAACAGAAAC TGAGTGTGAG 2700
 AGTTGTGAAA TACAGGAAA TGCAGTAAAG CCAGGGAATT TACAATAACA TTTCCGTTTC 2760
 CATCAITGAA TAAGTCTTAT TCAGTCAATG GTGAGGTTAA TGCATTAATC ATGATTTTT 2820
 TGAACATGTT ATTGCAATG TTTCAAAAT AACTGTATG GTGTAAGATT TTTGTCATTA 2880
 AGTGTTAAG TGTATTCTG AATTTCTAC CTTAGTTATC ATTAATGTAG TTCCCTATTG 2940
 AACATGTGAT AATCTAATAC CTGTGAAAAC TGACTAATCA GCTGCCAATA ATATCTAATA 3000
 TTTTTCATCA TGCAGGAAT AATAATCATC ATACTCTAGA ATCTTGTCTG TCACTCACTA 3060
 CATGAATAAG CAAATATTGT CTTCAAAAGA ATGCACAAGA ACCACAATTA AGATGTCTA 3120
 TTAATTTGAA AGTACAAAAT ATACTAAAAG AGTGTGTGTG TATTCACGCA GTTACTCGCT 3180
 TCAATTTTCA TGACCTTTCA ACTATAGGTA ATAACCTCTA GAGAAATTA TTTAATATTA 3240
 GAATTTCTAT TATGAATCAT GTGAAAGCAT GACATTGTT CACAATAGCA CATTATTTAA 3300
 TAAATTTAA GCTTTAAGGT ACGAAGTATT TAATAGATCT AATCAAAAT GTTGATTCT 3360
 GGCTATAATA AAGCAGGAGC AATTATAAAA TCTTCAATCA ATTGAACCTT TACAAAACCA 3420
 CTGAGGAATT TTAGAGCAT TTTAAATCT GAACCTTCAA AGCTTGCTAT TAAATCATT 3480
 AGAATGTTTA CATTACTTAA GGTGTGCTGG GTCATGTAAA ATATTAGACA CTAATATTTT 3540
 CATAGAAAT AGGCTGGAGA AAGAAGGAAG AAATGGTTTT CTTAAATACC TACAAAAAAG 3600
 TACTGTGGT ATCTATGAGT TATCATCTTA GCTGTGTAA AAATGAATT TTAATATGGC 3660
 AGATATGGTA TGGATCGTAA AATTTTAAAG ACTAAAAAT TTTTCATAAC CTTTCTAAT 3720
 AAAGTTTAAAT AATAGGTTTA TTAAGTGAAT TTCATTAGTT TTTTAAAGT GTTTTGTGTT 3780
 TGTGTATATA TACATATACA AATACAACAT TTACAATAAA TAAATACTT GAAATCTCA 3840
 AAAAAAAAAA AAAAAAAAAA AAAAA

65 Seq ID NO: 450 Protein sequence
 Protein Accession #: NP_003807.1

70
75
80

1 11 21 31 41 51
 1 MSGARFSPG TLRVRWLLLL GLVGPVLGAA RFGFQQTSHL SSYEIITPWR LTRERREAPR 60
 2 PYSKQVSYVI QAEQKEHIIH LERNKDLLPE DFVVTYTNKE GTLITDHPNI QNHCHYRGYV 120
 3 EGVHNSIAL SDCFLRLGLL HLENASYGIE PLQNSHFEH IYRMDVYK EPLKCGVSNK 180
 4 DIEKETARDE EEEPPSMTQL LRERRAVLPQ TRYVELFIVV DKERYDMGR NQTAVEREMI 240
 5 LLANYLDSMY IMLNIRIVLV GLEIWTGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS 300
 6 AQLVLKKFGP GTAGMAFVGT VCSRSHAGGI NVFGQITVET PASIVAHELG HNLGMHDDG 360
 7 RDCSCGAKSC INNSGASGR NFSSCSAEDF EKLTLNKGNN CLNLIKPDE AYSAPSCGNK 420
 8 LVDAGEECDC GTFKCELDLP CCEGSTCKLK SPACAYGDC CKDCRFLPGG TLCRGKTSFC 480
 9 DVPEYCNSS QFCQPDVPIQ NGYPCQNNKA YCINGMCQY DAQCQVIPS KAKAAPKDCF 540
 10 IBVNSKGRDF GNGPSGNEY KKCATGNALC GLQCEVQBE IPVFGIVPAI IQTPSRGTFC 600
 11 WGVDPQLGSD VPDPMVNEG TKCGAGKICR NFQCVDAVL NYDCDVQKKC HGHGVCSNKK 660
 12 NCHCENGWAP NCNETKGYGG SVDSGPITYE MNTALRDGLL VFFFLIVPLI VCAIFPIKR 720
 13 DQLWRSYFRK KRSQTYESDG KNQANPSRQP GSVPRHVSVP TTPREVPPIA NRPAPVPTAA 780
 14 KQPPQFPRP PPPQPKVSSQ GNLIAPRAP APPLYBSLT

Seq ID NO: 451 DNA sequence
Nucleic Acid Accession #: NM_016650.1
Coding sequence: 196..789

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5      1      11      21      31      41      51
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      GGTTC AATA TATGCAGATG TCTCGATATA GGAATGAAAT TACGTCCTTG GAACAACCTTA 60
      AATAAGTCAA ATATACTTGG AGCTTTAAAA ATTAAGAAGA GAGAGATTCC AGCACCTTTT 120
      CTGCTGCCAT GACAACCATG CAAGGAATGG AACAGGCCAT GCCAGGGTTG GCCTGGTGTG 180
10     CCCACAGCTGG GAAACATGGC TGTCAATCAT TCACATCTGT GGAAGAGGATT GCAAGAGAAG 240
      TTCTTGAAGG GAGAAACCAA AGTCCTTGGG GTTGTGCAGA TTCTGACTGC CCTGATGAGC 300
      CTTAGCATGG GAATAACAAT GATGTGTATG GCATCTAATA CTTATGGAAG TAACCCATT 360
      TCCGTGCATA TCGGGTACAC AATTTGGGGG TCAGTAATGT TTATTATTTC AGGATCCTTG 420
      TCAATTGCAG CAGGAATTAG AACTACAAAA GGCCTGGTCC GAGGTAGTCT AGGAATGAAT 480
15     ATCACCAGCT CTGTACTGGC TGCATCAGGG ATCTTAATCA ACACATTAG CTTGGCGTTT 540
      TATTCAATGC ATCACCTTA CTGTAACCTAC TATGGCAACT CAAATAATTG TCATGGGACT 600
      ATGTCCATCT TAATGGGTCT GGATGGCATG GTGCTCCTCT TAAGTGTGCT GGAATTCTGC 660
      ATTGCTGTGT CCTCTCTGCT CTTTGGATGT AAAGTGCTCT GTTGACCCC TGGTGGGGTT 720
      GTGTTAATTC TGCCATCACA TTCTCACATG GCAGAAACAG CATCTCCAC ACCACTTAAT 780
20     GAGGTTTGGG GCCAACAAA GATCAACAGA CAAATGCTCC AGAAATCTAT GCTGACTGTG 840
      ACACAAGAGG CTCACATGAG AAATTACCAG TATCCAACTT CGATACTGAT AGACGTGTGT 900
      ATATTATTAT TATATGTAAT CCAATTATGA ACTGTGTGTG TATAGAGAGA TAATAAATTC 960
      AAAATTATGT TCTCATTTT TTCCCTGGAA CTCATAACT CACTTCACCT GCTCTTTATC 1020
      GAGAGTACTA GGAGTTAAAT TAATAAATAA TGCATTTAAT GAGGCCACAG GAAAAA

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Seq ID NO: 452 Protein sequence
Protein Accession #: NP_057734.1

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30     1      11      21      31      41      51
      |      |      |      |      |      |
      MAVIHSWLWK GLQEKFLKGE PKVLGVVQIL TALMSLSMGI TMMCMASNTY GSNPISVHIG 60
      YTINGSVPMFI ISGSLSLAIG IRTTKGLVRG SLGMNITSSV LAASGILINT FSLAFYSFHH 120
      PYCNYYGNSN NCHGTMSILM GLDGMVLLLS VLEFCIAVSL SAFGCKVLCC TPGGVVLILP 180
      SHSHMAETAS PTPLINEV

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Seq ID NO: 453 DNA sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..503

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40     1      11      21      31      41      51
      |      |      |      |      |      |
      AGTCTCTGCT CTCCAGGCC TCTCCGGGCG GCTCCAAGGG CTTCCTCGTG GGACCATGCG 60
      CGGCAGTGAG CTCCTCGTGG TCTGTCTGCG GCTGTCTCTC TGCTTAGGCG CCCGGGGGCG 120
      AGCGGTCCCG CTGCTCGCG GCGGAGGGAC CGTGTGACC AAGATGTACC CGCGCGGCAA 180
45     CCACCTGGCG GTGGGGCACT TAATGGGAAA AAAGAGCACA GGGGAGTCTT CTTCTGTTTC 240
      TGAGAGAGGG AGCCTGAAGC AGCAGCTGAG AGAGTACAT AGGTGGGAAG AAGCTGCAAG 300
      GAATTTCTGT GGTCTCATAG AAGCAAAGGA GAACAGAAAC CACCAGCCAC CTCACCCCAA 360
      GGCTTGGGCG AATCAGCAGC CTTCTGTGGG TTCAGAGGAT AGCAGCAACT TCAAGATGTT 420
      AGGTTCAAAA GGCAAAGTTG GTAGACTCTC TGCTCCAGGT TCTCAACGTG AAGGAAGGAA 480
50     CCCCAGCTG AACCAAGCAAT GATAATGATG GCCTCTCTCA AAAGAGAAAA ACAAAACCCC 540
      TAAGAGACTG AGTTCTGCAG GCATCAGTTC TACGGATCAT CAACAAGATT TCCTTGTCGA 600
      AAATATTGTA CTATTCTGTA TCTTTTATCC TTGACTAAAT TGTGATTTT CAAGCAGCAT 660
      CTCTGTGTTT AAACCTGTTT GCTGTGAACA ATTGTGAAA AGAGTCTTCC AATTAATGCT 720
      TTTTATATC TAGGTACCT GTTGGTTAGA TTCAAGGCCCG CGAGCTGTGA CCATTACAAA 780
      TAAAGCTTA AACACAT

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Seq ID NO: 454 Protein sequence
Protein Accession #: NP_002082.1

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60     1      11      21      31      41      51
      |      |      |      |      |      |
      MRGSELPLVL LALVLCIAPR GRAVPLPAGG GTVLTKMYPR GNHMAVGHLM GKKTGESSS 60
      VSRGSLKQQL LREYIRWEEA ARNLLGLIEA KENRNHQPQ PKALGNQOPS WDSDESSNFK 120
      DVGSKGVQGR LSAFGSQREG RNPQLNQ

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Seq ID NO: 455 DNA sequence
Nucleic Acid Accession #: NM_016522.1
Coding sequence: 265..1299

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70     1      11      21      31      41      51
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      CTGGCAAAG CGAGGCTGAG ATTTGGGGGA GGAATATTAG ACTCGGAGGA GTCTGCGCGC 120
      TTTTCTCCTC CCCGCGCTC CGGTGCGCG CGGTTTACC GCTCAGTCCC CGCGCTCGCT 180
75     CGCACCCCAA CCCACTTCTT GTGCTCGCCC GGGGGGCGTG TGCGGTGCGG CTGCGGAGT 240
      TCGGGGAAGT TGTGCTGTG GAGAATGGGG GTCTGTGGGT ACCTGTTTCT GCCCTGGAAG 300
      TGCTCTGTGG TCGTGTCTCT CAGGCTGCTG TTCCTGTGAC CCACAGAGT GCCCGTGGCG 360
      AGCGGAGATG CCACCTTCCC CAAAGCTATG GACAAAGTGA CGGTCCGGCA GGGGAGAGC 420
      GCCACCTCA GGTGCACTAT TGACAACCGG GTCACCCGGG TGGCTGGCT AAACCGCAGC 480
80     ACCATCTCT ATGCTGGGAA TGACAAGTGG TGCTGGATC CTCGTGTGTT CTTCTGAGC 540
      AACACCCAAA CGCTGACAG CATCGAGATC CAGAAGCTGG ATGTGTATGA AGAGGCGCT 600
      TACACCTGCT CGGTGCAGAC AGACAACCAC CCAAGACCT CTAGGGTCCA CCTCATTGTG 660
      CAAGTATCTC CCAAAATTGT AGAGATTCTC TCAGATATCT CCATTAATGA AGGGAACAA 720
      ATTAGCCTCA CCGTCATAGC AACTGGTAGA CCAGAGCCTA CGGTTACTTG GAGACACATC 780

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TCTCCCAAAG CGGTGGCTT TGTGAGTGAA GACGAATACT TGGAAATCA GGGCATCACC 840
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 5 OTCCCGTGG GACAAAAGGG GACACTGCAG TGTGAAGCCT CAGCAGTCCC CTCACAGAA 1020
 TTCCAGTGGT ACAAGGATGA CAAAGACTG ATTGAAGGAA AGAAAGGGGT GAAAGTGGAA 1080
 AACAGACCTT TCCTCTCAAA ACTCATCTTC TTCAATGTCT CTGAACATGA CTATGGGAAC 1140
 TACACTTGGC TGGCCTCCAA CAAGCTGGGC CACACCAATG CCAGCATCAT GCTATTGGT 1200
 CCAGGCGCCG TCAGCGAGGT GAGCAACGGC ACGTGAAGGA GGGCAGGCTG CGTCTGGCTG 1260
 10 CTGCTCTTC TGGTCTTGA CCTGCTTCTC AAATTTTGAT GTGAGTGCCA CTTCGCCACC 1320
 CGGGAAGGC TGGCGCCACC ACCACCACA ACACAACAGC AATGGCAACA CCGACAGCAA 1380
 CCAATCAGAT ATATACAAAT GAAATTAGAA GAAACAAGC CTCATGGAC AGAAATTTGA 1440
 GGGAGGGGAA CAAAGAATAC TTTGGGGGGA AAAGAGTTT AAAAAGAAA TTGAAAATTG 1500
 CCTTGCAAT ATTTAGGTAC AATGGAGTTT TCTTTTCCCA AACGGGAAGA ACACAGCACA 1560
 15 CCGGCTTGG ACCCACTGCA AGCTGCATCG TGCAACCTCT TTGGTGCCAG TGTGGGCAAG 1620
 GGCTCAGCCT CTCTGCCAC AGACTGCCCC CAGGTGGAAC ATTCTGAGC TGGCCATCCC 1680
 AAATTCATC AGTCCATAGA GACGAACAGA ATGAGACCTT CCGGCCCAAG CGTGGCGCTT 1740
 CCGGCCCAAG GTGGCGCTG CGGGCACTT GGTAGACTGT GCCACCAAG CGTGTGTGT 1800
 GAAACGTGAA ATAAAAAGAG CAAAAAAGG AAAAAAAGG

20 Seq ID NO: 456 Protein sequence
 Protein Accession #: NP_057606.1

1 11 21 31 41 51
 25 MGVOGYLFLP WKCLVVSRLR LLFLVPTGVP VRSGDATFPK AMDNVTVROG ESATLRCTID 60
 NRKTRVANLN RSTILYAGND KWCLDPRVVL LSNQTQYSI EIQNVVDVDE GPYTCSVQTD 120
 NHPKTSRVHL IVQVSPKIVE ISSDISINEG NNISLTICAT GRPEPTVTWR HISPKRAGFV 180
 SEDEYLEIQG ITRREGSGDYE CSASNDVAAP VVRRVKVTVN YPPYISEAKG TGVFVGQKGT 240
 30 LQCEASAVPS AEFQWYKDDK RLIEGKKGVK VERNPFLSKL IFFNVSEHDY GNYTCVASNK 300
 LGHTNASIML POPGAVSEVS NGTSRRAGCV WLLPLLVHL LKLF

Seq ID NO: 457 DNA sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 203..1045

1 11 21 31 41 51
 35 GATTGTCTCT GCCAGCAGCT GTGGGTGCGG CGCTCGACAC AGAGTCCTAG CTAGGCGCTC 60
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 40 CACTCCAGCG GCGACTTTGA GGGATTCCTC CTCTGGCGGC CTCTGCAGCA GCACAGCCGG 180
 CTTCTATTGG GGCAGCTGGA GTATGGATCT CCAAGGAAGA GGGGTCCCCA GCATCGACAG 240
 ACTTCGAGTT CTCTGATGT TGTTCATAC AATGGCTCAA ATCATGGCAG AACAAAGAA 300
 GGAAATCTC TCAGGCTTTT CCACTAACCC TGAAGAAAGT ATATTGTGG TGGCGGAAAA 360
 TGGACGACG TGTCTCATGG CAGAGTTTGC AGCCAAATT ATTGTACCT ATGATGTGTG 420
 45 GGCCAGCAAC TACGTAGATC TGATCACAGA ACAGGCCGAT ATCGCATTGA CCCGGGGAGC 480
 TGAGGTGAAG GGCCTGCTGT GCCACAGCCA GTGCGAGCTG CAAAGTGTCT GGGTGGATCG 540
 CGCATATGAC CTCAAAATGC TCTTTGTAAA GGAAGGCCAC AACATGTCCA AGGGAACCTG 600
 GCGCACTTGG AGGCTGAGCA AAGTGCAGTT TGTCTAGCAC TCCTCGGAGA AAACCCACTT 660
 CAAAGACCGA TGTCTCATGG GGAAGCACAC AGCCAACTCG CACCACTCT CTGCTTGGT 720
 50 CACCCCGCTG GGAAGTCTT ATGAGTGTC AACTCAACAA ACCATTTCAC TGGCTCTAG 780
 TGATCCGACG AAGACGCTCA CCATGATCTT GTCTGCGGTC CACATCCAAC CTTTTGACAT 840
 TATCTCAGAT TTTGTCTTCA GTGAAGAGCA TAAATGCCCA GTGGATGAGC GGGAGCAACT 900
 GGAAGAAACC TTGCCCCGTA TTTTGGGGCT CATCTTGGGC CTCGTATCA TGTAAACACT 960
 55 CGGATTTTAC CAGTCCACC ACAAAATGAC TGCCAAACAG GTGCAGATCC CTCGGGACAG 1020
 ATCCAGTAT AAGCACATGG GCTAGAGGCC GTTAGGCAGG CACCCCTAT TCCTGCTCCC 1080
 CCAACTGAT CAGGTAGAAC AACAAAAGCA CTTTTCATC TTGTACACGA GATACACAA 1140
 CATAGCTACA ATCAACAGG CCTGGGTATC TGAGGCTTGC TTGGCTTGT TCCATGCTTA 1200
 AACCCACGGA AGGGGGAGAC TCTTTCGAT TTGTAGGGTG AAATGGAAT TATTCTCTCC 1260
 60 ATGCTGGGGA GGAGGGGAGG AGGGTCTCAG ACAGCTTTCG TGCTCATGGT GGCCTTGGCT 1320
 TGACTCTCCA AAGAGCAATA AATGCCACTT GGAGCTGTAT CTGCCCCAA AGTTTAGGGA 1380
 TTGAAAACAT GCTTCTTTGA GGAGGAAACC CTTTAGGTT CAGAAGAATA TGGGGTGCTT 1440
 TGTCTCCCTG GACACAGCTG GCTTATCCTA TACAGTTGTC AATGCACACA GAATACAACC 1500
 TCATGTCTCC TGACGACAGA CCCCTGAAAG TGATTCTATG TCTGTGGTGG CATTCGCAT 1560
 65 GTTGTAGTAT GTCTTGGGA ATGTTTCACT GCTACCGCA TCCAGCGACT GCAGCACCAG 1620
 AAAACGACTA ATGTAACAT GCAGAGTTGT TTGGACTTCT TCCTGTGCCA GGTCCAAGTC 1680
 GGGGACCTG AAGAAATCAAT CTGTGTGAGT CTGTTTTTCA AAATGAAATA AAACACACTA 1740
 TTCTCTGGC

70 Seq ID NO: 458 Protein sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 75 MDLQGRGVPS IDRLRVLLML PHTMAQIMAE QEVENLSGLS TNPEKDIPVV RENGITCLMA 60
 EFAAKFIVPY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSEIQVFW VDRAYALRML 120
 PVKESHNSMK GPEATWRLSK VQFVYDSSEK THFKDAVSAG KHTANSHLS ALVTPAGKSY 180
 ECQAQQTISL ASSDPQKTVT MILSAVHIQF PDIIISDFVFS BEHKPCVDER EQLEETLPLI 240
 LGLILGLVIM VTLAIYHVHR KMTANQVQIP RDRSQYKIMG

80 Seq ID NO: 459 DNA sequence
 Nucleic Acid Accession #: NM_001169.1
 Coding sequence: 85..870

1 11 21 31 41 51

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	TAGAGATAA		GAGTATCTTG		CACAGCAGGT		GCAGGTTTCC		CAGCAGCTCA		GGCAAGAGTC	60
	CGATGTTTGT		GCCATCTGAT		CCTGATGTCT		GGAGAGATAG		CCATGTGTGA		GCCTGAATTT	120
	GGCAATGACA		AGGCCAGGGA		GCCGAGCGTG		GGTGGCAGGT		GGCGAGTGTC		CTGGTACGAA	180
	CGGTTTGTGC		AGCCATGTCT		GGTCGAACTG		CTGGGCTCTG		CTCTCTTCAT		CTTCATCGGG	240
	TGCTGTGTGG		TCATTGAGAA		TGGGACGGAC		ACTGGGCTGC		TGCAGCGGCG		CCTGGCCAC	300
	GGGCTGGCTT		TGGGGCTCGT		GATTGCCACG		CTGGGGAATA		TCAGTGGTGG		ACACTTCAAC	360
	CCTGCGGTGT		CCCTGGCAGC		CATGCTGATC		GGAGGCCCTCA		ACCTGGTGAT		GCTCCTCCCG	420
	TACTGGGTCT		CACAGCTGCT		CGGGGGGATG		CTCGGGGCTG		CCTTGGCCAA		GGTGGTGAGT	480
	CCTGAGGAGA		GGTCTGGGAA		TGCATCTGGG		GCGGCCTTTG		TGACAGTCCA		GGAGCAGGGG	540
	CAGGTGGCAG		GGGCGTTGGT		GGCAGAGATC		ATCCTGACGA		CGCTGCTGSC		CCTGGCTGTA	600
	TGCATGGGTG		CCATCAATGA		GAAGACAAAG		GGCCCTCTGG		CCCCGTTCTC		CATCGGCTTT	660
	GCGGTCAACG		TGGATATCCT		GGCTGGGGGC		CCTGTGTCTG		GAGGCTGCAT		GAATCCCGCC	720
	CGTGTCTTTG		GACCTGCGGT		GGTGGCCAAC		CACTGGAAC		TCCACTGGAT		CTACTGGCTG	780
	GGCCACTCC		TGGCTGGCCT		GCTTGTGGA		CTGCTCAITA		GGTGTTCAT		TGGAGATGGG	840
	AAGACCCGCG		TCATCTTGAA		GGCTCGGTGA		GCAGAGCTCG		TGGGATTCCT		GCTGCTCCAG	900
	GTGTCTCTCAG		CTACCTGTGC		CCAGACTGAG		GACAGGGGAG		TTCTTGCAAT		TCTTCCCAGG	960
	GCAGAGGCGC		AGAGGAGCGA		CCCCCTGCTT		CCACTGTCTG		GGCCTGTCTT		CTCAGATAGA	1020
	CTGACTGTCT		AGGAGGCTCT		AGGTCTCTTG		AATTCCTTTG		TGCTCATCAG		AGACCCGAGC	1080
	CTGGGGAACA		CGCTGCCCGC		ACTGCCCAGA		GAGCAGTGCA		AACACCACAA		CACGAGCGTG	1140
	TTTCTTGAGA		GGAAATGTCC		CGAGTTGGAC		AAGGAGGCTG		TTTCTGCACA		TCAGCTCATT	1200
	TCCGCGACCC		CATTCTCTGC		TTGATTGCTT		TGTGGGGGCG		CTGGCCACTT		CCTTGTCTCT	1260
	CAAGCTGACA		ATTCTCACTT		TGCAATAAAT		AGTCCAGTGT		TTCTTCAT			

Seq ID NO: 460 Protein sequence
Protein Accession #: NP_001160.1

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	1		11		21		31		41		51	
	MSGEIAMCEP		EFGNDKAREP		SVGGRWRVSW		YERFVQPCLV		ELLGSALEP		IGCLSVIENG	60
	TDTLGLQPAL		AHGLALGLVI		ATLGNISGGH		FNPAVSLAAM		LIGGLNLVLM		LPYVWSQLLG	120
	GMLGAALAKV		VSPERFPWNA		SGAAFVTQBE		QGGVAGALVA		EIILITLLAL		AVCMGAINEK	180
	TKGPLAPFSI		GFAVTVDILA		GGFVSGGCMN		PARAFGPVAV		ANHWNEHWIY		WLGPLLGLLL	240
	VGLLIRCFIG		DGKTRILILKA		R							

Seq ID NO: 461 DNA sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

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	1		11		21		31		41		51	
	GATGCTGGGG		CTGGTCTCTG		CCTTGCTGTC		CTCCAGCTCT		GCTGAGGAGT		ACGTGGGCCT	60
	GTCTGCAAAC		CAGTGTGCCG		TGCCGGCCAA		GGCAGGGTGG		GACTGCGGCT		ACCCCATGTT	120
	CACCCCAAG		GAGTGCAACA		ACCGGGGCTG		CTGCTTTGAC		TCCAGGATCC		CTGGAGTGCC	180
	TTGGTGTTC		AAGCCCTTGA		CTAGGAAGAC		AGAATGCACC		TTCTGAGGCA		CCTCCAGCTG	240
	CCCTGTGGAT		GCAGGCTGAG		CACCTTGCC		CGGCTGTGAT		TGCTGCCAGG		CACGTTCAT	300
	CTCAGTTTCT		TGCTCCCTTT		GCTCCCGGCA		AGCTTCTGCG		TGAAAGTTCA		TATCTGGAGC	360
	CTGATGTCTT		AAGCAATAAA		GCTCCCATGC		TCCACCCG					

Seq ID NO: 462 Protein sequence
Protein Accession #: NP_003217.1

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	1		11		21		31		41		51	
	MLGLVLALLS		SSSAEEYVGL		SANQCAVPAK		DRVDCGYPHV		TPKECMNRGC		CFDSRIPGVF	60
	WCFKPLTRKT		ECTP									

Seq ID NO: 463 DNA sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

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70
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	1		11		21		31		41		51	
	GGCACGAGCC		AGTCTCCGCG		CCTCCACCCA		GCTCAGGAAC		CGCGAACC		TCTCTTGACC	60
	ACTATGAGCC		TCCCGTCCAG		CCGCGCGGCC		CGTGTCCCGG		GTCTTCCGG		CTCCTTGTGC	120
	GCGCTGCTCG		CGCTGCTGCT		CCTGCTGACG		CCGCGGGGCG		CCCTGCCAG		CGCTGGTCTT	180
	GTCTCTGCTG		TGCTGACAGA		GCTGCGTTGC		ACTTGTTTAC		GCGTTACGCT		GAGAGTAAAC	240
	CCCAAAACGA		TTGTTAAACT		GCAGGTGTTT		CCCGCAGGCC		CGCAGTGCTC		CAAGTGGGAA	300
	GTGTGAGCCT		CCCTGAAGAA		CGGGAAGCAA		GTTTGTCTGG		ACCCGGAAGC		CCCTTTCTTA	360
	AAGAAAGTCA		TCCAGAAAAA		TTTGGACAGT		GGAAACAAAG		AAAACAGAGT		AACAAAAAAG	420
	ACCATGCATC		ATAAAATTGC		CCAGTCTTCA		GCGGAGCAGT		TTTCTGGAGA		TCCCTGGACC	480
	CAGTAAGAAT		AAGAAGGAAG		GGTGGTCTTT		TTTCCATTTT		CTACATGGAT		TCCCTACTTT	540
	GAAGAGTGTG		GGGGAAGGCC		TACGCTTCTC		CCTGAAGTTT		ACAGCTCAGC		TAATGAAGTA	600
	CTAATATAGT		ATTTCACCTA		TTTACTGTTA		TTTTACCTGA		TAAATTAATG		AACCCCTTGG	660
	CAATTGACCA		TATTGTGAGC		AAAGAAATCAC		TGGTTATTAG		TCTTTCAATG		AATATTGAAT	720
	TGAAGATAAC		TATTGTATTT		CTATCATACA		TTCTTAAAG		TCTTACCGAA		AAGGCTGTGG	780
	ATTTCGTATG		GAATAATGT		TTTATTAGTG		TGCTGTTGAG		GGAGGTATCC		TGTTGTTCTT	840
	ACTCACTCTT		CTCATAAAAT		AGGAAATATT		TTAGTTCTGT		TTTCTTGGGG		AATATGTTAC	900
	TCCTTACCCCT		AGGATGCTAT		TTAAGTTGTA		CTGTATTAGA		ACACTGGGTG		TGTCATACCG	960
	TTATCTGTGC		AGGAATATAT		TCCTTATTCA		GAATTTCTAA		AAATTTAAGT		TCTGTAAGGG	1020
	CTAATATAT		CTCTTCTCTAT		GGTTTATAGT		GTTTGATGTC		TTCTTAGTAT		GGCATAATGT	1080
	CATGATTTAC		TCATTAAACT		TGATTTTGT		ATGCTATTTT		TTCACTATAG		GATGACTATA	1140

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ATTCTGGTCA CTAATATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
 TGATTGCTAA TTACATAGA AATGTATTCT CTGGTTTTT TAAATAAAG CAAATTAAC 1260
 AATGATCTGT GCTCTGCAAA GTTTTGAAAA TATATTGAA CAATTTGAAT ATAAATTCAT 1320
 CATTTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
 TTTAAAGGTT TTGACCATTT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
 AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGGTTT TTGGTACTTG TATTGTCAAT 1500
 TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAA AAAAAA

Seq ID NO: 464 Protein sequence
 Protein Accession #: NP_002984.1

1 11 21 31 41 51
 MSLEPSSRAAR VPGPSGSLCA LLALLLLLP PGPLASAGPV SAVLTELRCT CLRVTLRVNP 60
 KTIGKLQVPP AGPQCSKVEV VASLKNGKQV CLDPEAPPLK KVIQKILDSG NRKN

Seq ID NO: 465 DNA sequence
 Nucleic Acid Accession #: NM_002038.2
 Coding sequence: 108..500

1 11 21 31 41 51
 GAACCGTTTA CTCGCTGCTG TGCCCATCTA TCAGCAGGCT COGGGCTGAA GATTGCTTCT 60
 CTCTCTCTCT CCAAGGTCTA GTGACGAGC CGCGCGCGG CGCCACCATG CGGCAGAAAG 120
 CGGTATCGCT TTTCTTGTGC TACCTGCTGC TCTTCACCTG CAGTGGGGTG GAGGCAGGTA 180
 AGAAAAAGTG CTCGAGAGAG TCGACAGCG GCTCGGGGTT CTGGAAGGCC CTGACCTTCA 240
 TGGCCGTCGG AGGAGGACTC GCAGTCGCGG GGTGCGCCG GCTGGGCTTC ACCGGCGCGG 300
 GCATCGCGGC CAATCGGGT GCTGCTCGC TGATGAGCTG GTCTGCGATC CTGAATGGGG 360
 GCGCGGTGCC CGCGGGGGG CTAGTGGCCA CGCTGCAGAG CCTCGGGGCT GGTGCAGCA 420
 GCGTCGTCTA AGGTAATATT GGTGCCCTGA TGGGCTACGC CACCCACAAG TATCTCGATA 480
 GTGAGGAGGA TGAGGAGTAG CCAGCAGCTC CCAGAACCTC TTCTTCTTTC TTGGCCTAAC 540
 TCTTCCAGTT AGGATCTAGA ACTTTGCTT TTTTTTTTT TTTTGGATGG 600
 GTTCTCACTA TATTGTCCAG GCTAGAGTGC AGTGGCTATT CACAGATGCG AACATAGTAC 660
 ATCGCAGCTT CCAACTCCTA GCTCAAGTG ATCTCTCTGT CTCACCTCC CAAGTAGGAT 720
 TACAAGCATG CGCCGACGAT GCCCAGAAAT CAGAACTTTG TCTATCACTC TCCCCAACAA 780
 CCTAGATGTG AAAACAGAAAT AAACCTTACC CAGAAAA

Seq ID NO: 466 Protein sequence
 Protein Accession #: NP_002029.3

1 11 21 31 41 51
 MRQKAVSLPL CYLLLFCTSG VEAGKKKCE SSDSGSGFWK ALTFMAVGGG LAVAGLPALG 60
 FTGAGIAANS VAASLMSWSA ILNGGGVPAG GLVATLQSLG AGGSSVVIGN IGALMGYATH 120
 KYLDSEEDBE

Seq ID NO: 467 DNA sequence
 Nucleic Acid Accession #: NM_003469.2
 Coding sequence: 92..1945

1 11 21 31 41 51
 GAAACGGCCC GAGAAGCTCG CCGGAGAAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60
 CATATAAACA AAAAGAGGAA ATCTTTCAA CATGGCTGAA GCAAAGACCC ACTGGCTGG 120
 AGCAGCCCTG TCTCTATGCC CTTTAATTTT CCTCATCTCT GGGGCTGAAG CAGCTTCATT 180
 TCAGAGAAAC CAGCTGCTTC AGAAAGAAC AGACCTCAGG TTGGAATAATG TCCAAAGTT 240
 TCCCATCTCT GAATGATACA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAAGTCA 300
 TAAGGAAGAA AGCAGCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360
 AAAAGAAAT GCGATGAA GGCACCTGCC CGAGAGGAT TCACTGAGTG AAGAAGACTG 420
 GATGAGAATA ATACTGAA GCTTGAGACA GGTGAAAT GAGCCTCAGT CTGCACCAA 480
 AGAAATAAG CCTATGCC TGAATTCAGA AAAGAACTT CCAATGGACA TGAGTGATGA 540
 TTATGAGACA CAGCAGTGGC CAGAAAGAAA GCTTAAGCAC ATGCAATTCC CTCCTATGTA 600
 TGAAGAGAA TCCAGGGATA ACCCTTTAA ACGCACAAT GAAATAGTGG AGGAACAATA 660
 TACTCTCAA AGCCTTGCTA CATTGGAATC TGTCTTCAA GAGCTGGGGA AACTGACAGG 720
 ACCAAACAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTTATA CGGATGATGA 780
 AGATGATATC TACAAGGCTA ATAAATTCG CTATGAAGAT GTGGTCGGGG GAGAAGACTG 840
 GAACCCAGTA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGA 900
 GAATATAGGA AAAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGGCAT 960
 CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020
 AATTGCTAT TTGAAAAGGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
 AAAATGGGAA AGGGCCACCA GGCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
 GCTGATTTGA ATCTCAAGGA ATTTACAGAT ACCCCAGAA GACTTAATTG AGATGCTCAA 1200
 AACTGGGGAG AAGCCGAATG GATCAGTGGG ACCGGAGCGG GAGCTTGACC TTCTGTGTA 1260
 CCTAGATGAC ATCTCAGAGG CTGACTTGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320
 CTCACAGAGT GGCTACCTTA AAACACCTGG TGTGCTGGG ACTGAGGCC TACCAGACGG 1380
 GCTCAGTGT GAGGATATTT TAAATCTTTT AGGGATGGAG AGTGAGCAA ATCAGAAAG 1440
 GTGATTTT CCATATCCAT ATAACAGGA GAAAGTTCTG CCAAGGCTCC CTTATGGTGC 1500
 TGGAGATCT AGATGGAACC AGCTTCCCAA AGCTGCTGG ATTCCACATG TTGAAAACAG 1560
 ACAGATGGCA TATGAAAACC TGAACGACA GGATCAAGAA TTAGGTGAGT ACTTGGCCAG 1620
 GATGCTAGTT AAATACCTG AGATCATTAA TTCAAACCA GTGAAGCGAG TTCCTGGTCA 1680
 AGGCTCATCT GAAGATGACC TGACGAGA GAACAAATT GAGCAGGCCA TCAAGAGCA 1740
 TTTGAATCAA GGCAGCTCTC AGGAGACTGA CAAGCTGGCC CGGTGAGCA AAAGGTTCC 1800
 TGTGGGGCCC CGAAGAAATG ATGATACCCC AAATAGGCAG TACTGGGATG AAGATCTGTT 1860
 AATGAAAGTG CTGGAATACC TCAATCAAGA AAAGCAGAAA AAGGGAAGG AGCATATTGC 1920

5 TAAGAGAGCA ATGGAATAA TGTAAGCTGC TTTCATTAAT TACCTACTT TCATTCTCC 1980
 CACCCCAAGC AAATCCCAAC ATTTCTCTTC AGTGTGTTGA CTCTATCTCT GTTAACACTG 2040
 TAATATCTTT AAATGATGTA CAGGCAGATG AAACAGGCTC ACTGGGAGT CTGCTTCATT 2100
 TCCTCTGAGC TGTATCTTG TGTATGATA TGTGTAATG TTATGACTCC TTGATAAAAA 2160
 ATTTATTATG TCATTATTTC AAGAAAGATA TCTATGACTG TGTTAATAG TATATCTAAT 2220
 GGCTGTGCA TGTGTGATG TCACATATGA TAAAAAGTG TCCTATAATT CTATTGAAAG 2280
 TTTTAAATAT TTATTGAATT ATTTTGTAC TGTCTGTAGC GTTTTGTGGA GTACTGGACC 2340
 AAAAAATAA AGCATTATAA ATATA

10 Seq ID NO: 468 Protein sequence
 Protein Accession #: NP_003460.1

15 1 11 21 31 41 51
 MAEAKTHWLG AALSLIPLIF LIISGAEAAAF ORNQLLQKEP DLRLLENVQKP PSEPMIRALE 60
 YIENLRQQAQ KEESPDPYNP YQGVSVPLQQ KENGDBSHLP ERDSLSEEDW MRIILEALRQ 120
 AENEPQSAPE ENKPYALNSE KNFPMDSDD YETQQWPERK LKHMQFPFMY EENSNDNPFK 180
 RTNEIVEEQY TPQSALTLES VFQELGKLTG FNNQKRERMD EEQKLYTDDE DDYKANNIA 240
 YEDVVGGEOW NPVEEKIESQ TQBEVRDSKE NIGKNEQIND EMKRSQGLGI QEEDLRKESK 300
 20 DQLSDVSKV IAYLKRLLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRLNI 360
 PPEDLIEMLK TGEKPNQSVF PERELDLFVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420
 RAGTEALPDG LSVEDILNLL GMESAANQKT SYFPNPNQBE KVLPRLPYGA GRSRSNQLPK 480
 AAWIPHVENR QMAYENLNDK DQELGEYLAR MLVKYPEIIN SNQVKRVPQG GSSEDDLQBE 540
 25 EQIEQAIKEH LNQGSSEETD KLAPVSKRFP VGPPKNDTTP NRQVWDELL MKVLEYLNQE 600
 KAEKGREHIA KRAMENM

30 Seq ID NO: 469 DNA sequence
 Nucleic Acid Accession #: NM_006398.1
 Coding sequence: 19..516

35 1 11 21 31 41 51
 GGCCCTTGT CTGCAGAGAT GGCTCCCAAT GCTTCCCTGCC TCTGTGTGCA TGTCCGTTCC 60
 GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAAATCAA 120
 GAACATGTCC GGTCTAAGAC CAAGGTTCTCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
 AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240
 CACCTTACCC TGAAGTGGT GAAGCCCAAT GATGAGGAGC TGCCCTTGT TCTTGTGGAG 300
 TCAGGTGATG AGGCAAGAG GCACCTCTCT CAGGTGCGAA GGTCCAGCTC AGTGGCACAA 360
 GTGAAGCAAT TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420
 40 AATGGAAGA GACTGGAAGA TGGGAAGATG ATGCGCAGAT ACGGCATCAG AAAGGGCAAC 480
 TTAATCTTCC TGGCATCTTA TTGTATTGGA GGTGACCCAC CCTGGGGATG GGTGTTGGC 540
 AGGGGTCAA AAGCTTATTT CTTTAAATCT CTTACTCAAC GAACACATCT TCTGATGATT 600
 TCCCAAAAT AATGAGAATG AGATGAGTAG AGTAAGATT GGTGGGATG GGTAGGATGA 660
 45 AGTATATTGC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAA TGACATGATT 720
 TTTACTAATG TATTACTGAG ACTAGTAAT AAATTTTAA GGCAAAATAG AGCATTTC

Seq ID NO: 470 Protein sequence
 Protein Accession #: NP_006389.1

50 1 11 21 31 41 51
 MAPNASCLCV HVRSEEWDLN TFDANPYDSV KRIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
 RSLSSYGIDK EKTILHLTKV VKPSDEELPL FLVESGDRAK RHLLQVRRSS SVAQVKAMIE 120
 55 TKTGIIPETQ IVTCNGKRLD DQKMMADYGI RKGNNLFLAS YCIGG

Seq ID NO: 471 DNA sequence
 Nucleic Acid Accession #: XM_094741.1
 Coding sequence: 1..948

60 1 11 21 31 41 51
 ATGAAGGCCA ACTACAGGCG AGAGGAGGCG TTTCCTCTGC TGGGTTTCTC CGACTGGCCT 60
 TCCTCTGAGC CGCTCTCTCT CGCCCTTGTC CTCTGTGCT ACCTCTGAC CTGACGGGCG 120
 65 AACTCGGCGC TGGTCTGCTT GCGGTGCGC GACCGGCGCC TGCAACGCC CATGTACTAC 180
 TTCTCTGCTG ACCTGGCCTT GGTAGACGCG GGCTTCACTA CTAGCGTGGT GCCGCCGCTG 240
 CTGGCCAAAC TGGCGGAGC AGCGCTCTGG CTGCGCGCA GCCACTGCAC GGCCAGCTG 300
 TGGCATCGC TGGCTCTGGG TTCGGCGGAA TGGCTCTCTC TGGCGGTGAT GGCTCTGGAC 360
 CGCGCGGCGC CAGTGTGCGC CCGCTGCGC TATGCGGGGC TCGTCTCCCG GCGCTATGT 420
 CGCACTCTGG CCAGCGCTCT CTGGCTAAGC GGCTTCACTA ACTGGTTCG GCAACCGCG 480
 70 CTCTGGCTG AGCGGCGGCT GTGCGGCGCC CGCTGCTGG ACCACTTCTAT CTGTGAGCTG 540
 CCGCGGTTCG TCAAGCTGGC CTGCGGAGGC GACGAGACA CTACCGAGAA CCAGATGTTT 600
 GCGGCGCGCG TGGTCTCTCT GCTGCTGCGG TTTGCGGTCA TCCTGGCTCT CTACGCTGCC 660
 GTGGCGCGAG CTGTCTGTTG CATGCGGTTT AGCGGAGGCC GAGGAGGCG GGTGGGCAAG 720
 75 TGTGGGTCCC ACCTGACAGC CGTCTGCTGG TTCTACGCTG CGCCATCTA CACTACCTG 780
 CAGCGCGCGC AGCGCTACAA CCAGGACGCG GGCAAGTTG TATCGCTCTT CTACACCGTG 840
 GTCAACACTG CTCTCAACCC GCTCATCTAC ACCCTCAGGA ATAAGAAAGT GAAGGGGGCA 900
 GCGAGGAGGC TGCTGCGGAG TCTGGGGAGA GGCCAGGCTG GGCACTGA

80 Seq ID NO: 472 Protein sequence
 Protein Accession #: XP_094741.1

1 -11 21 31 41 51
 MKANYSABER FLLLGFSWDP SLQPVLPALV LLCYLLTLTG NSALVLLAVR DPLRLTFMY 60

FLCHLALVDA GFTTSVVPPL LANLRGPALW LPRSHCTAQL CASLALGSAB CVLLAVMALD 120
 RAAAVCRPLR YAGLVSPRLC RTLASASWLS GLTNSVAQTA LLAERPLCAP RLDDHFICEL 180
 PALLKLACGG DGDITENQMF AARVVILLLP FAVILASYGA VARAVCCMRP SGGRRRAVOT 240
 CGSHLTAVCL FYGSAITYYL QPAQRYNQAR GKFVSLFTTV VTPALNPLIY TLRNKKVKGA 300
 ARLLRLSLGR GQAGQ

Seq ID NO: 473 DNA sequence
 Nucleic Acid Accession #: NM_001062.1
 Coding sequence: 76..1380

1 11 21 31 41 51
 | | | | |
 GCTCTCATT CCTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60
 TACACTGTTG GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTTACTGTTT 120
 TCTTTTATTC CAAGCCAACT ATGCGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180
 CTAAGACCTC TGTGAAATC AATGATCCAG TCAAACATA ACAGGGGAAC CAGCGCTGTC 240
 AATGTTGTGT TGTCCCTCAA ACTTGTGTGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300
 ATCCAACAAA TCAAAATCAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACTT AATATATGAT 420
 TACCACCTGA CTGCAAGCT AGAAAAATAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480
 CCAATGGCA CTCCCTGAC TAACTACTAC CAGCTCAGCC TGGAGTTT GGCCTTGTGT 540
 CTGTTCAATG GGAAGTACTC AACCCGCCAA GTTGTCAACC ACTTCACTCC TGAAAAATAA 600
 AACTATTATT TTGTTAGCCA GTTCTCAGTA GATCTGGTGT CAATGGCTGT CCTGGCTCTG 660
 ACGTGTGTTA AGAAGAGTCT AATAAATGGG CAGATCAAG CAGATGAAG CAGTTTAAAG 720
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTC TGTCTGAGAA AAAAGAAAAT 780
 GGTCTCATG GAAACACATT TAGCACAGGA GAAGCCATG AGGCCCTCT TGTATCATCA 840
 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAACTC TGAATACAGT GCTCACGGAA 900
 ATTTCTCAAG GAGCATTCAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960
 GGAAAGACCT TCTTGATAT TAACAAAGAC TCTTCTTGG TCTCTGCTTC AGGTAACCTC 1020
 AACATCTCCG CTGATGAGCC TATACTGTG ACACCTCCTG ACTCACAATC ATATATCTCC 1080
 GTCAATTACT CTGTGAGAAT CAATGAAACA TATTTCAACA ATGTCTGT GCTAAATGGT 1140
 TGTGCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320
 GGTAGTTACG TTGTCGCAA TGGAGAAAC TTGGAGGTTG GCTGAGCAA ATACTAATAA 1380
 GCCCAAACCT TCCTCAGCTG CATAAAATCC ATTGCACTG GAGTTCATG TTTATTGTCC 1440
 TTATGCTTTC TTCTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCTTCTC 1500
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAC

Seq ID NO: 474 Protein sequence
 Protein Accession #: NP_001053.1

1 11 21 31 41 51
 | | | | |
 MRQSHQLPLV GLLLFSPIPS QLCEICEVSE ENYIRLKPLL NTMIQSNYNR GTSAVNVVLS 60
 LKLVGIIQIT LMQKMIQIK YNVKSRLSDV SSGELALIL ALGVCRAE NLIYDYHLTD 120
 KLENKQABE ENMEAHNGTP LTNYQLSLD VLALCLFNGN YSTAENVNH TPENKNYYPG 180
 SQPSVDTGAM AVLALTCVKK SLINGQIKAD ESSLKNISY TKSLVEKILS EKKENGLIGN 240
 TFSGTGAMGA LFWSSDYNE NDWNCQQLN TVLTBISQGA FSNPNAAAQV LPALMGRTFL 300
 DINKSSSCVS ASGNFNISAD EPITVTPPDS QSYISVNSV RINETYFTNV TVLNGSVFLS 360
 VMEKAQKMD TIFQFTMBER SWGPYITCIQ GLCANMDRT YWELSSGEP LSQAGSYVV 420
 RNGENLEVRW SKY

Seq ID NO: 475 DNA sequence
 Nucleic Acid Accession #: NM_004852.1
 Coding sequence: 89..1546

1 11 21 31 41 51
 | | | | |
 GCCCGCGCCC GCCCGGGGCC CTGATGGACT GAATGAAGGC TGCCTACACC GCCTATCGAT 60
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 GCCGCTGGGC AACGGGCTAG GCGGCTCCA CAACGCGCAG CAGAGTCTCG CCAACTACGG 780
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5 Seq ID NO: 476 Protein sequence
Protein Accession #: NP_004843.1

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DERGLPAMNN LYSFYKEMPG MSQSLSPALAA TPLGNGLGGL HNAQQSLPNY GPPGHDKMLS 240
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15 SCSQVATSGQ LEBINTKEVA QRITAEIKRY SIPQAIAPAQR VLCSRSQGLS DLLRNPKPWS 360
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20 Seq ID NO: 477 DNA sequence
Nucleic Acid Accession #: NM_013271.1
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45 Seq ID NO: 478 Protein sequence
Protein Accession #: NP_037403.1

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55 Seq ID NO: 479 DNA sequence
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Coding sequence: 681..2990

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 Protein Accession #: NP_002205

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 50 SRDFRLGPOS YVDRTVSPYI SIHPERIHQV CSDYNLDQMP PHGYIHVLSL TENITRFEKA 240
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 VPNDGCHLKL NNVTYVRSSTM EHPSLGQLSE KLIDNNINVI PAVQKGQFHW YKDLLPLLP 360
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Seq ID NO: 482 Protein sequence
 Protein Accession #: NP_003309.1

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Seq ID NO: 484 Protein sequence
 Protein Accession #: NP_003658.1

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 TLKLYCNLDK DLENIMDCSM VKHIALLLFT NCILNCPVAF LSPFSSLINLT FISPEVIKFI 780
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Seq ID NO: 485 DNA sequence
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	TATACAGGGT	CTATCTTGCT	TCCTACCTAC	ATCTGCTTGA	GCAGTGCCTC	AAGTACATCC	4440
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Seq ID NO: 486 Protein sequence

Protein Accession #: NP_005747.1

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	NACAVIAALE	RVKIRPMEHC	CCSVRIPCPS	SPEELEKIQ	DLQDPVCL	DHPRGPPFSS	240
	SQSIPIVPPA	TVLSQVFKAT	SFAEPPDYS	VTHNVPSPIG	BIQPLSPQPS	APIASSPAID	300
	MPPQSETISS	PMPQTHVSQT	PPPVKASPS	PTVSAPANVN	TTSAPPVQTD	IVNTSSISDL	360
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50	NTTISLTSFS	LALAVIRVNA	SSFNTTTFVA	QDPANLQVSL	ETQAPENSIG	TITLEPSSLMN	480
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55	VFLLDSEIAL	YMQQLCISV	AVFLHYFLV	SFTNMGLEAF	BMYLALVKVF	NTYIRKYILK	720
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	FLNVMSPFIV	VLVQLCRIK	KKQLGAGRK	SIQDLRSIAG	LTFLLGITWG	PAFPWGFVN	840
	VTFMYLFAIF	NTLQGFIF	FYCVAKENVR	KQWRRLCCG	KLRLENSDW	SKTATNGLKK	900
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Seq ID NO: 487 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..2904

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70	AACGAAACAG	AAAAAATAA	AATCACTATA	GTAACAACTT	TCAATGCTTC	AGGCGTCAAA	240
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	GGCACTTAA	CTGAGTCCT	GTCCTAAGT	GAATTAACA	CATTAAATG	TACATTCA	420
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 Protein Accession #: Eos sequence

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5
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 25

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Seq ID NO: 490 Protein sequence
 Protein Accession #: Eos sequence

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1 11 21 31 41 51
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LSLSELKRSE LKNTLQLTSE TYPIMCATAE AQSTINCTFT IKLNNMTNAC AVIAALERVK 180
IRPMEHCCCS VRIPCPSSE ELKQLQDLQ DPIVCLADHP RGPFFSSSSQ IPVVPRTATV 240
SQVFKATGFA EPPYPSPVTH NVPSPIGEIQ PLSPQPSAPI ASSPALDMPP QSETISSPMP 300
QTRVSGTPPP VKASFSSPTV SAPANVNTS APFVQTDIVN TSSISDLENQ VLQMEKALSL 360
GSLEPNLAGE MINQVSRLLH SPPDMLAPLA QRLLKVVDDI GLQLNFSNTT ISLTSPLSL 420
AVIRVNASSP NTTTTFVAQDP ANLQVLELQ APENSIGTIT LPSSLMNNLP AHDMELASRV 480
QNFFFETPAL PQDPSLENLS LISYVISSSV ANLTVRNLTR NVTVLKHIN PSQDELTVRC 540
VFMDLGRNGG RGGWSDNGCS VKDRRLNETI CTCSHLTSFG VLLDLRSTSV LPAQMMALTF 600
ITYIGCGLSS IPLSVTLVTV IAFEKIRRDY PSKILQLCA ALLLNLVFL LDSWIALYKM 660
QGLCISVAVF LHYFLVSVFT WMGLEAFHMY LALVKVFNTY IRKYILKPCI VGNVGPVAVV 720
TIILTISPDN YGLGSYKFP NGSPDDPCWI NNNAVFYITV VGYFCVIFLL NVSMFIVVLV 780
QLCRIKKGKQ LQAQRKTSIQ DLRSLAGLTF LLGITWGFAP FANGPVNVTF MYLPAIFNTL 840
QGFFPIFYFC VAKENVRKQW RRYLCOGKLR LAENSGNAST ERNGVSFSVQ NGDVCLHDFP 900
GRQHMPNEKE DSCNGKGRMA LRRTSKROSL HPLEQM
  
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Seq ID NO: 491 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..3045

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1 11 21 31 41 51
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GATACTGATA ATTCCAGTTT GTCAACCACA CCGTCTAAAT TATCTGTTGT CAGTTTGGCC 180
CCCTCTCCA ATGAGGTTGA AACAAACAGC CTCAATGATG TTACTTTAAG CTTACTCCCT 240
TCAAAAGAAA CAGAAAAAAC TAAATCACT ATAGTAAAAA CCTTCAATGC TTCAGGCGTC 300
AAACCCGACA GAAATATCTG CAATTGTGCA TCTATTGCA ATGACTCAGC ATTTTGTAGA 360
GGTGAGATCA TGTTTCAATA TGATAAGAA AGCACTGTTC CCCAGATCA ACATATAACG 420
AATGGCACTT TAATCGAGT CCGTCTCTTA AGTGAATTAA AACGCTCAGA GCTCAACAAA 480
ACCTGCAAAA CCTAAGTGA GACTTACTTT ATAATGTGTG CTACAGCAGA GGCCCAAGC 540
ACATTAATTT GTACATTAC AATAAACTG AATAATACAA TGAATGCATG TGTGCAATA 600
CGCGCTTTGG AAGAGTAAA GATTGACCA ATGGAACACT GCTGCTGTTT TGTGAGATA 660
CCCTGCCCTT CCTGCCAGA AGAGTTGGGA AAGCTTCAGT GTGACCTGCA GGATCCCAT 720
GTCTGTCTTG CTGACCATCC ACGTGGCCCA CCAATTTCTT CCAGCCAAAT CATCCAGTG 780
GTGCTGTGGG CCACTGTGCT TTCCAGGTC CCCAAAGCTA CCTCTTTTGC TGAGCCTCCA 840
GATTATTCAC CTGTGACCCA CAATGTTCCC TCTCCATAG GGGAGATTCA ACCCTTTTCA 900
CCCGAGCTTG CAGTCCCAT AGCTTCCAGC CTGCTCATG ACATGCCCC ACAGTCTGAA 960
ACGATCTCTT CCCCTATGCC CCAAACCAT GTCTCOGGA CCCCACCTCC TGTGAAAGCC 1020
TCATTTTCTT CTCCACCGT GTCTGCCCTT GCGAATGTCA ACATACCAG CGCACCTCT 1080
GTCCAGCAG ACATAGTCAA CACCAGCAGT ATTTCTGATC TTGAGAACCA AGTGTTCAG 1140
ATGGAAGAGG CTCTGTCTT GGGCAGCTG GAGCCTAAC TCGCAGGAGA AATGATCAAC 1200
CAAGTCAGTA GACTCCTTCA TTCCCGCTT GACATGCTGG CCCCTCTGG TCAAGATTG 1260
CTGAAAGTAG TGGATGACAT TGGCCTACAG CTGAACCTTT CAACACGAC TATAAGTCTA 1320
ACCTCCCTTT CTTTGGCTCT GGTGTGTATC AGAGTGAATG CCAGTAGTTT CAACACACT 1380
ACCTTTGTGG CCCAAGACCC TGCAATCTT CAGGTTTCTC TGGAAACCCA AGCTCCTGAG 1440
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TGGTCAGACA ATGGCTGCTC TGTCAAAGAC AGGAGATTGA ATGAAACCAT CTGTACTGCT 1800
AGCCATCTAA CAAGCTTCGG CGTTCTGCTG GACCTATCTA GGACATCTGT GCTGCTGCT 1860
  
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5 CAAATGATGG CTCTGACGTT CATTACATAT ATTGGTTGTG GGCTTTTCATC AATTTTTCCTG 1920
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 10 TGATTTGCTC TGATTAAGAT GCAAGGCTCT TGCATCTCAG TGGCTGTATT TCTTCATTAT 2100
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 CAGCACATGT TTAACGAGAA GGAAGATTCC TGCAATGGGA AAGGCCGTAT GGCTCTCAGA 3000
 AGGACTTCAA AGCGGGGAAG CTTACACTTT ATTGAGCAAA TGTGA

Seq ID NO: 492 Protein sequence
 Protein Accession #: Eos sequence

25 1 11 21 31 41 51
 MVPSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPF PAKLSVVSFA 60
 PSSNEVETTS LNDVTLGSLP SNETEKTKIT IVKTFNASGV KPQRNICNLS SICNDSAPFR 120
 30 GEIMFPQYDKE LMDVTLGSLP NGTLTGVLST SELKRSELNK TLQTLSETYP IMCATAEAQS 180
 TLNCTFTIKL NNTMNAACAI AALERVKIRP MEHCCCSVRI PCPSPPEELG KLQCDLQDPI 240
 VCLADHPRGP PFSSSQSPV VPRATVLSQV PKATSFAPFP DYSPVTHNVP SPIGEIQPLS 300
 PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTFFPVKA SFSSPTVSAP ANVNTTSAPP 360
 VQTDIVNTSS ISDLENQVLQ MEKALSLGSL EPNLAGEMIN QVSRLLHSPP DMLAPLAQRL 420
 35 LKVVDDIGLQ LNFSTTISL TSPSLALAVI RVNASSFNIT TFVAQDPANL QVSLETQAPE 480
 NSIGITILPS SLMMNLPAHD MELASRVQFN PFETPALPQD PSLENLSLIS YVSSSVANL 540
 TVRNLTRNVT VTLKHINPSQ DELTVRCVFW DLGRNGGRGG WSDNGCSVKD RRLNETICTC 600
 SBLTSFGVLL DLSRTSVLPA QMMALTFITY IGCGLSIFL SVTLVTYIAF EKIRRDYPSK 660
 ILIQLCAALL LLNLVFLDLS WIALYKMQGL CISVAVFLHY PLLVSPTWMG LEAFHMYLAL 720
 40 VKVPNTYIRK YLKLFCIVGW GVPVAVVTII LTISPNDNYL GSYGKFPNGS PDDFCWINNN 780
 AVFYITVVG YFCVIFLLNVS MPVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840
 ITWGFAPFAW GPNVTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKLRLAE 900
 NSDWSKTATN GLKKQTVNQG VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGMASTER 960
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45 Seq ID NO: 493 DNA sequence
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241..1902

50 1 11 21 31 41 51
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 55 GGGTCCGGCC GGGCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGGCAGA 240
 ATGCCTCTGC CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
 GGGAAACGGG CAGGTGCAAG GCATCAAGGG TTGTAGCAT CGGCACGTCA GCGTGGGGTC 360
 TGTCACTATG GAACTAAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
 TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAAT GCGTGGGACC AAACAAATGC 480
 60 AGATGCTTTC CAGGATACAC CGGAAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAAG GAAGCTACAA GTGCTTTTGC 600
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
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 ATCCCTGAAA ATTCGTGTGA GGAAGTCCCT AGAGCACCTG GTACCATCAA AGACAGAATC 1080
 70 AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAAGAGG CAAAAATTAA AAATGTTACC 1140
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 75 CTGCTCCAAA GGAAAGCGCT AACCTCCAAA CTGGAAACATA AAGATTAAAA TATCTCGGTT 1440
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 TGGAACTGTA CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGGCA 1560
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5 TCTTGATATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
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10 Seq ID NO: 494 Protein sequence
 Protein Accession #: NP_056322

15 1 11 21 31 41 51
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 LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEPQCLCPSS SGLRLAPNGR DCLDIDECAS 180
 GKVICPNYRR CVNTFGSYVC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNQ 240
 GSPKCKCKQG YKGNLRCBA IPENSVKEVL RAPGTIKDRI KLLLAHKNSM KKKAKIRNVT 300
 PEPRTPTPK VNLQPPNYEE IVSRGGNSHG GKKGNNEKMK EGLEDEKRER KALKNDIEER 360
 SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGIC WKQDREDDFD 420
 WNPADRNDAI GFYMAVPAIA GHKKDIGRLK LLLPDLQFQS NFCLLFQYRL AGDKVGLKRV 480
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25 Seq ID NO: 495 DNA sequence
 Nucleic Acid Accession #: NM_003506.1
 Coding sequence: 259..2379

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 GGCCAAGTGC AATTGACTCT CTTTITTTAA TGTTCATGA CCACCCATTG ATTGTATTAT 3240

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5 Seq ID NO: 496 Protein sequence
Protein Accession #: NP_003497.1

1 11 21 31 41 51
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CAPPCPMNMF KSDLELEPAKS FIGTVSIFCL CATLPTFLTP LIDVRRFRYP ERIPIIYSVC 240
YSIVSLMYFI GFLLGDSSTAC NKADEKLEBLG DTVVLGSONK ACTVLFMLLY FPMAGTVNM 300
15 VILTITWFLA AGRKWSCRAI EQKAVMPHAV AWGTPGFLTV MLLALNKVEG DNISGVCFVG 360
LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVROVI QHDGRNQEKI KKFIRIGVFP 420
SGLYLVPLV LLGCYVVEQV NRITWEITWV SDRCRQYHIP CPYQAKAKAR PELALFMIKY 480
LMTLIVGISA VWVGSKKTC TEWAGFFKRN RKRDPISESR RVLQESCRFP LKHNSKVKKH 540
KHYKPSSEHK LKVISKSMGT STGATANHGT SAVAITSHDY LGQETLTBIQ TSPETSMREV 600
20 KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKQAG SVGESARSEG RISPKSDITD 660
TGLAQSNLQ VPSSEPSL KGSTSLLVHP VSGVRKEQGG GCHSDT

25 Seq ID NO: 497 DNA sequence
Nucleic Acid Accession #: NM_005046
Coding sequence: 16..777

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GAGAGCGTCC TGGTCAATGA GCGCTGGGTG CTCACTGCCG CCCACTGCAA GATGAATGAG 240
TACACCGTGC ACCCTGGGAG TGATACGCTG GGCACAGGA GAGCTCAGAG GATCAAGGCC 300
TCGAAGTCAT TCGCCACCCC CGGCTACTCC ACACAGACCC ATGTTAATGA CCTCATGCTC 360
35 GTGAAGCTCA ATAGCCAGGC CAGGCTGTCA TCCATGGTGA AGAAAGTCAG GCTGCCCTCC 420
CGCTGCGAAC CCCTCGAAC CACTGTACT GTCTCGGCT GGGGCACTAC CACGAGCCCA 480
GATGTGACT TTCCCTCTGA CCTCATGTGC GTGGATGTCA AGCTCATCTC CCCCCAGAC 540
TGCAAGAGG TTTACAAGGA CTTACTGGAA AATTCATGC TGTGCGCTGG CATCCCCGAC 600
TCCAAGAAAA ACGCTTCGAA TGGTGACTCA GGGGACCGT TGGTGTGCAG AGGTACCTG 660
40 CAAGGTCTGG TGTCTGGGG AACTTTCCCT TGGCGCCAAC CCAATGACCC AGGAGTCTAC 720
ACTCAAGTGT GCAAGTTCAC CAAGTGGATA AATGACACCA TGAAAAAGCA TCGCTAACGC 780
CACACTGAGT TAATTAACCTG TGTGCTTCCA ACAGAAAAATG CACAGGAGTG AGGACGCGA 840
TGACCTATGA AGTCAAAATTT GACTTTACCT TTCCTCAAAG ATATATTTAA ACCTCATGCC 900
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45 AACCTCAA

50 Seq ID NO: 498 Protein sequence
Protein Accession #: NP_005037

1 11 21 31 41 51
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QARLSMWVK VRFPSCRPEP GTTCTVSGWG TTTSPDVTFP SDLMCVDVKL ISPQDCTKVY 180
55 RDLLENSMLC AGIPDSKRNA CNGDSGGPLV CRGTLQGLVS WGTFFPCGQFN DPGVYTVCK 240
FTKNINDTKK KHR

60 Seq ID NO: 499 DNA sequence
Nucleic Acid Accession #: NM_007196
Coding sequence: 182..962

1 11 21 31 41 51
GTTCCAGAA GCTCCCCAGG CTCTAGTGCA GGAGGAGAAG GAGGAGGAGC AGGAGGTGGA 60
65 GATTCCCAAT TAAAGGCTC CAGAAATCGT TACCAGGCAG AGAACTGAAG TACTGGGGCC 120
TCCTCCACTG GGTCCGAATC AGTAGGTGAC CCGGCCCTG GATTCTGGAA GACCTCACCA 180
TGGGAGCCCC CGACCTCGT GGGGCCAAGA CGTGGATGTT CCTGCTCTTG CTGGGGGGAG 240
CCTGGGCAGG ACACCTCCAG GCACAGGAGG ACAAGGTGCT GGGGGGTCT GAGTGCCAAAC 300
CCCATTGCGA GCCTTGGCAG GCGGCCTTGT TCCAGGGCCA GCAACTACTC TGTGGCGGTG 360
70 TCCTTGTAGG TGGCAACTGG GTCCCTTACAG CTGCCCACTG TAAAAAACCG AAATACACAG 420
TACGCGTGGG AGACCAACAG CTACAGAATA AAGATGGGCC AGAGCAAGAA ATACCTGTGG 480
TTCAGTCCAT CCAACACCCC TGCTACAACA GCAGCGATGT GGAGGACCAC AACCATGATC 540
TGATGCTTCT TCACTGCGT GACCAGGCAT CCCTGGGGTC CAAAGTGAAG CCCATCAGCC 600
TGGCAGATCA TTGCACCCAG CCTGGCCAGA AGTGACCGT CTCAGGCTGG GGCATGTCA 660
75 CCAGTCCCCG AGAGAAATTT CCTGACACTC TCAACTGTGC AGAAGTAAAA ATCTTTCCCC 720
AGAAGAAAGT TGAGGATGCT TACCAGGGGC AGATCACAGA TGGCATGTGC TGTGACGGCA 780
GCAGCAAGG GCGTGACACG TGCCAGGGCG ATTCTGGAGG CCCCCTGGTG TGTGATGGTG 840
CACTCCAGGG CATCACATCC TGGGGCTCAG ACCCTGTGG GAGGTCCGAC AAACCTGGCG 900
80 TCTATACCAA CATCTGCCG TACCTGGACT GGATCAAGAA GATCATAGGC AGCAAGGGCT 960
GATTCTAGGA TAAGCACTAG ATCTCCCTTA ATAACTCAC AACTCTC

Seq ID NO: 500 Protein sequence
Protein Accession #: NP_009127

1 11 21 31 41 51

5 MGRPRPRAAK | TNPFLLLGG | AWAGHSRAQE | DKVLGGHECQ | PHSQPMQAL | FQGQQLLOGG 60
 VLVGGNMVLT | AAKCKPKYTT | VRLGDHSLQN | KDGPEQEIFV | VQSIPHCYN | SSDVEDHNHD 120
 LMLQLRQDA | SLGSRVKPIS | LADHCTQPGQ | KCTVSGWGTV | TSPRENFDT | LNCAEVKIFP 180
 QKKCEADYPG | QITDGMVCAG | SSRGADTCQG | DSGGPLVCDG | ALQGITSNWS | DPCGRSDKPG 240
 VYTNICRYLD | WIKKIIGSRG

Seq ID NO: 501 DNA sequence
 Nucleic Acid Accession #: NM_006103
 Coding sequence: 29..406

15 1 | 11 | 21 | 31 | 41 | 51
 CACCTGCACC | CCGCCCCGGC | ATAGCACCAT | GCCTGCTTGT | CGCCTAGGCC | CGCTAGCCGC 60
 CGCCCTCTCT | CTCAGCCTGC | TGCTGTTCGG | CTTCACCCCTA | GTCTCAGGCA | CAGGAGCAGA 120
 GAAGACTGGC | GTGTGCCCGG | AGCTCCAGGC | TGACCAGAAC | TGACGCAAG | AGTGOGTCTC 180
 GGACAGCGAA | TGGCCGACG | ACCTCAAGTG | CTGCAGCGCG | GGCTGTGCCA | CCTTCTGCCT 240
 TCTCTGCCCA | AATGATAAGG | AGGGTTCCTG | CCCCAGGTG | AACATTAACT | TTCCCCAGCT 300
 CGGCCCTCTG | CGGGACCAGT | GCCAGGTGGA | CAGCCAGTGT | CCTGGCCAGA | TGAAATGCTG 360
 CGGCAATGGC | TGTGGGAAGG | TGTCTGTGT | CACTCCCAAT | TTCTGAGTTC | CAGCCACCAC 420
 CAGGCTGAGC | AGTGAGGAGA | GAAAGTTTCT | GCCTGGCCCT | GCATCTGTTT | CCAGCCACC 480
 TGCCCTCCCC | TTTTTCGGGA | CTCTGTATTG | CCTCTTGGGC | TGACCACAGC | TTCTCCCTTT 540
 CCCAACCAAT | AAGTAACCA | CTTTCAGCAA | AAAAAAAAAA | AAAA

25 Seq ID NO: 502 Protein sequence
 Protein Accession #: NP_006094

30 1 | 11 | 21 | 31 | 41 | 51
 MPACRLGLPA | AALLSLLLF | GFTLVSGTGA | EKTGVCPBLQ | ADQNTQBEV | SDSECADNLK 60
 CCSAGACTFC | LLCPNDEKGS | CPQVNINFPQ | LGLCRDQCQV | DSQCPOQMKC | CRNGCGKVSC 120
 VTPNF

35 Seq ID NO: 503 DNA sequence
 Nucleic Acid Accession #: NM_002407
 Coding sequence: 65..352

40 1 | 11 | 21 | 31 | 41 | 51
 CCTCCACAGC | AACTTCCTTG | ATCCCTGCCA | CGCAGACTGT | AACACAGACA | GCAGCCGCCT 60
 GGCATGAAG | CTGCTGATGG | TCCTCATGCT | GCGCGCCCTC | CTCTGCACCT | GCTATGCAGA 120
 TTCTGGCTGC | AACTTCCTGG | AGGACATGGT | TGAAAGACCC | ATCAATTCGG | ACATATCTAT 180
 ACCTGAATAC | AAGAGAGTTC | TTCAAGAGTT | CATAGACAGT | GATGCCGCTG | CAGAGGCTAT 240
 GGGGAATTC | AAGCAGTGTG | TCCTCAACCA | GTCACATAGA | ACTCTGAAA | ACTTTGGACT 300
 GATGATGCAT | ACAGTGTACG | ACAGCATTTG | GTGTAATATG | AAGAGTAATT | AACTTTACCC 360
 AAGGCGTTTG | GCTCAGAGGG | CTACAGACTA | TGGCCAGAAC | TCATCTGTTG | ATTGCTAGAA 420
 ACCACTTTTC | TTTCTGTGTG | TGTCTTTTGA | TGTGGAAACT | GCTAGACAAC | TGTGAAACC 480
 TCAATTCAT | TTCCATTTC | ATAATAACT | GCAAAATC

50 Seq ID NO: 504 Protein sequence
 Protein Accession #: NP_002398

55 1 | 11 | 21 | 31 | 41 | 51
 MKLLMVLMLA | ALLLHCYADS | GCKLLEDMEV | KTINSDISIP | EYKELLQEP | DSDAAAEAMG 60
 KFKQCFLNQS | HRTLNPFGLM | MHTVYDSIWC | NMKEN

60 Seq ID NO: 505 DNA sequence
 Nucleic Acid Accession #: NM_014791.1
 Coding sequence: 171..2126

65 1 | 11 | 21 | 31 | 41 | 51
 TTGGCGGGCG | GAAGCGGCCA | CAACCGGCG | ATCGAAAAGA | TTCTTAGGAA | CGCCGTACCA 60
 GCGCGTCTC | TCAGGACAGC | AGGCCCTCTG | CCTTCTGTCT | GCGCGCGCTC | AGCCGTGCCC 120
 TCAGCGCTC | AGGTTCTTTT | TCTAATTCCA | AATAAACTTG | CAAGAGGACT | ATGAAAGATT 180
 ATGATGAAC | TCTCAATAT | TATGAATTAC | ATGAACTAT | TGGGACAGGT | GGCTTTGCAA 240
 AGGTCAAACT | TGCTGCCAT | ATCCTTACTG | GAGAGATGGT | AGCTATAAAA | ATCATGGATA 300
 AAAACACACT | AGGAGTGTAT | TTGCCCGGA | TCAAAACGGA | GATTGAGGCC | TTGAAGAACC 360
 TGAGACATCA | GCATATATGT | CAATCTACCC | ATGTGCTAGA | GACAGCCAAC | AAAATATTCA 420
 TGGTTCTTGA | GTACTGCCCT | GGAGGAGAGC | TGTTTGACTA | TATAATTTC | CAGGATCGCC 480
 TGTGAGAAGA | GGAGACCCGG | GTTGTCTTCC | GTCAGATAGT | ATCTGCTGTT | GCTTATGTGC 540
 ACAGCCAGGG | CTATGCTCAC | AGGGACCTCA | AGCCAGAAAA | TTTGCTGTTT | GATGAATATC 600
 ATAAATTAAA | GCTGATTGAC | TTTGGTCTCT | GTGCAAAACC | CAAGGTAAC | AAGGATTACC 660
 ATCTACAGAC | ATGCTGTGGG | AGTCTGGCTT | ATGAGCACC | TGAGTTAATA | CAAGGCAAAAT 720
 CATATCTTGG | ATCAGAGGCA | GATGTTTGGG | GCATGGGCAT | ACTGTTATAT | GTTCTTATGT 780
 GTGGATTCT | ACCATTGAT | GATGATAATG | TAATGGCTTT | ATACAAGAAG | ATTATGAGAG 840
 GAAATATGA | TGTTCCTCAAG | TGGCTCTCTC | CCAGTAGCAT | TCTGCTTCTT | CAACAAATGC 900
 TGCAAGTGA | GCTAAGAAA | CGGATTCTTA | TGAATAATCT | ATTGAACCAT | CCTTGATATG 960
 TGCAAGATTA | CAATATCTCT | GTTGAGTGGC | AAAGCAAGAA | TCTTTTATT | CACCTGATG 1020
 ATGATTGCT | AACAGAACTT | TCTGTACATC | ACAGAAACAA | CAGGCAACAA | ATGGAGGATT 1080
 TAATTTCACT | GTGGCAGTAT | GATCACCTCA | CGGCTACCTA | TCTTCTGCTT | CTAGCCAAGA 1140
 AGGCTGGGG | AAAACAGTT | CGTTTAAGGC | TTTCTTCTT | CTCTGTGGA | CAAGCCAGTG 1200
 CTACCCCAT | CACAGACATC | AAGTCAAATA | ATTGGAGTCT | GGAAGATGTG | ACCGCAAGTG 1260

5 ATAAAAATTA TGTGGCGGGA TTAATAGACT ATGATTGGTG TGAAGATGAT TTATCAACAG 1320
 GTGCTGCTAC TCCCGGAACA TCACAGTTTA CCAAGTACTG GACAGAATCA AATGGGGTGG 1380
 AATCTAAATC ATTAATCTCA GCCTTATGCA GAACACCTGC AAATAAATTA AAGAACAAG 1440
 AAAATGTATA TACTCCTAAG TCTGCTGTAA AGAATGAAGA GTACTTTATG TTCTCTGAGC 1500
 CAAGACTCC AGTTAATAAG AACAGCATA AGAGAGAAAT ACTCACTACG CCAAAATCGTT 1560
 ACACACACCC CTCAAAAGCT AGAAACCACT GCCTGAAAGA AACTCCAATT AAAATACCAG 1620
 TAAATTCAAC AGGAACAGAC AAGTTAATGA CAGGTGTGAT TAGCCCTGAG AGGCGGTGCC 1680
 GCTCAGTGGG ATTGGATCTC AACCAAGCAC ATATGGAGGA GACTCCAAA AGAAGGGGAG 1740
 10 CCAAAGTGTT TGGGAGCCTT GAAAGGGGGT TGGATAAGGT TATCACTGTG CTCACCAGGA 1800
 GCAAAAGGAA GGGTCTGCCC AGAGACGGGC CCAGAAGACT AAAGCTTCAC TATAATGTGA 1860
 CTACAACATG ATTAGTGAAT CCAGATCAAC TGTGAAATGA AATAATGTCT ATTCTTCCAA 1920
 AGAAGCATGT TGACTTTGTA CAAAAGGGTT ATACACTGAA GTGTCAAACA CAGTCAGATT 1980
 TTGGGAAAGT GACAATGCAA TTTGAATTAG AAGTGTGCCA GCTTCAAAA CCGATGTGG 2040
 15 TGGGIATCAG GAGGCAGCGG CTTAAGGGCG ATGCTCTGGT TTACAAAAGA TTAGTGAAG 2100
 ACATCCTATC TAGCTGCAAG GTATAATGA TGGATTCTCT CATCTGCGCG GATGAGTGTG 2160
 GGTGTGATAC AGCCTACATA AAGACTGTGA TGATCGCTTT GATTTTAAAG TTCATTGGAA 2220
 CTACCAACTT GTTTCTAAAG AGCTATCTTA AGACCAATAT CTCTTTGTTT TTAACAAAA 2280
 GATATTATTT TGTGTATGAA TCTAAATCAA GCCCATCTGT CATTATGTTA CTGCTTTTT 2340
 20 TAATCATGTG GTTTTGTATA TTAATAATTG TTGACTTTCT TAGATTCACT TCCATATGTG 2400
 AATGTAAGCT CTTAACTATG TCTCTTGTGA ATGTGTAATT TCTTCTGAA ATAAACCAT 2460
 TTGTGAATAT

Seq ID NO: 506 Protein sequence

Protein Accession #: NP_055606.1

25 1 11 21 31 41 51
 MKDYDELLKY YELHETIGTG GFAKVKLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
 30 LKRLRHQHC QLYHVLETAN KIFMVLEYCP GGELFDYIIS QDRLSEETR VVFRQIVSAV 120
 AYVHSQQYAH RDLKPENLLF DEYHKLKID FGLCAKPKGN KDYLQTCG SLAYAAPELI 180
 QGKSVLGS EA DWVSMGILLY VLMCGFLPF DDNVMALYKK IMRGKYDVPK WLSFSSILL 240
 QQMLQVDPKK RISMKNLLNH FWIMQDYNYP VEWQSKNFFI HLDGDCVTEL SVHRRNNRQT 300
 MEDLISLWQY DHLTATYLLL LAKKARGKPV RLRLSSPSCG QASATPPTDI KSNWMSLEDV 360
 35 TASDNKYVAG LDIDYDWCDD LSTGAATPRT SQPTKYWTES NGVESKSLTP ALCRTPANKL 420
 KKNENVYTFK SAVKNEEYFM PPEPKTFVNK NQHKREILLT PNRYTTPSKA RNQCLKETPI 480
 KIPVNSTGTD KLMTGVISPE RRCRSVELDL NQAHMEETPK RKGAKVFGSL ERGLDKVITV 540
 LTRSKRKGSA RDGPRRLKIH YNVTTRLVN PDQLNEIMS ILPKGHVDFV QKGYTLKQCT 600
 QSDFGKVTMQ FELEVQLQK PDVVGIRRRQ LKGDWVYKR LVEDILSSCK V

Seq ID NO: 507 DNA sequence

Nucleic Acid Accession #: NM_000582

Coding sequence: 88..990

45 1 11 21 31 41 51
 GCAGAGCACA GCATGCTGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
 AAGCGCGACC AAGGAAACT CACTACCATG AGAATTGCAG TGATTGTGCT TTGCTCCTA 120
 GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAGCAG 180
 50 CTTTACAACA AATACCCAGA TGCTGTGCCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
 CAGAATCTCC TAGCCCCACA GACCCCTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300
 GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
 AAGCACTCTG ATGATGTAGA TGCACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
 TCTGATGAAT CTGATGAAC GGTCACTGAT TTTCCACGCG ACCTGCCAGC AACCGAAGTT 480
 55 TTCACTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
 GGACTGAGGT CAAAATCTAA GAAATTTCCG AGACCTGACA TCCAGTACCC TGATGCTACA 600
 GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGGTGATA CAAGGCCATC 660
 CCGTGTGCC AGGACCTGAA CCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
 GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
 60 TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA 840
 CTTTCCAAGC TCAGCCGTGA ATTCCACAGC CATGAATTTT ACAGCCATGA AGATATGCTG 900
 GTTGTAGAAC CCAAAAGTAA GGAAGAAGAT AACACCTGA AATTTCTGAT TTCTCATGAA 960
 TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAAATT CTCACTTTGC 1020
 ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080
 65 CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
 ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAC TAAAAGCTTC AGGGTTATGT 1200
 CTATGTTTAT TCTATAGAAG AAATGCAAAAC TATCACTGTA TTTTAATATT TGTATTCTC 1260
 TCAATGAATG AAATTTATGT AGAAGCAAAC AAAATACITT TACCCACTTA AAAAGAGAAT 1320
 70 ATAACATTTT ATGTCACIAT AATCTTTTGT TTTTAAAGTT AGTGTATATT TTGTTGTGAT 1380
 TATCTTTTGG TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGTGTGC 1440
 AATTGCTTAT TTGTTTCCCC ACGGTGTGCC AGCAATTAAT AAAACATAAC CTTTCTTACT 1500
 GCCTAAAAAA AAAAAAAAAA AAAA

Seq ID NO: 508 Protein sequence

Protein Accession #: NP_000573

75 1 11 21 31 41 51
 MRAIVICFCL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLLAPQTL 60
 PSKSNESHSH MDDMDDEDD DHVDSQDSID SNDSDDVDPT DDSHQSDSH HSDESDELVT 120
 80 DFPTDLPAE VFTFPVVTVD TYDGRGDSV YGLRSKSKFP RRPDIQYFDA TDEDITSHME 180
 SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
 NEHSDVIDSQ ELKSVSREPH SHEFHSHEDM LVVDPKSKKE DKHLKFRISH ELDSASSEVN

Seq ID NO: 509 DNA sequence
Nucleic Acid Accession #: AB051390.1
Coding sequence: 34..2457

5	1	11	21	31	41	51	
	AGCGGCGCGG	GCACAAAGTT	GGGGGCGCGG	AAGATGAGGC	TGTCCCGCGC	GCCCCGGAAG	60
	CTGAGCGCGG	CTCGGCACT	GCTGGCCCTG	GCGCTGCCCC	TGGCGCGGCG	GCTGGCCCTC	120
10	TCCGACGAGA	CCCTGGACAA	AGTGCCCAAG	TCAGAGGGCT	ACTGCAGCGG	TATCTGCGCG	180
	GCCCAGGGCA	CGCGGCGCGA	GGGCTACACC	GAGTTGAGCC	TCCGCGTGGA	GGGCGACCCC	240
	GACTTCTACA	AGCCGGGAAC	CAGCTACCGC	GTAACTCTTT	CAGCTGCTCC	TCCCTCCTAC	300
	TTGAGAGGAT	TCACATTAA	TGCCCTCAGA	GAGAACAGAG	AGGGTGATAA	GGAAGAAGAC	360
	CATGCTGGGA	CCTTCCAGAT	CATAGACGAA	GAAGAAACTC	AGTTTATGAG	CAATTGCCCT	420
15	GTTGCACTCA	CTGAAAGCAC	TCCAAGGAGG	AGGACCCGGA	TCCAGGTGTT	TTGGATAGCA	480
	CCACCAGCGG	GAACAGGCTG	CGTGATTCTG	AAGGCCACGA	TCGTACAAAA	ACGCATTATT	540
	TATTTTCAAG	ATGAGGGCTC	TCTGACCAAG	AACTTTGTGT	AACAAGATTC	CACATTTGAT	600
	GGGGTGACTG	ACAAACCCAT	CTTAGACTGC	TGTGCTCTGG	GAACCTGCCA	GTACAGACTC	660
	ACATTTTATG	GGAAATGGTC	CGAGAAGACA	CACCCAAAGG	ATTACCTCTG	TCGGGCCAAC	720
20	CAGTGGTCTG	CGATCATCGG	AGGATCCCAC	TCCAAGAAAT	ATGTACTGTG	GGAATATGGA	780
	GGATATGCCA	GCGAAGCGGT	CAACAAGATT	GCAGAAITGG	GCTCACCCGT	GAAATGGAG	840
	GAAGAAATTC	GACAACAGAG	TGATGAGGTC	CTCACCCGTC	TCAAAGCCAA	AGCCCAATGG	900
	CCAGCCTGGC	AGCCTCTCAA	CGTGAGAGCA	GCACCTTCAG	CTGAATTTTC	CGTGGACAGA	960
	ACGCGCCATT	TAATGTCTTT	CCTGACCATG	ATGGGCCCTA	GTCCGAGCTG	GAACGTAGGC	1020
25	TTATCTGCA	AGATCTGTG	CACCAAGGAA	TGTGGCTGGG	TCCAGAAAGT	GGTGCAAGAC	1080
	CTGATTCCTT	GGGACGCTGG	CACCGACAGC	GGGGTGACCT	ATGAGTCACC	CAACAAACCC	1140
	ACCATTTCCC	AGGAGAAAAT	CCGGCCCTTG	ACCAGCCTGG	ACCATCTCTA	GAGTCTTTTC	1200
	TATGACCCAG	AGGGTGGGTC	CATCACTCAA	GTAGCCAGAG	TTGTCTCGA	GAGAACTGCA	1260
	CGGAAGGGTG	AACAATGCAG	TATTTGTACT	GACAATGTGC	ATGATATTGT	AGCTGACCTG	1320
30	GCTCCAGAG	AGAAAGATGA	AGATGACACC	CCTGAAACCT	GCATCTACTC	CAACTGGTCC	1380
	CCATGTCGCG	CCTGCAGCTC	CTCCAACCTG	GACAAAGGCA	AGAGGATGCG	ACAGGCGATG	1440
	CTGAAAGCAC	AGCTGGACCT	CAGCGTCCCC	TGCCCTGACA	CCCAGGACTT	CCAGCCCTGC	1500
	ATGGGCCCTG	CTGCGAGTGA	CGAAGACGGC	TCCACCTGCA	CCATGTCGGA	GTGGATCACC	1560
	TGGTTCGCTT	CGACATCTCT	CTGCGGCATG	GGCATGAGGT	CCCGGAGAGG	GTATGTGAAG	1620
35	CAGTTCCCGG	AGGACGGCTC	CGTGTGCACG	CTGCCCACTG	AGGAAACGGA	GAAGTGACAG	1680
	GTCAACGAGG	AGTGCTCTCC	CAGCAGCTGC	CTGATGACCG	AGTGGGCGGA	GTGGGACGAG	1740
	TGCAGCGCCA	CCTGCGGCAT	GGGCATGAAG	AAGCGGCACC	GCATGATCAA	GATGAACCCC	1800
	GCAGATGGCT	CCATGTGCAA	AGCCGAGACA	TCACAGGCAG	AGAAAGTCAT	GATGCCAGAG	1860
	TGCCACACCA	TCCCATGCTT	GCTGTCCCCA	TGGTCCGAGT	GGAGTGACTG	CAGCGTGACC	1920
40	TGCGGGAGGG	AGGTCGGAAG	CGACAGCGGG	ATGCTCAAGT	CTCTGGCAGA	ACTTGGAGAC	1980
	TGCAATGAGG	ATCTGGAGCA	GCTGGAGAAG	TGCTATGCTC	CTGAATGCCC	CATTGACTGT	2040
	GAGCTCACCG	AGTGGTCCCC	GTGGTCCGAA	TGTAACAAGT	CATGTGGGAA	AGGCCACGTG	2100
	ATTGGAACCC	GGATGATCCA	AATGGAGCCT	CAGTTTGGAG	GTGCACCCCTG	CCGAGAGACT	2160
	GTGCGAGGAA	AAAAGTCCCG	CATCCGAAAA	TGCCCTTGAA	ATCCATCCAT	CCAAAAGCTA	2220
45	CGCTGGAGGG	AGGCGCGAGA	GAGCGCGGGG	AGTGAGCAGC	TGAAGGAAGA	GTCTGAAGGG	2280
	GAGCAGTTCC	CAGGTTGTAG	GATGCGCCCA	TGACCGCCCT	GGTCAGAAATG	CACCAACCTG	2340
	TGCGGAGGTG	GAATTCAGGA	ACGTTACATG	ACTGTAAAGA	AGAGATTCAA	AAGCTCCCAG	2400
	TTTACCAAGT	GCAAAAGCAA	GAAGGAGATC	AGAGCATGCA	ATGTTCTATC	TTGTTAGCAA	2460
	GGGTACGAGT	TCCCGAGGGC	TGCACTCTAG	ATTCCAGAGT	CACCAATGGC	TGGATTATTT	2520
50	CGTCTTTTAA	GACAAATTAA	ATTGTTTACG	CTAGTTTTTA	TTTTTGAGT	GTGTTTCGCG	2580
	CAGTAGTCTT	GTGGATGCCA	GAGACATCCT	TTCTGAATAC	TTCTTGATGG	GTACAGGCTG	2640
	AGTGGGGCGC	CCTCACTCTC	AGCCAGCCCTC	TTCTGTCAGA	GGAGTAGTGT	CAGCCACCTT	2700
	GTACTAAGCT	GAAACATGTC	CCTCTGGAGC	TTCCACTCTG	CCAGGGAGGA	CGGAGACTTT	2760
	GACCTACTCC	ACATGGAGAG	GCAACCATGT	CTGGAAGTGA	CTATGCTCTA	GTCCAGGGGT	2820
55	GCGGCAGGTA	GAAACATATT	ACAGATGAAG	ACAGCAGATT	CCCCACATTC	TCATCTTTGG	2880
	CCTGTTCAAT	GAAACCATTT	TTTGGCCATC	TCTTCTTAGT	GGAACTTTAG	GTCTCTTTTC	2940
	AAGTCTCTCT	AGTCATCAAT	AGTTCTCTGG	GAAAAACAGA	GCTGTAGTAC	TTGAAGAGGA	3000
	GCAITGATGT	TGGGTGGCTT	TTGTTCTTTC	ACTGAGAAAT	TGGGAATACA	TTTGTCTCAC	3060
	CCCTGATATT	GGTCTCTGAT	GCCCCCCCCA	CAAAAATAAA	TAAATAAATT	ATGGCTGTCT	3120
60	TATTTAAATA	TAAGGTAGCT	AGTTTTTACA	CCTGAGATAA	ATAATAAGCT	TAGAGTGTAT	3180
	TTTTCCCTTG	CTTTGGGGGG	TTGAGAGGAG	TATGTACAAT	TCTTCTGGGA	AGCCAGCCCT	3240
	CTGAACCTTT	TGTTACTAAA	TCTTATTGGG	AACCAAGACA	AAGGAAGCAA	AATTGGTCTC	3300
	TTTGAAGACC	AATTTGCCCTA	AATTTTAAAA	TCTTCTTACA	CACATCTAGA	CGTTCAAGTT	3360
	TGCAATCAGT	TTTTTATGCA	GAAACATTTT	TTGCTATACA	AACATTTTGC	TAAGTCTGCC	3420
65	CAAGCCCCCC	CCAATGCATT	CCTTCAACAA	AATACAATCT	CTGTACTTTA	AAGTTATTTT	3480
	AGTCATGAAA	TTTTATATGC	AGAGAGAAAA	AGTTACCGAG	ACAGAAAAACA	AATCTAAGGG	3540
	AAAGGAATAT	TATGGGATTA	AGCTGAGCAA	GCAATTCTGG	TGGAAAGTCA	AACCTGTCTG	3600
	TGCTCCACAC	CAGGGCTGTG	GTCTCCCGAG	ACATGCAATG	GAATGGCCAC	AGGTTTACAC	3660
	TGCTTCCCA	GCAATTATAA	GCACCCAGCA	TTGAGGGAGA	CTGACCCACA	AGGGATAGTG	3720
70	TAAGAGGACA	TTTTCTCAGT	TGGGTCCATC	AGCAGTTTTT	CTTCTGCTAT	TTATTGTTGA	3780
	AAACTATTGT	TTCAATTCTT	CTTTTATAGG	CCTTATTACT	GCTTAATCCA	AATGTGTACC	3840
	ATTGGTGAGA	CACATCAAT	GCTCTGAATA	CACTACGAAT	TTGTATTAAA	CACATCGAAA	3900
	TATTTCCAAA	TACAACATAG	TATAGTCTCT	AATATGTACT	TTTAAACACA	GAGAGACTAT	3960
	TCAATAAAAA	CTCACTGGGT	CTTTCATGTC	TTTAAAGCTAA	GTAAGTGTTC	AGAAGGTCTT	4020
75	TTTTTATATT	GTCTCTCCAC	TCCATCATTT	TCAATAAAAG	ATAGGGCTTT	TGCTCCCTTG	4080
	TTCTTGGAGG	GACCATTAAT	ACATCTCTGA	ACTACCTTTG	TATCCAACAT	GTTTTAAATC	4140
	CTTAAATGAA	TTGCTTTCTC	CCAAAAAAGG	CACAAATATA	AGAAACACAA	GATTTAATTA	4200
	TTTTTCTACT	TGGGGGGAAA	AAAGTCTCTA	TGTAGAAGCA	CCCACTTTTG	CAATGTTGTT	4260
	CTAAGCTATC	TATCTAATCT	TCAGCCCATG	ATAAAGTTCC	TTAAGCTGGT	GATTCTTAAT	4320
80	CAAGGACAA	CCACCCTAGT	GTCTCATGTT	TGTATTGGGT	CCCACTTGGG	TACATTTTAA	4380
	AATCCTGATT	TTGGAGACTT	AAAACCAAGT	TAATGGCTAA	GAATGGGTAA	CATGACTCTT	4440
	GTTGGATTGT	TATTTTTTGT	TTGCAATGGG	GAATTTATAA	GAAGCATCAA	GTCTCTTTCT	4500
	TACCAAGTCT	TTGTTAGGTG	GTTTATAGTT	CTTTTGGCTA	ACAAATCAAT	TTGGAAATAA	4560
	AGATTTTTTA	CTACAAAAAT	G				

Seq ID NO: 510 Protein sequence
Protein Accession #: BAB18461.1

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5 1 11 21 31 41 51
MRLSPAPLKL SRTFALLALA LPLAALAFS DETLDKVPKS EGYCSRILRA QGTRREGYTE 60
PSLRVEGDDP FYKPGTSTYRV TLSAAPPSTYF RGFLLIALRE NREGDKKEEDH AGTFQIIDEH 120
ETQFMSCNCPV AVTESTPRRR TRIQVFWIAP PAGTGCVILK ASIVQKRIIY PQDEGSLTKK 180
LCEQDSTFDG VTDKPILDCC ACGTAKYRLT PYGNWSEKTH PKDYPRRANH WSAIIGGSHS 240
KNYVLWEYGG YASEGVKQVA ELGSPVKMBE EIRQQSDEVL TVIKAKAQWP AWQPLNVRAA 300
PSAEFSVDRT RHLMSFLTMM GPSPDWNVGL SAEDLCTKEC GWVQKVVDL IPWDAGTDSG 360
VTYESPNKPT IPQEKIRPLT SLDPQSPFFY DPEGGSITQV ARVVIERIAR KGEQCNIVPD 420
NVDDIVADLA PERKEDDTP ETCIYSNWSF WSACSSSTCD KGRMRQRLM KAQLDLSVPC 480
PDTQDFQPCM GPGCDEDEGS TCTMSEWITW SPCSISCGMG MRSRERYVKQ FPDGGSVCTL 540
PTEETKCTV NEECSPSSCL MTENGWDEC SATCGMGMKK RHRMIKMNPA DGSMDCAETS 600
QAEKCMPEEC HTIPCLLSFW SEWSDCSVTC GKGMRTQRM LKSLAELGDC NEDLEQVEKC 660
MLPECPIDCE LTESQWSEC NKSOGKHVI RTRMIQMEPO FGGAPCPFTV QRKKCRIRKC 720
LRNPSIQKLR WREARESRRS EQLKESSEGE QPPGCRMRPW TANSECTKLC GGGIQERYMT 780
VKRPFKSSQP TSCKDKKIR ACNVHPC

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Seq ID NO: 511 DNA sequence
Nucleic Acid Accession #: NM_003108.1
Coding sequence: 76..1401

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25 1 11 21 31 41 51
GGGGTGGGAG GGGGAGGGGG ACCTCCGCAC GAGACCCAGC GGGCCGGGTT GGAGCGTCCA 60
GCCCTGCAAC GGATCATGGT GCAGCAGGCG GAGAGCTTGG AAGCGGAGAG CAACCTGCCC 120
CGGGAGGGCG TGACACCGGA GGAGGGCGAA TTCATGGCTT GCAGCCCGGT GCCCTGGGAC 180
GAGAGCGACC CAGACTGGTG CAAGACGCGC TCGGGCCACA TCAAGCGGCC GATGAACGCG 240
TTCATGGTAT GGTCCAAGAT CGAACGCGAG AAGATCATGG AGCAGTCTCC GGACATGCAC 300
AAGCGCGAGA TCTCCAAGAG GCTGGGCAAG CGCTGGAAAA TGCTGAAGGA CAGCGAGAAG 360
ATCCGTTTCA TCCGGGAGGC GGAGCGGCTG CGGCTCAAGC ACATGGCCGA CTACCCCGAC 420
TACAAGTACC GGGCCCGGAA AAGACCCCAA ATGGACCCCT CGGCCAAGCC CAGCGCCAGC 480
CAGAGCCACG AGAAGAGCGC GGCCGGCGGC GCGCGGCGGA GCGCGGCGGG AGGCGCGGGC 540
GGTGCCACGA CCTCCAAGGG CTCCAGCAAG AAATGCGGCA AGCTCAAGGC CCGCGGGGCC 600
CGGGGGCCCA AGGCGGGCGC GGGCAAGGCG GCCCAGTCCG GGGACTACGG GGGCGGGGCG 660
GACGACTACG TGCTGGGCGG CCTGCGCGTG AGCGGCTCGG GCGGCGGGCG GCGGGGCAAG 720
ACGCTCAAGT GCGTGTCTCT GGATGAGGAC GACGACGACG ACGACGACGA CGACGAGCTG 780
CAGCTGATGT TCAACACGGA GCCGACGAG GAGGACGAGG AACCAACGCA CCAGCAGCTC 840
CTGACGCGCG CGGGGACGCA GCGGTGCGAG CTGCTGAGAC GCTACACGCT CGCCAAAGTG 900
CCCGCCAGCC CTACGCTGAG CAGCTCGGGG GAGTCCCCCG AGGGAGCGAG CCTCTACGAC 960
GAGGTGCGGG CCGGGCGGAC CTGGGGCGCC GGGGGCGGCA GCGGCTCTTA CTACAGCTTC 1020
AAGAAATACA CCAACGACGA CCGCGCGCGG CTGCGGCGAG CCGCGCTGTC GCCCGCGTCC 1080
TCGCGCTCGG TGTCACACTC CTGCTCCAGC AGCAGCGGCA GCAGCAGCGG CAGCAGCGGG 1140
GAGGACGCGG ACGACCTGAT GTTCGACCTG AGCTTGAATT TCTCTCAAAG CGGCGACAGC 1200
GCCAGCGAGC AGCAGCTGGG GGGCGGCGCG GCGGCGGGGA ACCTGTCCCT GTCGCTGGTG 1260
GATAAGGATT TGGATTGCTT CAGCGAGGGC AGCCTGGGCT CCCACTTGA GTTCCCGGAC 1320
TACTGCAAGC CGGAGCTGAG CGAGATGATC GCGGGGGACT GGTCTGGAGG GAACCTCTCC 1380
GACCTGATGT TCAACATTTG AAAGGCGGCC GCTGCTCGCT CTTTCTCTCG GAGGGTGCA 1440
AGCTGGGTTT CTGGGAGGA AGTTGTAGTG GTGATGATGA TGATGATGAT AATGATGATG 1500
ATGATGATGA TGTGATGATG GGCCTGTGTA GGGTGGAGGG GAGAGAAGAA GATGCTGATG 1560
ATATTGATAA GATGCTGATG CGCAAGAAAA TTGAAAAACA TGATGAAAAA TTTGGTGGAG 1620
TTAAAGTGAA ATGAGTAGTT TTTAAACATT TTCTCTGTC TTTTCTGTC CCCCCCTCC 1680
CTCTTTATCG TGCTCAAGG TAGTTGCATA CCTAGTCTGG AGTTGTGATT ATTTTCCCAA 1740
AAAAATGTTT TTTGTAATTA CTATTTCTTT TTCTGAAAT TCCTGATTGC AACAAAGGCA 1800
GAGGGGGCGG CGCGGCGGAG GGGAGGTAGG ACCCGCTCCG GAAGGCGCTG TTTGAAGCTT 1860
GTGCGTCTTT GAAGTCTGGA AGACGTCTGC AGAGGACCCCT TTTGGCAGCA CAACTGTTAC 1920
TCTAGGGAGT TGGTGGAGAT ATTTTTTTTT CTTAAGAGAA CTTAAGAAC TGGTGATTTT 1980
TTTTTAACAA AAAAAGGG

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Seq ID NO: 512 Protein sequence
Protein Accession #: NP_003099.1

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65 1 11 21 31 41 51
MVQQAESLEA ESNLPREALD TEEGEFMACS FVALDESDPD NCKTASGHK RPMNAFMVWS 60
KIERRKIMEQ SPDMEHAIS KRLGRWKML KDSEKIPPIR EAERLRLLKH ADYDPYKYRP 120
RKPKKMDPSA KPSASQSPKE SAAGGGGGGA GGGAGGAKTS KSSSKKCKGL KAPAAAGAKA 180
GAGKAAQSGD YGAGGDDYVL GSLRVSGSGG GGAGKTVKCV FLDEDDDDDD DDELQLQIK 240
QEPDEEDEEP FHQQLLQPPG QQPSQLLRRY NVAKVPASPT LSSSABSPBG ASLYDEVVRAG 300
ATSGAGGGSR LYYSPKNITK QHPPPLAQPA LSPASSRSVS TS9SSSSGSS SGSSSGEDADD 360
LMFDLSLWFS QSAHSASBQ LGGGAAAGNL SLSLVDKDLD SFSEGLSGSH FEPFDYCTPE 420
LSEMIAGDWL EANFSDLVFT Y

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Seq ID NO: 513 DNA sequence
Nucleic Acid Accession #: CAT Cluster

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80 1 11 21 31 41 51
GGTCGACCTA AATCTGATAA CTGGCTTATT ATGTAATTTA TTGGTGTATT TATAGTAGAG 60
ATTGTAATTC TACAGTAAGA TTTTCAGTTA GGATTGAGA TTATGATAAT AACTAATAGA 120
ATATTTCTAA ATTGGAATTA GAAGATTGTT GTATGACAGA GAGTCAGGAC TTGCCATTTG 180

```

5 GCAAACATCA AAGTCATTGT TTGGTGTGTA ATAGTACAAA ATCATCTTGC TTAACAGAGA 240
AAGGATATCT GTTGCTCCCG AATGAAACAA TTTTCTGAA ATAGAGGGCC CAGAATTGGT 300
CTCTGCAAT TAATAAAGAC ATCAAAGATA GCAAAATGAT TTTTATATCT TAGGGCCAAT 360
ACTACCAATT TAATAATTAA AACAGTTCT GTTGAGCTCT GAACTTGGCA GAATTGGTGG 420
CAACATAGAC TTGTGATTTT CCAAAATCCC CACATAAAAC AAAGGGGATC AACTAGATAG 480
AAAAACCAGA AACCTTTGGA AATATCTGTT TAAAAAATAA AAAAAGTCGA CGGGGGCC

Seq ID NO: 514 DNA sequence
Nucleic Acid Accession #: CAT cluster

10

1 11 21 31 41 51
15 GGAGCCACAG TGAAGTCAA GAATGTCACT GATTCCACAT TTAATATCTA CATTTTGTCA 60
GGGCACTTAC TCTTTGTAG TATAACATTG AGCTGATAGC ACATAGTGTA GACAAGTGAA 120
TACAGGATTC TCTGGGTTGT ATTCCAGAA GTCTGGAGGT CATTGTGATA TTTGTGGGCC 180
CTTGGCTTCA CTCTGAGTTG TGTGACACAT AAAAATTGTG ATGAAATGTC CTATAGATGT 240
CTGTCAGGTC TTAAAGAAC CTTTCCAAAC TATGAAACAG CCCAGCAGCA CTGAGTTAGA 300
GGTAAATTCT GAACCTTGA AACTAAAAAC TATTCTAAT GCACATAGAA TTGGCAAGTA 360
GCATTCTATG TCTATGAACA GTATGTCTTT TCTATATAAC AGAGAAAAATC TTTTAAAGCA 420
AACTACTCAG TTTAAACCT AATTCTTCTC ATAATCTCAG TACTTTTGAA TGAAGACATA 480
TCAATGCAAC AGTACACTCT TATTGAGGCA TTTGAAAGAA AGAATTGAG ATCTAGTTTG 540
TATCAGATAT TATAAATTAG TATGTTTAG TCTTTGTCT GAAATTCTAC TTAATTTTGT 600
GACTATAGGT TTAAGAATGT AAGCAGAAGT TCTGCCACCA TCAGAATAAG CTACATTATG 660
CTTGAGTGAC AACTACTGTA ATGACAAAT ATCAGTGGCT TAATACAATG GTTTTCTCT 720
CATACTTGT CATAAAGAGT CAGCAAGGAC CCTGCTCATT ATGGTCCCTC AGGGACCCAG 780
GGTTGTTGGA AGCTCCACCA TTTTAGATAG CTCCCTTCAA AGTCAGCCAT CTTTGGCAGT 840
CATGTGCCCT CAACAGGCTG GCAAAATTTG GCTCTGGATG GCTCAAGGA TTGAGCATCG 900
GGCAGTTTAA ATGCTTTCAA CATGGAAGT GGACACCGGC CACTCCCACT CACATCCCTT 960
GGGCCAGAAC TAGGTCACTG GGGCCGAGCC TAACCTCGGA GGGTTGGGGA ATTTGTAATTC 1020
CTCCATGTAC CCAAGATGGA GAGAAGCCAG ATACTGAGAA ACATCAATAA TGGCTAACAG 1080
AAATCCATTC TACCATTTCC TTTGCCATAA GTGAAAGAT GAGTACTTTC ATCAATTGT 1140
AACTGTACT TTTGAAGTAA ATCCTGOTAG CTGTGATGG GGCTGATTI CCAGAAAGCC 1200
ATATGTAATT TGGGAATGAC ATTCACCTAA GCTCATAGAA TATCATTATT TGATGTAAAA 1260
TGCCCTCATT TGCAATACAG GACCAAAATG CACTAACCCAC AAAACCCCCC TCCCCACGGG 1320
GCCCGGGGTC CCTATTCCCC TCCATCCCTT TAAATGAGGC ATTCTATGAT TTGGAATGGA 1380
AGCCCACTG TAGTCGTAAG AATTTTACTT AATTCAAGAA TTATCTCTAC TGAATATGTG 1440
CCAGTCTGTA AAGGAATGCA AAGTCAAAT TTGCATCTTC TTTGCTCAAG GGCCTTAGA 1500
TGTAACAACA CAGACATGAT ACAGGCTGA CAATGACATT ATGATTTAAA TATGTTAAAC 1560
AACTATTAA ATTGTGAATC AAAAAAAT TATGTTCTT ATTTTATGGT TTTGCATAGT 1620
CTGACTCAC TGCATACATA CCCCCTTGT TCCTCAGTTC TTATCCCTGA TTTCTACAG 1680
GATGGCTAA GACAGCTGTA GATGTTTTA TTTAGCAAAA AAAAAAATAA AAAAGTCGAC 1740
GCGGCGGGA ATTTAGTAG

45 Seq ID NO: 515 DNA sequence
Nucleic Acid Accession #: NM_012427
Coding sequence: 43..924

50 1 11 21 31 41 51
CTTGTGGTTC CTCTCTACTT GGGGAAATCA GGTGCAGCGG CCATGGCTAC AGCAAGACCC 60
CCCTGATGAT GGGTGTCTTG TGCTCTGATC ACAGCCTTGC TTCTGGGGGT CACAGAGCAT 120
GTTCTCGCCA ACAATGATGT TTCTCTGTAC CACCCCTCTA ACACCGTGCC CTCTGGGAGC 180
AACCAGGACC TGGGAGCTGG GGGCGGGGAA GACGCCGGGT CGGATGACAG CAGCAGCCGC 240
ATCATCAATG GATCOGACTG CGATATGCAC ACCAGCCCGT GGCAGCGCGC GCTGTGTGTA 300
AGGCCCAACC AGCTCTACTG CGGGGCGGTG TTGTTGCATC CACAGTGGCT GCTCAGCGCC 360
GCCCACTGCA GGAAGAAAGT TTTCAAGATC CGTCTCGGCC ACTACTCCCT GTCAACAGTT 420
TATGAATCTG GGCAGCAGAT GTTCCAGGGG GTCAAATCCA TCCCCACCC TGGCTACTCC 480
CACCCCTGGC ACTCTAAAGT CCTCATGCTC ATCAAACTGA ACAGAAAGAT TCGTCCCACT 540
AAAGATGTCA GACCCATCAA CGTCTCTCTT CATTGTCCCT CTGCTGGGAC AAAGTGCTTG 600
GTGCTGGCT GGGGACAAAC CAAGAGCCCC CAAGTGCACT TCCCTAAGGT CCTCCAGTGC 660
TTGAATATCA GGTGCTAAG TCAGAAAAGG TGCGAGGATG CTTACCCGAG ACAGATAGAT 720
GACACCATGT TCTGCGCCGG TGACAAAGCA GGTAGAGACT CCTGCCAGGG TGATTCTGGG 780
GGGCTGTGTT TCTGCAATGG CTCCCTGCAG GGACTCGTGT CTTGGGGAGA TTACCCCTTG 840
GCCCCGCCCA ACAGACCGGG TGTCTACAGC AACCTCTGCA AGTTCACCAA GTGGATCCAG 900
GAAACCATCC AGGCCAACTC CTGAGTCATC CCAGGACTCA GCACACCGGC ATCCCACT 960
GCTGCAAGGA CAGCCCTGAC ACTCCTTTCA GACCTCATT CCTTCCAGA GATGTTGAGA 1020
ATGTTCTACT CTCCAGCCCC TGACCCCATG TCTCTGGAC TCAGGGTCTG CTTCCCCCAC 1080
ATTGGGCTGA CGTGTCTCT CTAGTTGAAC CCTGGGAACA ATTTCCAAAA CTGTCCAGGG 1140
CGGGGGTTC GTCTCAATCT CCGTGGGCA CTTTCATCCT CAAGCTCAGG GCCCATCCCT 1200
TCTCTGAGC TCTGACCAA ATTTAGTCCC AGAAATAAAC TGAGAAGTGG AAAAAAATAA

Seq ID NO: 516 Protein sequence
Protein Accession #: NP_036559

75

80 1 11 21 31 41 51
MATARPPMMV VLCAALITALL LGVTEHVLAN NDVSCDHPSN TVPSGSNQDL GAGAGEDARS 60
DDSSRIING SDGMHTQPW QAALLLRPNQ LYCGAVLVHP QWLLTAHCR KKVFRVRLGH 120
YSLSPVYESG QMFGVKSII PHPGYSHPG SNDLMLIKLN RRIPTKQVR PINVSSHCPS 180
AGTKCLVSGV GTTKSPQVHP PKVLQCLNIS VLSQKRCEDA YPRQIDTME CAGKAGRDS 240
CQDGGGPPV CNGSLQLLVS WQDYPCARPN RPOVYTNLCK PTKWQETIQ ANS

Seq ID NO: 517 DNA sequence
Nucleic Acid Accession #: NM_001719
Coding sequence: 123..1418

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5 1 11 21 31 41 51
| | | | |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACOGACGGCC GGGACGGCCG CCTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GGTAGCGCGT AGAGCCGGCG 120
CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
CCCTGTTCCT GCTGCGCTCC GCGCTGGCCG ACTTCAGCCT GGACAACGAG GTGCACCTCGA 240
GCTTCATCCA CGCGCGCTC CGCAGCCAGG AGCGGGCGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTTGCCCCAC CGCCCGCGCC CGCACTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGGACCTG TACAACGCCA TGGCGGTGGA GAGGGGCGCG GGGCCCGGGG 420
GCCAGGGCTT CTCTACCCCG TACAAGGCCG TCTTCAGTAC CCAGGGCCCG CCTCTGGCCA 480
GGCTGCAGGA TAGCCATTTC CTCAACGAGC CCGACATGCT CATGAGCTTC GTCAACCTCG 540
TGGAAACATGA CAAGGAATTTC TTCCACCCAC GGTACCACTA TCGAGAGTTC CGGTTTGATC 600
TTTCCAGAT CCACGAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGGTACCCCT TGGGCTTCGG 780
AGGAGGGCTG GCTGTGTGTT GACATCAGAG CCACAGGCAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT CAAGCGCTCAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CTTGATTGGG CGGCAGGGG CCCAGAACAA GCAGCCCTTC ATGTTGGCTT 960
TCTTCAAGCG CACGAGGTC CACTTCCGCA GCATCCGCTC CACGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCAGAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACGAG AGGCAGGCTT GTAAAGACA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCCTGAAAG CTACGCGGCC TACTACTGTG 1200
AGGGGAGGTG TGCTTCCCT CTGAATCTCT ACATGAAGCG CACCAACCCG GCCATCGTGC 1260
AGACGCTGCT CCACTTCATC AACCCGGAAG CGGTGCCCAA GCCCTGCTGT GCGCCCAAGC 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACTGCTAT CTGAAGAAAT 1380
ACAGAAACAT GGTGTGCCGG GCGTGTGGCT GCCACTAGCT CCTCGAGAA TTCAGACCTT 1440
TTGGGGCCAA GTTTTCTGCG ATCTCCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCTCAACAGC TGTGAGGCA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
CGCGGGCCAG GTCAATGGCT GGGGAAGTCT AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACCAAGCA GGCCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCTGTGA ATAAATGTCA 1860
CAATAAAACG AATGAATG
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Seq ID NO: 518 Protein sequence
Protein Accession #: NP_001710

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45 1 11 21 31 41 51
| | | | |
MHVRSRLRAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRLRSQRE REMQREILS 60
ILQLPFRPRP HLOGKHSAP MFMLDLNAM AVEEGGGPGG QGFSYPYKAV PSTQPPPLAS 120
LQDSHPLTDA DMVMSFVNLV EHDKEFPHPR YHREPRFDL SKIPEGEAVT AAEFRIVKDY 180
IRERFQNETF RIVSYVQLQE HLGRESLDLFL LDSRTLWASE EGMVLVFDITA TSNHWVNVNR 240
HNLLGLQSVB TLDGQINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
QNRSKTFKQK EALRMANVAE NSSSDQRQAC KKHLYVVSFR DLGWQDWILA PEGYAAYYCE 360
GECAPPLNSY MNATNHAIVQ TLVHPINPET VFKPCAPTQ LNAISVLYPD DSENVILKKY 420
RMVMVRACGC H
```

Seq ID NO: 519 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 264..782

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60 1 11 21 31 41 51
| | | | |
CCCTGCTCCA GTCACACCCG GAAGCTGACT GGTCCACGCA CAGCTGAAGC ATGAGGAAAC 60
TCATCGPRPP ACTAATTTC CTTAAATTT AGACTTGAC AGTAAGGACT TCAACTGACC 120
TTCTCAGAC TGAGAACTGT TTCCAGTATA TACATCAAGT CACTGAGATC TCCAGCACCC 180
TGCCGGTGGC ACTACTGAGA GACGAGGTGC CAGGGTGGTT CCTGAAAGTG CCTGAGCCCC 240
AACTTATCAG CAAGGAGCTC ATCATGCTGA CAGAAGTCAAT GGAGGTCTGG CATGGCTTAG 300
TGATCGCGGT GGTGTCCCTC TTCTGCAAGC CTGCTTCTCT CACCGCCATC AACTACCTGC 360
TCAGCAGGCA CATGGCCAC AAGAGTGAAC AGATACTGAA AGCGGCCAGT CTCAGGTTTC 420
CCAGGCCAGC CCTGGCCAC CATCATCCAC CTGCTGTCAA AGAGATGAAG GAGACTCAGA 480
CAGAGAGAGA CATCCCAATG TCTGATTCCC TTACAGGCA TGACAGCGAC ACACCTCAG 540
ATAGCTTGGG TAGCTCTGCG AGTTGCGCTC CTGCTGCCA GGCCACAGAG GATGTGGATT 600
ACACACAAGT GGTCTTTTCT GACCTGGGAG AACTAAAAAA TGAATCCCG CTGGACTATG 660
AGAACATAAA GGAATCACA GATTATGTCA ATGTCAATCC AGAAAGACAC AAGCCAGTTT 720
TCTGGTATTT TGTCAACCTT GCTCTGTCTG AGCCAGCGGA ATATGATCAA GTGCCATGT 780
GAATTCACAA TATTTTAAAT GGGGTCCAGT TCTTATGGA TTCTTACATT TAATTTTAG 840
GGAATGCGCA TTTTCCCCC TTAAACAAGG CATGGGGCTC ACAAGTCTAT GGAGACAGCG 900
CAAAAGAAGT GTGAGAGA AACTGATATA ATACACAGAG GTCCCTCAGA CCCATGGACT 960
CTCGTCTGT ACCCAAAAA GCTGTTCGTT CCTCAAAAC AAAACACAGG CTGGCTGGG 1020
AAAAAGGCC AATGCCCCG CAAGAAAGGT TGAGATCAGA TGTAGGAAG AACTTTTCAG 1080
TAAAGTATGA GAACATGGA GTCCATCAGC AGAGATAGTA GTGAAGTCTC TCCCCAGGGA 1140
AAATTTTAAA AAGGTTGAAT CAGCTGTGT AGAGTCTAT TTGGCAATCT CATGTTAAA 1200
TGACTTCCCT TTGAGCTCTT TAATTATTGG CAATAAACAA CTCTTTAAA AGTTTAAAAT 1260
AAAATAGCAA CACCAACA
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Seq ID NO: 520 Protein sequence
Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
5  MLTEVMSVNH GLVIAVVSLE LQACPLTAIN YLLSRHMAHK SEQILKAASL QVPRPSPGHH 60
    HPPAVKEMKE TQTERDIPMS DSYLRHSDST PSDSLDSSCS SPPACQATED VDYTQVVFSD 120
    PGLRKRDSPL DYENIKSITD YVNVNPERHK PSFWYFVNPA LSEPAEYDQV AM

```

Seq ID NO: 521 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 107..328

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1      11      21      31      41      51
|      |      |      |      |      |
15 CTGCTCTGTC TGAGCCAGCG GAATATGATC AAGTGGCCAT GTGAATTCOA AATATTTTAA 60
    ATGGGGTCCA GTTCTCTATG GATTCTTACA TTTAATTTGT AGGGAATGC CATTTTTCCC 120
    CCTTAAACAA GGCATGGGCG TCACAAGTCT ATGGAGACAG GCCAAAAGA ATGTGGAGAA 180
    GAAACTGAT AAATACACAG AGGTCTCTCA GACCCATGGA CTCCTGGTCT GTACCCAAAA 240
    AAGCTGTTCG TTCTCTAAAA AAAAAACAA GGCTTGGCTG GAAAAACAG CCAATGCCCC 300
    GGCAAGAAAG GTTGAGATCA GATGTTAGGA AGAAGCTTCA GGTAAAGTAT GAGAACTATG 360
    GAGTCCATCA GCAGAGATAG TAGTGAAGTC TCTCCCAGG GAAATTTTAA AAAAGGTTGA 420
    ATCAGCTGTT GTAGAGTTCT ATTTGGCAAT CTCATGGTTA AATGACTTCC CTTTGAGCTC 480
    TTTAATTATT GGCAATAAAC AACTTCTTTA AAAGTTTAA ATAAATAGC AACCAACCAC 540
    A

```

Seq ID NO: 522 Protein sequence

Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
30 MPFFFLKQGM GLTSLWRQAK KNVEKKTDKY TEVLKTHGLL VCTQKSCSFL KNKNKAWLGK 60
    QANAPARKVE IRC

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Seq ID NO: 523 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 211..1895

```

1      11      21      31      41      51
|      |      |      |      |      |
40 GGATCTGAGG GGCGCCAGT CACTTCCTCC ACGTTCCTGT GCTGGGCGGG AGGAGCGGAT 60
    GGGGCTTGGG AGGCAGCCTG CTCTCCAGTC CCTATCCACC CACAGGTTT TTGGGTCGGA 120
    GAGGAATTAAT CTGATAAAAT TCCTGGGTTA ATATTTTAA AAACGGAGAG TTTTAAAAA 180
    TGATTTTTTT CCCTCGAAAA TGACCTTTTT ATGCTTCGAA GCAAGTTGTC AACCAGCATA 240
    GTGCTTTTTT TTTTCTCTTC TTTTCTACG ATAAATGAAA GCATTTCTTC AAGAAAAAGG 300
    CACAGGTTCG TTGAACAGCT GGATTCGAT GGCACCATTA CTATAGAGGA GCAGATTGTC 360
    CTTGTGCTGA AAGCGAAAGT ACAATGTGAA CTCACATCA CAGCTCAACT CCAGGAGGGA 420
    GAAGGTAAAT GTTTCCTCGA ATGGGATGGA CTCATTGTGT GGCCGAGAGG AACAGTGGGG 480
    AAAATATOGG CTGTTCCATG CCCTCCTTAT ATTTATGACT TCAACCATAA AGGAGTTGCT 540
    TTCCGACACT GTAACCCCAA TGGAACTGCG GATTTTATGC ACAGCTTAAA TAAACATGG 600
    GCAATTAAT CAGACTGCCT TCGCTTCTG CAGCCAGATA TCAGCATAGG AAAGCAAGAA 660
    TTCTTTGAAC GCCTCTATGT AATGTATACC GTTGGCTACT CCATCTCTTT TGGTTCCTTG 720
    GCTGTGCTTA TTCTCATCAT TGCTTACTTC AGACGATTGC ATTGCACTAG GAACTATATC 780
    CACATGCACT TATTTGTGTC TTTCATGCTG AGAGCTACAA GCATCTTGT CAAAGACAGA 840
    GTAGTCCATG CTCACATAGG AGTAAAGGAG CTGGAGTCCC TAATAATGCA GGATGACCCA 900
    CAAAATTCCA TTGAGGCAAC TTCTGTGGAC AAATCACAAT ATATCGGGTG CAAGATTGCT 960
    GTTGTGATGT TTAATTAATT CCTGGCTACA AATTATTATT GGATCCTGGT GGAAGSTCTC 1020
    TACCTGCTAT ATCTCATCTT TGTGGCTTTC TTTTGGACA CCAATACCT GTGGGCTTC 1080
    ATCTTGATAG GCTGGGGGTT TCCAGCAGCA TTTGTTGAG CATGGGCTGT GGCAGCAGCA 1140
    ACTCTGGCTG ATGCGAGGTG CTGGGAACCT AGTGTGAGG ACATCAAGTG GATTTATCAA 1200
    GCACGATCT TAGCAGCTAT TGGGCTGAAT TTTATTCTGT TTCTGAATAC GGTTAGAGTT 1260
    CTAGCTACCA AATCTGSGA GACCAATGCA GTTGGGCATG ACACAGGAA GCAATACAGG 1320
    AAACCTGCCA AATCGACACT GGTCTGTGTC CTAGTCTTTG GAGTGCAATTA CATGTTGTTT 1380
    GTATGCTGCT CTCACCTCTT CACTGGGCTC GGTGGGAGA TCCGCATGCA CTGTGAGCTC 1440
    TTCTTCAACT CCTTTCAGGG TTTCTTTGTG TCTATCATCT ACTGCTACTG CAATGGAGAG 1500
    GTTCAGGCAG AGGTGAAGAA GATGTGGAGT CGGTGGAATC TCTCGTGGG CTGGAAAAGG 1560
    ACACCGCCAT GTGGCAGCCG CAGATGCGGC TCAGTGCTCA CCACGCTGAC GCACAGCACC 1620
    AGCAGCCAGT CACAGGTGGC GGCCAGCACA CGCATGGTGC TTATCTCTGG CAAAGCTGCC 1680
    AAGATCGCCA GCAGACAGCT TGACAGCCAC ATCATTACCT CTGGCTATGT CTGGAGTAAC 1740
    TCAGAGCAGG ACTGCTGCC ACACCTTTTC CACGAGGAGA CCAAGGAAGA TAGTGGGAGG 1800
    CAGGGAGATG ATATTCTAAT GGAGAAGCCT TCCAGGCCTA TGAATCTAA CCCAGACATC 1860
    GAAGGATGCC AAGGAGAAAC TGAGGATGTT CTCTGA

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Seq ID NO: 524 Protein sequence

Protein Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
75 MLRSSLSSTSI VLFLPSSFST INESISSRRK HRFLEQLDSD GTITIEEQIV LVLKAKVQCE 60
    LNTIAQLQEG EGNCFPEWDG LICWPRGTVG KISAVPCPPY IYDFNHKGVA FRHCPNPGTW 120
    DFMBSLNTW ANYSDCLRFL QPDISIGKQE FFERLYVMYT VGYISFGSL AVAILIIGYF 180
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    FVAAMAVARA TLADARCWEL SAGDIKIWIYQ APILAAIGLN FILPLNTVRV LATKIWETNA 360
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TACCTGTGGG	CTAATTTAGC	TGCTGCCGAT	TTCTTGGCTG	GAATTGCCCTA	TGTATTCCTG	300
ATGTTTAAAC	CAGGCCCACT	TTCAAAAAC	TTGACTGTCA	ACCGCTGGTT	TCTCCGTCAG	360
GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCAACT	TGCTGGTTAT	CGCCGTGGAG	420
AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTTATGG	GGGCGGTCCC	CACACTGGGC	540
TGGAATTGCC	TCTGCAACAT	CTCTGCTGTC	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
TACCTTGTIT	TCTGGACAGT	GTCCAACCTC	ATGGCCCTCC	TCACTCATGT	TGTGGTGATC	660
CTGCGGATCT	ACGTGTACGT	CAAGAGGAAA	ACCAAGTCTT	TGCTCCGCA	TACAAGTGGG	720
TCCATCAGCC	GCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGCTTAGGG	780
GCGTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCTTCGACGG	CCTGAACCTG	840
AGGCAGTGTG	GCGTCAGACA	TGTGAAAAGG	TGGTTCTGCG	TGCTGGCGCT	GCTCAACTCC	900
GTCTGAACCC	CCATCATCTA	CTCTACAAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGCGTC	CCTCTCGCAT	CCCCCCACA	1020
GTCTTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
GTCTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCCTCT	GGCCACCCA	GGTGATGACT	1140
GTCTTAGG						

Seq ID NO: 532 Protein sequence

Protein Accession #: NP_036284

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1	11	21	31	41	51	
MNECHYDKHM	DPFYNSRNTD	TVDDWTOTKL	VIVLCVGTFF	CLPIFFNSNL	VIAAVIKMRK	60
FHFPPYYLLA	NLAADFPFAG	IAYVFLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIIVERHMS	IMRMVRHSHL	TKKRVTLLIL	LVWAIAPFMG	AVPTLGNWCL	CNISACSSLA	180
PIYSRSLVLF	WTYSNLMFAL	IMVVYLRIY	VYVKRKTNLV	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CMTPGLVLL	LDGLNCRQCG	VQHVKNWFL	LALLNSVNP	IISYKDEDM	300
YGTMKMIMCC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

Seq ID NO: 533 DNA sequence

Nucleic Acid Accession #: NM_002821

Coding sequence: 150..3362

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1	11	21	31	41	51	
AACTCCCGCC	TGGGAGCGCC	TGGGGGTGCG	GCTCCGGCTG	CGGCTGCTGC	TGCGGCGCCC	60
GCGCTCCGGT	GCGTCCGCTC	CCTGTGCCCG	CCGCGGAGCA	GTCTGCGGCC	CGCGGTGCGC	120
CCTCAGCTCC	TTTTCTGTAG	CCCGCCCGGA	TGGGAGCTGC	GCGGGGATCC	CCGCGCAGAC	180
CCCGCCGGTT	GCGTCTGCTC	AGCGTCTCTG	TGCTGCGCGT	GCTGGGCGGT	ACCCAGACAG	240
CCATGTCTTT	CATCAAGCAG	CCGTCTCTCC	AGGATGCACT	GCAAGGGCGC	CGGGCGCTGC	300
TTGCTGTGTA	GTTTGTAGGT	CCGGGCGCGG	TACATGTGTA	CTGGCTGCTC	GATGGGGGCC	360
CTGTCCAGGA	CACGGAGCGG	CGTTTCCGCC	AGGGCAGCAG	CCTGAGCTTT	GCAGCTGTGG	420
ACCGGCTGCA	GGACTCTGGC	ACCTTCCAGT	GTGTGGCTCG	GGATGATGTC	ACTGGAGAAG	480
AAGCCCGCAG	TGCCAAGCGC	TCCTTCAACA	TCAATGGAT	TGAGGCAGGT	CCTGTGGTCC	540
TGAAGCATCC	AGCCTCGGAA	GCTGAGATCC	AGCCACAGAC	CCAGGTCACT	CTTCGTTGCC	600
ACATTGATGG	GCACTCTCGG	CCCACTACCC	AATGGTTCCG	AGATGGGACC	CCCCTTCTCG	660
ATGGTCAGAG	CAACCACACA	GTGAGCAGCA	AGGAGCGGAA	CCTGAAGCTC	CGGCCAGCTG	720
GTCTTGAGCA	TAGTGGGCTG	TATTCCTGCT	GCGCCACAG	TGCTTTTGGC	CAGGCTTGCA	780
GCAGCCAGAA	CTTCACTCTG	AGCATGCTG	ATGAAAGCTT	TGCCAGGGTG	GTGCTGGCAC	840
CCCAGGAGCT	GGTAGTAGCG	AGGTATGAGG	AGGCCATGTT	CCATTGCCAG	TTCTCAGCCC	900
AGCCACCCCC	GAGCCTGCA	TGGCTCTTTG	AGGATGAGAC	TCCCATCACT	AACCGCAGTC	960
GCCCCCACA	CCTCCGAGCA	GCCACAGTGT	TTGCCAACGG	GTCTCTGCTG	CTGACCCAGG	1020
TCCGGCCAGC	CAATGCAAGG	ATCTACCGCT	GCAATTGGCA	GGGGCAGAGG	GGCCCAACCA	1080
TCATCTGGGA	AGCCACACTT	CACCTAGCAG	AGATTGAAGA	CATGCCGCTA	TTTGAGCCAC	1140
GGGTGTTTAC	AGCTGGCAGC	GAGGAGCGTG	TGACCTGCTT	TCCCCCAAG	GCTCTGCCAG	1200
AGCCCGAGCT	TGGTGGGAG	CACGCGGGAG	TCCGGCTGCC	CACCCATGGC	AGGGCTTACC	1260
AGAAGGGCCA	CGAGCTGGTG	TTGGCCAATA	TTGCTGAAG	TGATGCTGGT	GTCTACACCT	1320
GCCAGCGCGC	CACCTGGGCT	GGTCAGCGGA	GACAGGATGT	CAACATCACT	GTGGCCACTG	1380
TGCCCTCCTG	GCTGAAGAGG	CCCCAAGACA	GCCAGCTGGA	GGAGGGCAAA	CCCGGCTACT	1440
TGGATTGCTT	GACCCAGGCC	ACACCAAAAC	CTACAGTTGT	CTGGTACAGA	AACCATGATG	1500
TCATCTCAGA	GGACTCAGCG	TTGAGGTCTT	TCAAGAATGG	GACCTTGGCG	ATCAACAGCG	1560
TGGAGGTGTA	TGATGGGACA	TGGTACCGTT	GTATGAGCAG	CACCCAGGCC	GGCAGCATCG	1620
AGGCGCAGAG	CGGTGTCCAA	GTGCTGGAAG	AGCTCAAGTT	CACACCACCA	CCCCAGCCAC	1680
AGCAGTGCA	GGAGTTTGAC	AAGGAGGCCA	CGGTGCCCTG	TTCAAGCCCA	GGCCGAGAGA	1740
AGCCCACTAT	TAAAGTGGAA	CGGGCAGATG	GGAGCAGCCT	CCAGAGTGGG	GTGACAGACA	1800
ACGCTGGGAC	CCTGATTTT	GCCCGGGTGA	CTGAGATGA	CGCTGGCAAC	TACACTTGCA	1860
TTGCTTCCAA	CGGGCCGAG	GGCCAGATTC	GTGCCCATGT	CCAGCTCACT	GTGGCAGTTT	1920
TTATCACCTT	CRAAGTGGA	CCAGAGCGTA	CGACTGTGTA	CCAGGGCCAC	ACAGCCCTAC	1980
TGCACTGCGA	GGCCAGGGG	GAACCCAAAG	CGCTGATTC	GTGGAAGGCG	AAGGACCGCA	2040
TCTTGAGCCC	CACCAAGCTG	GAACCCAGGA	TGCACATCTT	CCAGAAATGGC	TCCCTGGTGA	2100
TCCATCAAGT	GGCCCTCAG	GACTCAGGCC	GCTACACCTG	CAITGCAGGC	AACAGCTGCA	2160
ACATCAAGCA	CACGGAGGCC	CCCCCTCTATG	TCTTGACAA	GCCTGTGCCG	GAGGAGTCGG	2220
AGGGCCCTGG	CAGCCCTCCC	CCCTACAAGA	TGATCCAGAC	CATTGGGGTTG	TGGTGGGGTG	2280
CGCTGTGGCG	CTACATCAT	GCGGTGCTGG	GCCTCATGTT	CTACTGCAAG	AAGCGCTGCA	2340
AAGCCAAGCG	GCTGCAGAG	CAGCCCGAGG	GCGAGGAGCC	AGAGATGGAA	TGCTTCAACG	2400
GAGGCGCTTT	GCAGAACGGG	CAGCCCTCAG	CAGAGATCCA	AGAAGAAGTG	GCCTTGACCA	2460
GCTTGGGCTC	CGGCCCCCGG	GCCACCAACA	AACGCCACAG	CACAAGTGAT	AAGATGCACT	2520
TCCACGCGTC	TAGCTTGACG	CCCATCACCA	CGCTGGGGAA	GAGTGAGTTT	GGGGAGGTGT	2580
TCTTGGCAAA	GGCTCAGGCG	TTGGAGGAGG	GAGTGGCAGA	GACCCCTGGTA	CTTGTGAAGA	2640

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GCGTCGACAG  GAAGGATGAG  CAGCAGCAGC  TGGACTTCCG  GAGGGAGTTG  GAGATGTTTG  2700
GGAAGCTGAA  CCACGCCAAC  GTGGTGCGGC  TCCTGGGGCT  GTGCGGGGAG  GCTGAGCCCC  2760
ACTACATGGT  GCTGGAATAT  GTGGATCTGG  GAGACCTCAA  GCAGTTCCCT  AGGATTTCOA  2820
AGAGCAAGGA  TGAAAAATTG  AAGTCACAGC  CCCTCAGCAC  CAAGCAGAAG  GTGGCCCTAT  2880
GCACCCAGGT  AGCCCTGGGC  ATGGAGCACC  TGTCCAACAA  CCGCTTTGTG  CATAAGGACT  2940
TGGCTGCGCG  TAACTGCTGT  GTCACTGCCC  AGAGACAAGT  GAAGGTGTCT  GCCCTGGGCC  3000
TCAGCAAGGA  TGTGTACAAC  AGTGAGTACT  ACCACTTCCG  CCAGGCTCGG  GTGCGCTGCG  3060
GCTGGATGTC  CCCCGAGGCC  ATCTGGAGG  GTGACTTCTC  TACCAAGTCT  GATGTCTGGG  3120
CCTTCGGTGT  GCTGATGTGG  GAAGTGTITA  CACATGGAGA  GATGCCCAT  GGTGGGCAGG  3180
CAGATGATGA  AGTACTGGCA  GATTTCAGG  CTGGGAAGGC  TAGACTTCCT  CAGCCCGAGG  3240
GCTGCCCTTC  CAACTCTTAT  CGGCTGATGC  AGGCTGCTG  GGCCCTCAGC  CCGAAGGACC  3300
GGCCCTCCTT  CAGTGAGATT  GCCAGCGCCC  TGGGAGACAG  CACCGTGGAC  AGCAAGCGGT  3360
GAGGAGGGAG  CCCGCTCAGG  ATGGCTGGG  CAGGGGAGGA  CATCTCTAGA  GGGAAAGCTCA  3420
CAGCATGATG  GGCAGATGCC  CTGTCTCCT  GGGCCCTGAG  GTGCCCTAGT  GCAACAGGCA  3480
TTGCTGAGGT  CTGAGCAGGG  CCGTGGCTTT  CCTCTCTTC  CTCACTCTCA  TCCTTTGGGA  3540
GGCTGAGTGG  GAGCCAAACT  GGGCGACTAG  GGCCTTGAGC  TGGGCGAGTT  CCCCTGCCAC  3600
CTCTCTCTCT  ATCAGCGACA  GTGTGGGTGC  CACAGGTAAC  CCAATTTCT  GGCCTTCAAC  3660
TTCTCCCTCT  GACCGGGTCC  AACTCTGCCA  CTCATCTGCC  AACTTTGCC  GGGGAGGGCT  3720
AGGCTTGGGA  TGAGCTGGGT  TTGTGGGGAG  TTCTTAATA  TTCTCAAGT  CTGGGCACAC  3780
AGGGTTAATG  AGTCTCTTGC  CCACTGGTCC  ACTTGGGGGT  CTAGACCAGG  ATTATAGAGG  3840
ACACAGCAGG  TGAGTCTCTC  CCACTCTGGG  CTGTGCACA  CTGACCCAGA  CCAAGCTCT  3900
CCCCACCTCT  CTCTCTCTTC  CTCATCTAA  GTGCCTGGCA  GATGAAGGAG  TTTTCAGGAG  3960
CTTTTGACAC  TATATAAACC  GCCCTTTTGT  TATGCACCAC  GGGCGGCTTT  TATATGTAAT  4020
TTCAGCGTGG  GGTGGGTGGG  CATGGGAGGT  AGGGGTGGGC  CCGGAGATG  AGGAGGGTGG  4080
GCCATCCTTA  CCCCACACTT  TTATTGTTGT  CGTTTTTGT  TTGTTTTGTT  TTTTGTTTT  4140
TGTTTTTGT  TTTACACTCG  CTGCTCTCAA  TAAATAAGCC  TTTTTTA

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Seq ID NO: 534 Protein sequence
Protein Accession #: NP_002812

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1      11      21      31      41      51
|      |      |      |      |      |
MGAARGSPAR  FRLPLLSVL  LPLLLGQTQT  AIVFIKQFSS  QDALQRRAL  LRCEVEAPGP  60
VHVYWLDDGA  PVQDTERRFA  QGSSLSFAAV  DRLQDSGTFQ  CVARDDVTGE  EARSANASFN  120
IKWIEAGPVV  LKHPASEAEI  QPQTQVTLRC  HIDGHPRTY  QWFRDGTPLS  DGQSNHTVSS  180
KERNLTLRFA  GPEHSGLYSC  CAHSAPGQAC  SSQNFLLSIA  DESFARVULA  PQDVVVARYE  240
EAMPHCQFSA  QPPPSLQWLF  EDETPITNRS  RPPHLRRATV  FANGSLLLTQ  VRPRNAGIYR  300
CIQQGQRGPP  IILEATLHLA  EIEDMPLFEP  RVFTAGSEER  VTCLPPKGLP  EPSVWWEHAG  360
VRLPETHGRVY  QKGHELVLAN  IAESDAGVYT  CHAANLAGQR  RQDVNITVAT  VPSWLKKPQD  420
SQLSEBKPGY  LDCLTQATPK  PTVVWYRNQM  LISEDSRFEV  FKNGTLRLNS  VEVDYDGTWYR  480
QMSSTPAGSI  EAQARVQVLE  KLKFTPPPOP  QQCMFQKEA  TVPCSATGRE  KPTIKWERAD  540
GSSLPFWVTD  NAGTLHFARV  TRDDAGNYTC  IASNGPQQQI  RAHVQLTVAV  FITFKVEPER  600
TTYVQGHATL  LQCEAGQDPK  PLIQWKGKDR  ILDPKLGKPR  MHIFQNGSLV  IHDVAPEDSG  660
RYTCLAGNSC  NIKHTEAPLY  VVDKFPVPEES  EGPSPPPPYK  MIQTIGLSVG  AAVAYIIAVL  720
GLMFYCKKRC  KAKRLQKQPE  GEEPEMECLN  GGPLQNGQPS  AEIQEEVALT  SLGSGPAATN  780
KRHSTDGKH  PFRSSLPFIT  TLGSEFGEV  FLAKAQGLEE  GVAETLVLVK  SLQTKDEQQQ  840
LDFRRELEMF  GKLNHANVVR  LLGLCREAEP  HYMVLEYVDL  GDLKQFLRIS  KSKDEKLKSK  900
PLSTKQKVAL  CTQVALGMEH  LSNRFRVHKD  LAARNCLVSA  QRQVKVLSAL  LSKDVYNSEY  960
YHFRQAWPL  RWSFPAILE  GDFSTKSDVV  AFGVLMWEVF  THGEMPHGQV  ADDEVLDLQ  1020
AGKARLPQPE  GCPKLYRLM  QRCWALSPKD  RPSFSEIASA  LGDSTVDSKP

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Seq ID NO: 535 DNA sequence
Nucleic Acid Accession #: NM_013952
Coding sequence: 161..1357

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1      11      21      31      41      51
|      |      |      |      |      |
TTCAGAAGGA  GGAGAGACAC  CGGGCCCAGG  GCACCCTGCG  GGGCGGGCGG  ACCCAAGCAG  60
TGAGGGCCCTG  CAGCCGGCCG  GCCAGGGCAG  CGGCAGGGGC  GGCCCGGACC  TACGGGAGGA  120
AGCCCCGAGC  CCTCGGCGGG  CTGCGAGCGA  CTCCCGGGCG  ATGCCCTACA  ACTCCATCAG  180
ATCTGGCCAT  GGAGGGCTGA  ACCAGCTGGG  AGGGGCTTTT  GTGAATGGCA  GACCTCTGCC  240
GGAAGTGGTC  CGCCAGCGCA  TCGTAGACCT  GGCCACCAGG  GGTGTAAGGC  CCTGCGACAT  300
CTCTCGCCAG  CTCCGCGTCA  GCCATGGCTG  CGTCAGCAAG  ATCCTTGCCA  GGTACTACGA  360
GACTGGCAGC  ATCCGCGCTG  GAGTGATAGG  GGGCTCCAAG  CCAAGGTGG  CCACCCCAAA  420
GGTGGTGGAG  AAGATTGGGG  ACTACAAAG  CCAGAACCT  ACCATGTTTG  CCTGGGAGAT  480
CCGAGACCGG  CTCTGGCTGT  AGGGCGTCTG  TGACAAATGAC  ACTGTGCCCA  GTGTCACTGC  540
CATTAAATAGA  ATCATCCGGA  CCAAAGTGCA  GCAACCATTC  AACCTCCCTA  TGGACAGCTG  600
CGTGGCCACC  AAGTCCCTGA  GTCCCGGACA  CAGCTGATC  CCGAGCTCAG  CTGTAACCTC  660
CCCGGAGTCA  CCCCAGTCGG  ATTCCCTGGG  CTCCACCTAC  TCCATCAATG  GGCTCCTGGG  720
CATCGCTCAG  CCTGGCAGCG  ACAAGAGGAA  AATGGATGAC  AGTGATCAGG  ATAGCTGCGG  780
ACTAAGCATT  GACTCACAGA  GCAGCAGCAG  CGGACCCGGA  AAGCACCTTC  GCACGGATGC  840
CTCAGCCAG  CACCACCTCG  AGCCGCTCGA  GTGCCCATTT  GAGCGGCAGC  ACTACCCAGA  900
GGCCTATGCC  TCCCCAGGCC  ACACCAAAGG  CGAGCAGGGC  CTCTACCCGC  TGCCCTTGCT  960
CAACAGCACC  CTGGAAGACG  GGAAGGCCAC  CCTGACCCCT  TCCAACACGC  CACTGGGGCG  1020
CAACTCTCG  ACTACACAGA  CCAACCCGT  GGTGGCAGCT  CCGCCCTTTT  GATCTGCGAG  1080
CAAGTCGGCT  CCGGGTCCC  GCGCTTCAAT  GCCTTTCCCC  ATGCTGCCTC  CGTGTACGGG  1140
CAGTTTACGG  GCCAGGCCCT  CCTCTCAGGG  CGAGAGATGG  TGGGGCCAC  GCTGCCCGGA  1200
TACCCACCCC  ACATCCACAC  CAGCGGACAG  GGCAGCTATG  CCTCTCTGCG  CATGCGAGGC  1260
ATGGTGGCAG  GAAAGTAAATA  CTCTGGCAAT  GCGTATGGCC  ACACCCCTCA  CTCTCTACT  1320
AGCGAGGCCT  GGGGCTTCCC  CAACTCCAGC  TTGCTGAGTT  CCCCATAATTA  TTACAGTTCC  1380
ACATCAAGGC  CGAGTGACAC  GCCCACCCT  GCCACGGCTT  TTGACCATCT  GTAGTTGCCA  1440
TGGGACAGT  G

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Seq ID NO: 536 Protein sequence
Protein Accession #: NP_039246

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5      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQPPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD SDQDSCRLSI DSQSSSSGPR KHLRTDAPSQ HHLPLECPFP 240
10 ERQHYPEAYA SPSHTKGEGQ LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYFVVAA 300
PPFWLCCKSA PGRSPMPFP MLFPCTGSSR ARPSQGERW WGPCRCPDTHP TSPPADRAAM 360
PPLPSQANWQ EVNTLAMPMA TPPTPTTARP GASPTPAC

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Seq ID NO: 537 DNA sequence
Nucleic Acid Accession #: NM_003466.1
Coding sequence: 11..1363

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20      1      11      21      31      41      51
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GAATTCGGGG ATGCCTCACA ACTCCATCAG ATCTGGCCAT GGAGGGCTGA ACCAGCTGGG 60
AGGGGCCCTTT GTGAATGGCA GACCTCTGCC GGAAGTGGTC CGCCAGCGCA TCGTAGACCT 120
GGCCCAACCA GGTGTAAGGC CCTGCGACAT CTCTCGCCAG CTCGCGCTCA GCCATGGTTG 180
CCTCAGCAAG ATCCTTGGCA GGTACTACGA GACTGGCAGC ATCGGCGCTG GAGTGTATAG 240
GGGCTCCAA GCGAAGGTGG CCACCCCAAA GGTGGTGGAG AAGATTGGGG ACTACAAAG 300
25 CCAGAACCTT ACCATGTTTG CCTGGGAGAT CCGAGACCGG CTCTCGCTG AGGGCGTCTG 360
TGACAAAGAC ACTGTGCCCA GTGTGAGCTC CATTAATAGA ATCATCCGGA CCAAAGTGCA 420
GCAACCATTC AACCTCCCTA TGGACAGCTG CGTGGCCACC AAGTCCCTGA GTCCCGGACA 480
CAGCGTGATC CCAGCTCAG CTGTAATCC CCCGAGTCA CCCAGTCCG ATTCCTTGGG 540
TCCACCTAC TCATCAATG GGCTCCTGG CATCGCTCAG CCTGGCAGCG ACAAGAGGAA 600
30 AATGATGAC AGTATCAGG ATAGCTGCC ACTAAGCATT GACTCAGAGA GCAGCAGCAG 660
CGAGCCCGGA AAGCACCCTC GCACGGATGC CTTACGCCAG CACCACTCG AGCCGCTCGA 720
GTGCCCATTT GAGCGGCAGC ACTACCCAGA GGCTATGCC TCCCCAGGCC ACACCAAAG 780
CGAGCAGGGC CTCTACCCGC TGCCCTTGCT CAACAGCACC CTGGACGAGG GGAAGGCCAC 840
CCTGACCCCT TCCAACACGC CACTGGGGCG CAACCTCTCG ACTCACGGA CTTACCCCTG 900
35 GTGTGGCAGT CCTCACTCAC CCTTCGCCAT AAGCAGGAA ACCCCGAGG TGTCCAGTTC 960
TAGCTCCACC CTTTCTCTT TATCTAGCTC CGCTTTTGG GATCTGCAGC AAGTCGGCTC 1020
CGGGTCCCG CCCTTCAATG CCTTCCCA TGCTGCTCC GTGTACGGC AGTTACGGG 1080
CCAGGCCCTC CTCTCAGGGC GAGAGATGTT GGGGCCACG CTGCGCGGAT ACCCAACCCA 1140
40 CATCCCAAC AGCGGACAGG GCAGCTATGC CTCTCTGCG ATCGCAGGCA TGGTGGCAGG 1200
AAGTGAATG TCTGGCAATG CCTATGGCCA CACCCCTAC TCCTCTTACA GCGAGGCTG 1260
CGGCTTCCC AACTCAGCT TGCTGAGTTC CCCATATTAT TACAGTTCCA CATCAAGGCC 1320
GAGTGCACCG CCCACCACTG CCAAGGCTT TGACCATCTG TAGTTGAAGC TT

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Seq ID NO: 538 Protein sequence
Protein Accession #: NP_003457

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50      1      11      21      31      41      51
|      |      |      |      |      |
MPHNSIRSGH GGLNQLGGAF VNGRPLPEVV RQRIVDLAHQ GVRPCDISRQ LRVSHGCVSK 60
ILGRYYETGS IRPGVIGGSK PKVATPKVVE KIGDYKRQNP TMFAWEIRDR LLAEGVCDND 120
TVPSVSSINR IIRTKVQPPF NLPMDSCVAT KSLSPGHTLI PSSAVTPPES PQSDSLGSTY 180
SINGLLGIAQ PGSDKRKMD SDQDSCRLSI DSQSSSSGPR KHLRTDAPSQ HHLPLECPFP 240
ERQHYPEAYA SPSHTKGEGQ LYPLPLLNST LDDGKATLTP SNTPLGRNLS THQTYFVVAD 300
55 PHSPFAIKQE TPEVSSSSST PSSLSAFL DLQVVGSGVP PFNAFPHAA SSVYQFTGQAL 360
LSGREMVGPT LPGVPHIPT SGQGSYASSA IAGNVAGSEY SGNAVHTFP SSVSEAWRFP 420
NSSLLSPFY YSSTSRPSAP PTTATAFDHL

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Seq ID NO: 539 DNA sequence
Nucleic Acid Accession #: NM_006799
Coding sequence: 19..963

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65      1      11      21      31      41      51
|      |      |      |      |      |
GCGCGGGGAG AGGAGGCCAT GGGCGGCGC GGGCGGCTGC TGCTGGGCT GCTGCTGGCT 60
CGGGCTGAGC TCAGGAAGCC GGAGTCGAG GAGGCGGCGC CGTTATCAGG ACCATGCGGC 120
CGACGGGTAC TCACGTGCG CATCTGCGT GAGAGGACG CGAACTCGG GCGTTGGCCG 180
TGGCAGGGGA GCTGCGCCT GTGGGATTCC CAGTATGCG GAGTGAGCT GCTCAGCCAC 240
CGCTGGGAC TCACGGGCGC GCATGCTTT GAAACCTATA GTGACCTTAG TGATCCCTCC 300
GGGTGGATGG TCCAGTTTGG CCAGCTGACT TCCATGCCAT CCTCTGGAG CCTGCAAGGC 360
70 TACTACACCC GTTACTTGT ATCGAATATC TATCTGAGCC CTGCTACCT GGGGAATTCA 420
CCCTATGACA TTGCTTGGT GAAGCTGTCT GCACCTGTCA CCTACATAA ACACATCCAG 480
CCCATCTGTC TCCAGGCTC CACATTGAG TTTGAGAACC GGACAGACTG CTGGGTGACT 540
GGCTGGGGGT ACATCAAGA GATGAGGCA CTGCCATCTC CCCACACCT CCAGGAAGTT 600
CAGGTGCGCA TCATAACAA CTCTATGTGC AACCACTCT TCCTCAAGTA CAGTTTCCG 660
75 AAGGACATCT TTGAGACAT GGTTTGTGCT GGCAATGCC AAGCGGGAA GATGCTGCTG 720
TTGCGTGACT CAGGTGAGC CTTGGCTGT AACAAAGAT GACTGTGTA TCAGATTGGA 780
GTGCTGAGCT GGGGAGTGG CTGTGCTCG CCCAATCGG CCGGTGTCTA CACCAATATC 840
AGCCACCACT TTGAGTGGAT CCAGAAAGCT ATGGCCCAAG GTGGCATGTC CCAGCCAGAC 900
CCTCTGCTG GCTACTCTT TTTCCTCTT CTCTGGGCTC TCCCACTCT GGGGCGGCTG 960
80 TGAGCCTACC TGAGCCCATG CAGCCTGGG CCACTGCCAA GTCAGGCCCT GGTCTCTCTC 1020
TGCTCTGTTT GGTAATAAAC ACATTCCAGT TGATGCCTTG CAGGCGATTC TTCAAAA

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Seq ID NO: 540 Protein sequence
Protein Accession #: NP_006790

1 11 21 31 41 51
 5 MGARGALLLA LLLARAGLRK PESQBAAPLS GPCGRRVITS RIVGGEDAEL GRWPWQGSILR 60
 LADSHVCGVS LLSHRWALTA AHCPEYSDL SDPSGWMVQF GQLTSMPSFW SLQAYYTRYF 120
 VSNLYLSPRY LGNSPYDIAL VKLSAPVITY KHIIQICLQA STFEFENRTD CWVTGNGVIK 180
 EDEALPSPHT LQEVQVAIIN NEMCNHLPLK YSFRKDIPGD MVCAGNAQGG KDACFGDSGG 240
 PLACNKNGLW YQIGVVSNGV GCGRPNRPGV YTNISHHFEW IQKLMAQSGM SQPDPSWPLL 300
 10 FFPLLWALPL LGPV

Seq ID NO: 541 DNA sequence
 Nucleic Acid Accession #: NM_014344
 Coding sequence: 131..1444

15 1 11 21 31 41 51
 GGGGCGCGA TGGGCGGAA GCGCCGGAAG CCCCGAGCC CACAACTGC GGGGCGCGC 60
 TCGCTGCGG GACCGGGTG CTTGGGCTCG GCTTGAAGCG GCGGCGGCG ACCGCGACAG 120
 CGCGCGGAGC ATGGGCGAGG GATGCGGGG CGCGCGCGC ACCGCGGGC TCTGGCTGCT 180
 20 GCGCTGCGG TCGCTGCTGG CGCTGTGGG AGGCTCTCTG CGCGCGCGA CCGAGCTGCC 240
 CGCTCTCCG CGCGCGGAG ACCGACTCCC ACGGCGCGC GCGCGAGCG GCGGCGCGC 300
 GCGCGCGCT CGCTTCCCTC TGCCCGCGC CTTGGGCTGG GACGCGCGG GGGCTCCCT 360
 GAAAACTTC CGGCGCTGC TCACCTTGG GCGCGCGCG GACGCGCGC CCCGCGAGTC 420
 CGGAGCGCG CGGAGCTGG ACCTGTGAG CAGGCGCGC CGCGCGGAG AGAGCGCGC 480
 25 GGTGACGCG GCGCTCTCT GAGCGCGCG CTTGGAGGAG CAGGTGCCCC CGGCTTTTC 540
 GGAGGCCAG CGCGCGGCT GCTGGAGGC GCTCGCGCG GCGCGGATG TGGCGCTGGA 600
 GCGCGGGGT TGGCGGCGA GCTCCACCG ACTGGCGCG TTTGCGGAG GCACCGCGC 660
 CTGCTGCGC TACGCGATCA ACCCGAGCA GATTGAGGC GAGGCGCTGT CTTACTATCT 720
 GCGCGCGCT CTGCGCTCC AGCGCCACG CCGCGCGCT GCACTGGCTC GGGTGGAGGC 780
 30 TCGCGCGCG CAGTGGGCG AGGTGAGGA GAGCTGCGC GCTGCGCACT GGACCGAGGG 840
 CAGCGTGTG AGCTTGACAC GCTGGCTGCC CAACCTCAG GACGTGGTGG TGCCGCGCG 900
 CTGCGCTCG GAGGACGCG GTCTGCGCC CTTCCGGAT GCGCGGGTG AGCTGGCAA 960
 CCTCAGCCG CGCGAGCTG TGGACCTAGT ACAATGAGC GACTTAATCC TTTTCGACTA 1020
 CCGTACGCG AACTTCGACC GCTCTGTAAG CAACCTCTC AGCTTCGAGT GGGACCGCG 1080
 35 CGTATGCGC CGTGGCCCA GCAACCTGCA CCGCGTCCG GCGCGGCGC TGGTCTTCT 1140
 GGACATGAG GCGGCTTGG TGCACGGCTA CCGGTAGCA GGCATGTGG ACAAGTATAA 1200
 CGAGCGCGT TTAGCTGAG TGTGCGTGT CCGCGAGCG ACCGCGCGC GGTCTCTGGA 1260
 GCTGACGCG GGACAGGAG CCGCGCGCG GCTGCTGCG CTCTACCGCG GCCACGAGCC 1320
 TGCTTCTCG GAGGACGAA TCACCGAGG GAGAAAGTGA ACATTCTCT CACCCAGCTT 1380
 40 GCACTTCTC GCCAAGACA TTTTGCACTG TAAGGCCAAG TACGCGCGC GGTCTGGGAC 1440
 TTAGTGTGAG CGGAGGAAA AGAGAGAGT CTGGGCTGG GGTATGATG ATGGGGGAA 1500
 GGGCGGTGC CTCTGCCACT GTCAGGAGC AGCGCGCAA CGCCCAACCG CAAAGGTGTC 1560
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 AAAAGTTTG GAGGACGAA TCACCGAGG GAGAAAGTGA ACATTCTCT CACCCAGCTT 1680
 45 ATAAAGAGT TCTTTACTG GCCAGCAGG GATTTGGATC GAAAGAACT GGTACTGGG 1740
 GTTGGCCCG CGAGTGGCG TCCTGTGGG AGATGACCC CATTCTTGG CCCCCTCAT 1800
 TCCCTTTCCG AAAAAGAAA ACTTGCGTT GAGCGTGA GCTAATCTG CAATTTCTA 1860
 CCAACAGAG CGCTGTGGC CCGGAGCAG GGTGTGACA TTGGCTGGT GAGCCCTTC 1920
 50 CTGTGTCTC CTTTGTTC AGCGCGCGA TGGTGAGAT ACTGTTCAA GCAGGGGAG 1980
 GGCTCGGAT AGGACAAAG GAGCAGGAC TCCAGACTCT GGGGAGCCCT GCAGACCTT 2040
 ACAATTGCT TGACTCATC CTGACCTCT GTCATTTTG CCGTGAAGCT ACAATTCTG 2100
 GGTCACTGT ATGCACTAG TCAATAATG AATTTCTTC TCCCTCTGC AACCGACCA 2160
 AATTTTGAC ACAGATGAT TCACAGAGG GAAAAAATA TCAGTTTAT GCACCTTAT 2220
 55 TTGTTTGAT TTTTATTTT TATTAAGAAA AAATTTTAT TTACAGAAAT TACCTTCTC 2280
 GTATATATG GCATAAAGT TGGTGTAAT ATACTAAACA AACTATATT TCAATAAAG 2340
 GGAGTTAAA ATTTAAAAA AAAAAA

Seq ID NO: 542 Protein sequence
 Protein Accession #: NP_055159

60 1 11 21 31 41 51
 MGRMRGAAA TAGLWLLALG SLLALWGLL PPRTELPASR FPEDRLPRRP ARSGGPAPAP 60
 RFPPLPPFLAW DARGGSLKTF RALLTLAAGA DGPFRQSRSE PRWHVBARQP RPERSAAVHG 120
 65 GVFWSRGLEE QVPPGFSEAQ AAAMLEAARG ARMVALERGG CGRSSNRLAR FADGTRACVR 180
 YGINPEIQIG EALSYYLARI LGLQRHVPL ALARVEARGA QWAQVOELR AAHWTEGSVV 240
 SLTRWLENLT DVVVPAPWRS EDGRLRPLRD AGGELANLSQ AELVDLVQWT DLILFDYLT 300
 NFDRLVSNLF SLQWDPRVMQ RATSNLHRGP GGALVFLDNE AGLVHGVRVA GMWDKYNEPL 360
 70 LQSVCFRER TARREVLHLR QDAAARLLR LYRREPRFP ELAALADPEA QLLQRRLDPL 420
 AKHILHCKAK YGRRSGT

Seq ID NO: 543 DNA sequence
 Nucleic Acid Accession #: XM_007652.4
 Coding sequence: 1..1290

75 1 11 21 31 41 51
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 80 TCTCGGTTCA ACAAACTTC AGTTGTGGT GCCGATGAG GTTCCGAGC CCGGAAAGG 180
 CTGTTAACG GGGCGCACCG GACCTCCAG GCCAGCATG ATTCTTACT GGACCAAGC 240
 TTACCTTTGA CCAACAGTCA GCTGAGTTT AAGGTGGACT CTTGTGACAA CTGCAGCAA 300
 CAGAGAGAGA TACTGAAGCA GAGAAAGGT AAAGCCAGGT TGACCATTCG TGCCGTTCT 360
 TACTTGCTTT TCATGATGG AGAACTGTA GGTGGATACA TTGCAATAG CTAGCAATC 420

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ATGACAGATG CACTTCATAT GTTAAGTAC CTAAGCGCCA TCATACTCAC CCTGCTTGCT 480
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GTTTTGTGAG CTATGATTAG TGTGCTGTTG GTGTATATAC TTATGGGATT CCTCTTATAT 600
GAAGCTGTGC AAAGAACTAT CCATATGAAC TATGAAATAA ATGGAGATAT AATGCTCATC 660
ACCGCAGCTG TTGGAGTTGC AGTTAATGTA ATAATGGGCT TTCTGTTGAA CCAGCTCTGGT 720
CACCGTCACT CCGATTCCCA CTCCCTGCGT TCAAATTCCC CTACCAGAGG TTCTGGGTGT 780
GAACTGAACC ATGGGCAGGA TAGCCTGGCA GTGAGAGCTG CATTGTGTACA TGCTTTGGGA 840
GATTGTGTAC AGAGTGTGTT TGTGCTAATA GCTGCATACA TCATACGATT CAAGCCAGAA 900
TACAAGATTG CTGATCCCAT CTGTACATAC GTATTTTCAT TACTTGTGGC TTTTACAACA 960
TTTGAATCA TATGGGATAC AGTAGTTATA ATACTAGAAG GTGTGCCAAG CCATTGTGAAT 1020
GTAGACTATA TCAAAGAAGC CTGTATGAAA ATAGAAGATG TATATTTCAGT CGAAGATTTA 1080
AATATCTGGT CTCTCACTTC AGGAAAATCT ACTGCCATAG TTCACATACA GCTAATTCCT 1140
GGAAGTTTCA TTAATGGGGA GGAAGTACAG TCCAAAGCAA ACCATTATT ATTGAACACA 1200
TTTGGCATGT ATAGATGTAC TATTGAGCTT CAGAGTTACA GGCAAGAAGT GGACAGAACT 1260
TGTGCAAAAT GTCAGAGTTC TAGTCCCTGA
  
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Seq ID NO: 544 Protein sequence
Protein Accession #: XP_007652.1

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1 11 21 31 41 51
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PUNGAPHTLQ ADDSLLDQD LPLTNSQLSL KVDSCDNCCK QREILKQRKV KARLTIAAVL 120
YLLFMIGELV GGYIANSLAI MTDALHMLTD LSAILLTLIA LMLSSKSPK RPTFGPHRL 180
VLSAMISVLL VYILMGFLLY EAVQRTIEMN YEINGDMLLI TAAVGVAVNV IMGFLNQSG 240
HRHSHSHSLP SNPSPTGSGC ERNHGQDLSA VRAAFVHALG DLVQSVGLI AAYIIRFKPE 300
YKIADPICYT VPSLLVAFIT FRIINDTVVI ILEGVPSHLN VDYIKSALMK IEDVYSVEDL 360
NINSLTSGKS TAIVHIQLIP GSSSKWEVQ SKANHLLNT FGMRYCTIQL QSYRQSEVDR 420
CANQSSSP
  
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Seq ID NO: 545 DNA sequence
Nucleic Acid Accession #: AB037765.1
Coding sequence: 1..2478

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1 11 21 31 41 51
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TACATGCCAA CAGTAACTC TTTACAGAA CTGAGTCTCT AGAAATATT TAGTACATTG 120
CAACAGAGAA AAGCCTCTTT AGCTTATTTT TGTCAGCTG ATTCCCCAAG AACATCTGTA 180
TTTCTTGAAG AACTGAATGA GGCTGTTAGA CCTCTGAGG ACTATGGAAT TTCAGTTGCC 240
AAGGTTAATT GTGTCAAAGA AGAATATCA AGATACTGTG GAAAAGAAA GGATTTGATG 300
AAGCATATT TATTCAAGGG CAACATAITG CTCAGAGAAT TCCCTACTGA CACCTTGTTT 360
GATGTGAATG CCAATGTGCG CCATGTCTCT TTTGCTCTTC TTTTATGTA AGTGAAATAT 420
ATTACCAACC TGAAGAAGCT TCAGAACATA GAAAATGCTC TGAAAGGAAA AGCAAAATAT 480
ATATTCTCAT ATGTAAGAGC CATTGGAATA CCAGAGCACA GAGCAGTCAT GGAAGCCGCT 540
TTTGTGTATG GGAATCATATA CCAATTGTGC TTAACACAG AAATTGCCCT TTTGAAAAGT 600
ATTGGCTCTG AGGATGTGGA ATATGCACAT CTCTACTTTT TTCATTGTAA ACTAGTCTTG 660
GACTTGACCC AGCAATGTAG AAGAACACTA ATGGAACAGC CATTGACTAC ACTGAACATT 720
CACCTGTTTA TTAAGACAA GAAAGCACCT CTGTTGACTG AAGTTGCTGA AGATCCTCAA 780
CAAGTTTCAA CIGTCCATCT CCAACTGGGC TTACCACTGG TTTTATTGTI TAGCCAACAG 840
GCTACTTATG AAGCTGATAG AAGAACAGCA GAATGGGTG CTGCGCTCT TCTGGGAAA 900
GCAGGAGTTC TACTCTGTG TAAAGGACTCT TTGGAAGTGA ACATTCCTCA AGATGCTAAT 960
GTGGTCTTCA AAGAGCAGA AGAGGGAGTT CCAGTGGAA TTTTGTATT ACATGATGTT 1020
GATTTAATAA TATCTCATGT GGAAAATAAT ATGCACATT AGGAAATACA AGAAGATGAA 1080
GACATGACA TGAAGGTCC AGATATAGAT GTTCAGGATG ATGAAGTGGC AGAACTGTT 1140
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TTTAATGCAA CAGTATGGC TTCTGACAGC ATAGTACTCT TCTATGCTGG TTGGCAAGCA 1260
GTATCCATGG CATTTTGTCA ATCCTATATT GATGTGGCAG TAAACTGAA AGGCACATCT 1320
ACTATGCTTC TTACTAGAAT AAACGTGTGA GATTGCTCT ATGTATGTAC TAAGCAAAAT 1380
GTTACTGAAT TTCCTATCAT AAAGATGTAC AAGAAAGCG AGAACCCAGT ATCTTATGCT 1440
GGAATGTTAG GAACCGAAGA TCTCCTAAAA TTTATCCAGC TCAACAGGAT TTCATATCCA 1500
GTGAATATAA CATOGATCCA AGAAGCAGAA GAATATTATA GTGGGGAATT ATATAAGAC 1560
CTCATCTTGT ATTCTAGTGT GTCAGTATTG GGACTATTTA GTCCCAACCAT GAAACACAGCA 1620
AAAGAAGATT TTAGTGAAGC AGGAAACTAC CTAAGAGGAT ATGTTATCAC TGAATTTAT 1680
TCTGAAGAAG ATGTTTGTCT ACTGTCAACC AAATATGCTG CAAGTCTTCC AGCCCTGCTG 1740
CTTGCCAGAC ACACAGAAAG CAAAATAGAG AGCATCCAC TAGCTAGCAC ACATGCACAA 1800
GACATAGTTC AAATAATAAC AGATGCACTA CTGGAAATGT TTCCGGAAAT CACTGTGGAA 1860
AATCTTCCCA GTTATTTCAG ACTTCAGAAA CCAATTATGA TTTTGTTCAG TGATGGCACT 1920
GTAAATCCTC AGTATAAAAA AGCAATATTG ACACGGTAA AGCAGAAATA CTTGGATTCA 1980
TTTACTCCAT GCTGGTTAAA TCTAAAGAA ACTCCAGTGG GGAGAGGAAT CTTGAGGGCA 2040
TATTTTGATC CTCTGCCTCC CCTTCTCTT CTGTGTTTGG TGAATCTGCA TTCAGGTGGC 2100
CAAGTATTTG CATTTCTCTC AGACCAAGCT ATAATTGAAG AAAACCTTGT ATTGTGGCTG 2160
AAGAAATTAG AAGCAGGAGT AGAAAATCAT ATCACAATTT TACCTGTCCA AGAATGGAAA 2220
CCTCTCTTC CAGCTTATGA TTTTCTAAGT ATGATAGATG CCGCAACATC TCAACGTGGC 2280
ACTAGGAAAG TTCCCAAGTG TATGAAGAA ACAGATGTGC AGGAGATGA TAAGGAACAA 2340
CATGAAGATA AATCGGAGT CAGAAAAGAA CCGATTGAAA CTCTGAGAAAT AAAGCATTGG 2400
AATAGAAGTA ATTGTTTAA AGAAGCAGAA AAATCATTTA GACGTGATAA AGAGTTAGGA 2460
TGCTCAAAAG TGAACATA
  
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Seq ID NO: 546 Protein sequence
Protein Accession #: BAA92582.1

1 11 21 31 41 51

5 MFSGFNVRV GISFVIMCIP YMPTVNSLPE LSPQKYFSTL QPGKASLAYF CQADSPTS SV 60
 FLEENNEAVR PLQDVGISVA KVNCKKEIS RYCGKEKDLN KAYLFKGNIL LREFPTDTLP 120
 DVNAIVARVL FALLPSEVKY ITNLEDQNI ENALKGKANI IFSVRAIGI PEHRAVMEAA 180
 FVYGTYYQFV LTTEIALLES IGSEDVEYAH LYFFHCKLVL DLTTQCCRIL MEQPLTTANI 240
 HLFIKTKAP LLEVAEDPQ QVSTVHLQLG LPLVFIVSQQ ATYEADRRTA EMVAMRLLGK 300
 AGVLLLLRDS LEVNIPQDAN VVFKRAESGV FVEPLVLHDV DLIISHVENN MHIESIQEDE 360
 DNDMEGPDID VQDDEVAETV FRDRKRKLPL ELTVLLEET FNATVMASDS IVLFYAGWQA 420
 VSMAPLQSYI DVAVKLKGTS TMLLTRINCA DWSOVCTKQN VTEFFIIMY KKGEPVSYA 480
 10 GMLGTEDLLK PIQLNRISYP VNITSIQEAE BYLSGELYKD LILYSSVSVL GLFSPTMKTA 540
 KEDPSEAGNY LKGYVITGIY SEEDVLLST KYAASLPALL LARHTEGKIE SIPLASTHAQ 600
 DIVQIITDAL LEMPEITVE NLPSYFRLQK PLLILFSDGT VNPQYKAIL TLVKQKYLDS 660
 FTPCNLNLKN TFGVGRILRA YFDPLPPLPL LVLVNLHSGG QVFAFPSDQA IIEENLVML 720
 KLEAGLEBNH ITILPAQEWK PPLPAYDFLS MIDAATSQRG TRKVPKCMKE TDVQENDKEQ 780
 15 HEDKSAVRKE PIETLRIKHW NRSNWFKEAB KSPRRDKELG CSKVN

Seq ID NO: 547 DNA sequence
 Nucleic Acid Accession #: NM_033102.1
 Coding sequence: 1..1662

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 ATGGTCCAGA GGCTGTGGGT GAGCCGCGCTG CTGGGGCACC GGAAGGCCA GCTCTGTCTG 60
 GTCAACCTGC TAACCTTTGG CCTGGAGGTG TGTTTGGCCG CAGGCATCAC CTATGTGCCG 120
 25 CCTCTGTGC TGGAGTGGG GGTAGAGGAG AAGTTCATGA CCATGTTGCT GGGCATTGGT 180
 CCACTGTGG GCTGTGCTG TGTCCCGCTC CTAGGCTCAG CCACTGACCA CTGGCTGGA 240
 CGCTATGGCC GCGCGCGGCC CTTCACTGCG GCACTGTCTT TGGGCATCCT GCTGAGCCTC 300
 TTTCTCATCC CAAGGGCGCG CTGGCTAGCA GGGCTGTCTG GCCCGATCC CAGGCCCTCT 360
 GAGCTGGCAC TGCTCATCTT GGGCGTGGG CTGCTGGACT TCTGTGGCCA GGTGTGCTCT 420
 30 ACTCACTGCT AGCCCTGTCT CTCTGACCTC TTCGGGACCC CGGACCACTG TCGCCAGGCC 480
 TACTCTGTCT ATGCTCTCAT GATCAGTCTT GGGGGCTGCC TGGGCTACCT CCTGCTGCTC 540
 ATTGACTGGG ACACCATGTC CTTGGGCGCC TACCTGGGCA CCGAGGAGGA GTGCTCTTT 600
 GGCTGCTCA CCTCATCTT CCTCACTGCT GTAGCAGCCA CACTGCTGCT GGCTGAGGAG 660
 CGAGCGCTGG GCGCCACCGA GCCAGCAGAA GGGCTGTCCG CCCCCTCCTT GTGGCCCTC 720
 35 TGCTGTCCAT GCGGGGCGCG CTTGGCTTTC CGGAACCTGG GCGCCTGCT TCCCGGCTG 780
 CACCACTGCT GCTGCGCAT GCGCCGCGCC CTGCGCGGCG TCTTCTGCTG TGAGCTGTGC 840
 AGCTGATGG CACTCATGAC CTTCACTGCT TTTTACAGG ATTTGCTGGG AGAGGGGCTG 900
 TACCAGGGCG TGCCAGAGC TGAGCCGGCG ACCGAGGCCG GGAGACACTA TGATGAAGGC 960
 GTTCGGATGG CGAGCTGGG GCTGTCTCTG CAGTGGGCCA TCTCCTGCT CTCTCTCTG 1020
 40 GTCATGGACC GCGTGTGCA GCGATTGGC ACTCGAGCAG TCTATTGGC CAGTGTGGCA 1080
 GCTTCTCCTG TGCTGCGCG TGCCACATGC CTGTCCACA GTGTGGCGT GGTGACAGCT 1140
 TCAGCCGCGC TCACGGGCTT CACCTTCTCA GCGCTGAGA TCTGCGCTA CACTGCGC 1200
 TCCTCTTACC ACCGGGAGAA GCAGGTGTTT CTGCCAAAT ACCGAGGGA CACTGGAGGT 1260
 GCTAGCAGTG AGGACAGCT GATGACAGC TTCTTCCAG GCCCTAAGCC TGGAGCTCCC 1320
 45 TTCCCTAATG GACACGTGGG TGCTGGAGGC AGTGGCCTGC TCCCACTCC ACCCGGCTC 1380
 TGCGGGGCTC CTGCTGTGA TGTCTCGTA CGTGTGTTG TGGGTGAGCC CACCGAGGCC 1440
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 CTGTCCAGG TGCGCCATC CTTGTTTATG GGCTCCATTG TCCAGCTCAG CCAGTCTGTC 1560
 ACTGCTTATA TGTGTCTGC CGCAGGCGCT GGTCTGTTG CCATTACTT TGCTACACAG 1620
 50 GTAGTATTGG ACAAGAGCGA CTTGGCCAAA TACTCAGCGT GA

Seq ID NO: 548 Protein sequence
 Protein Accession #: NP_149093.1

55 1 11 21 31 41 51
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 MVQLNLSRL LRHRKAQLLL VNLLTFGLEV CLAAGITYVP PLLLEVGVEE KFTMTVLGIG 60
 PVLGLVCPVL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGWLA GLLCPDPRPL 120
 ELALLILGVG LLDPCGVCF TPLEALLSDL PRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180
 60 IDWTSALAP YLGTQECLEP GLLTLIFLTC VAATLLVAEE AALGPTEPAR GLSAPSLSPH 240
 CCPCRARLAF RNLGALLPRL HQLCCRMPT LRRLFVAELC SWMALMTFTL FYTDFVGBGL 300
 YQGVFRAEPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFQ TRAVYLASVA 360
 APFVAAGATC LSHSVAVVTA SAALTGTFPS ALQILPYTLA SLYHREKQVP LPKYRGDTGG 420
 ASSEDSLMT FLPGPKPGAP PFNGHVAGG SGLLPPFPAL CGASACDVSV RVVVGEPTEA 480
 65 RVVPGRGICL DLALDLSAPL LSQVAPSLPM GSTVQLSQSV TAYMVAAGL GLVAIYPATQ 540
 VVFKSDLAK YSA

Seq ID NO: 549 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1389

70 1 11 21 31 41 51
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 75 GTTGTCAACT CGATTATAGG ATCTGGTATA ATAGGATTGC CTTATTCAAT GAAGCAAGCT 180
 GGGTTTCCCT TGGGAATAAT GCTTTTATTC TGGGTTTCAT ATGTACCGA CTTTCCCTT 240
 GTTTTATTGA TAAAGAGAGG GGCCTCTCTT GGAACAGATA CCTACCACTC TTTGCTCAAT 300
 AAAACITTCG GCTTTCAGG GTATCTGCTC CTCTCTGTTT TTCAGTTTAT GTATCTTTT 360
 80 ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420
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 ACAGTACCT TTACTCTGCC TTTATCTTTC TACCGAATA TAGCAAGCT TGGAAAGTTC 540
 TCCCTCATCT CTACAGGTTT AACAACTCTG ATCTTGGAA TTGTAAATGGC AAGGGCAATT 600
 TCACTGGGCT CACACATACC AAAACAGAA GAGCTTGGG TATTTCGAAA GCCCAATGCC 660
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5 TACAGTTCTC TAGAAGAAC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
 GTGATTTCTG TATTTATCTG TATATCTTTT GCTACATGTG GATACTTGAC ATTTACTGGC 840
 TTCACCCAGG GGGACTTATT TGAAAATTAC TGCAGAAATG ATGACCTGGT AACATTTGGA 900
 AGATTTTGTG ATGGTGTAC TGTCAATTTG ACATACCCCTA TGGAAATGCTT TGTGACAAGA 960
 GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTTCAT CGGTTTTCCTA CATTTGTGTA 1020
 ACAGTGATGG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTGGGGATA 1080
 GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
 TGTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCG ATAAGATTAT GTCTTGTGTC 1200
 10 ATGCTTCCCA TTGCTGCTGT GGTGATGGTT TTTGATTGCG TCATGGCTAT TACAAATACT 1260
 CAAGACTGCA CCCATGGGCA GGAATGTTC TACTGCTTTC CTGACAAATT CTCTCTACA 1320
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 TTCAATGA

15 Seq ID NO: 550 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 20 MGYQRQEPVI PPQRDLDDRE TLVSEHYEKE KTCQSAALFN VVNSIIGSGI IGLPYSMKQA 60
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 IAMISVNIIA GDTLSKVFQR IPGVDPENVP IGRHFIIGLS TVTPTLPLSL YRNIKLGKV 180
 SLISTGLTTL ILGLVMARAI SLGPHIPKTE DAWVPAKFNA IQAVGVSFA FICHNSFLV 240
 YSSLEPTVA KWSRLIHMSI VISVFICIFF ATCGYLTFGT FTQGLPFENY CRNDLVTFG 300
 25 RPYGVTVIL TYPMCEPVTB EVIANVFFGG NLSSVFHIVV TVMVITVATL VSLLDCLGI 360
 VLELNGVLCA TPLIFIIPSA CYLKLSEEPB THSDKIMSCV MLPIGAVVMV FGFVMAITNT 420
 QDCTHQEPMF YCFPDNPSLT NTSSEHVQQT TQLSTLNI SI PQ

30 Seq ID NO: 551 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1284

1 11 21 31 41 51
 35 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGGA GAGGATTGCC TTATTCAATG 60
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 TTTCCCTTG TTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AAATTTCCGG CTTTCCAGGG TATCTGCTCC TCTCTGTCTC TCAGTTTTTG 240
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAAGT 300
 40 TTTCAAAGAA TCCCAGGAGT TGATCCTGAA AAGGTGTTA TTGGTCGCCA CTTTATTATT 360
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 GGAAAGGTCT CCTCATCTC TACAGGTTA ACAACTCTGA TTCTTGAAT TGTAAATGGCA 480
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 45 TCTTAGTATT ACAGTTCTCT AGAAGAACCC ACAGTAGCTA AGTGGTCCCG CCTTATCCAT 660
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 TTTACTGGCT TCACCCCAAGG GACTTATTT GAAAATTACT GCAGAAATGA TGACCTGGTA 780
 ACATTTGGAA GATTTTGTGA TGGTGCTACT GTCATTTTGA CATACCTAT GGAATGCTTT 840
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTTCATC GGTTTCCAC 900
 50 ATTGTGTGTA CAGTGATGGT CATCACTGTA GCCAAGCTTG TGTCATTGCT GATTGATTGC 960
 CTCGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCTCAT TTTTATCAT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CACACTCGA TAAGATTATG 1080
 TCTGTGTGCA TGCTTCCCAT TGGTGCTGTG GTGATGGTTT TTGGATTGGT CATGGCTATT 1140
 ACAATACTC AAGACTGCAC CCATGGGCGG GAAATGTTCT ACTGCTTTCC TGACAATTTC 1200
 55 TCTCTACAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
 ATTAGTATCT TCAACTCGA GTAA

Seq ID NO: 552 Protein sequence
 Protein Accession #: Eos sequence

60 1 11 21 31 41 51
 MGYQRQEPVI PPQRGLPYSM KQAGFPLGIL LLEWVSIVTD PSLVLLIKGG ALSGTDYQS 60
 LVNKTGPPFG YLLSLVLQFL YPFIAMISYN ILAGDTLSKV PQRIPGVDP NVFIGRHFII 120
 65 GLSTVFTFLP LSLYRNIAKL GKVSLISTGL TTLILGIVMA RAISLGHPI KTEDAWVFAK 180
 PNAIQAVGVM SPAFICHNS FLVYSSLEEP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240
 FTGFTQGLDF ENYCRNDLV TFGRFCYGVV VILTYPMCEP VTREVIANVF FGGNLSSVPH 300
 IIVTVMVITV ATVLVSLIDC LGIVLELNGV LCATPLIPII PSACYLKLSE EPRTHSDKIM 360
 SCVMLPIGAV VMVFGFVMAI TNTQDCTHQG EMPYCFPDNF SLTNTSESHV QQTTLSTLN 420
 ISIFQLE

75 Seq ID NO: 553 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1203

1 11 21 31 41 51
 80 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGAGT TTTCCCTGT TTTATTGATA 60
 AAAGGAGGGG CCTCTCTCTG AACAGATACC TACCACTCTT TGGTCAATAA AACTTTCCGC 120
 TTTCCAGGGT ATCTGCTCTT CTCTGTTCTT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
 AGTTACAATA TAATAGCTCG AGATACTTTG AGCAAAAGTT TTTCAAGAAT CCCAGGAGTT 240
 GATCCTGAAA ACGTGTATTAT TGGTCGCCAC TTCAATTATG GACTTTCCAC AGTTACCTTT 300
 ACTCTGCTCT TATCCTTGTA CCGAAATATA GCAAGCTTG GAAAGGTCTC CCTCATCTCT 360
 ACAGGTTTAA CAACTCTGAT TCTTGGAAAT GTAATGGCAA GGGCAATTTC ACTGGGTCCA 420
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAGC CCAATGCCAT TCAAGCGTCT 480

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GGGGTTATGT CTTTTCGATT TATTTGCCAC CATAACTCCT TCTTAGTTTA CAGTTCCTTA 540
GAAGAACCCA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGCCCATCGT GATTTCTGTA 600
TTTATCTGTA TATTCCTTTC TACATGTGGA TACTTGACAT TTACTGGCTT CACCCAAGGG 660
GACTTATTTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTTGGAAG ATTTTGTAT 720
GGTGTCACTG TCATTTTGAC ATACCCATAG GAATGCTTTG TGACAAGAGA GGTAAATGCC 780
AATGTGTTTT TTGGTGGGAA TCTTTTCATCG GTTTTCCACA TTGTTGTAAC AGTGATGGTC 840
ATCACTGTAG CCACGCTTGT GTCAATGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900
AATGTGTGTC TCTGTGCAAC TCCCTCATTT TTTATCAATC CATCAGCCTG TTATCTGAAA 960
CTGTCTGAAG AACCAAGGAC AACTCCGAT AAGATTATGT CTGTGTGCAT GCITCCCATT 1020
GGTGTCTGGG TGATGGTTTT TGGATTGGTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
CATGGGCAAG AATATTCTTA CTGCTTTTCT GACAATTTCT CTCTCACAAA TACCTCAGAG 1140
TCTCATGTTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
TAA

Seq ID NO: 554 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
MGYQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTGP FPGYLLLSVL QFLYPFIAMI 60
SYNIIAGDTL SKVFQRIQGV DPENVFIGRH PIIGLSTVTF TLPLSLYRNI AKLQKVSLLIS 120
TGLTTLILGI VMARAIQLGP HIPKTEDAWV FAKPNAIQAV GVMSFAPICH HNSFLVYSSL 180
EPTVAKWSR LIHMSIVISV FICIPFATCG YLTFTGFTQG DLFENYCRND DLVTPGRFCY 240
GVTVILTYPM ECFVTREVIA NVFFGGNLSS VFHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVGFV MAITNTQDCT 360
HGQEMFYCFP DNPSLTNTSE SHVQQTQLS TLNISIFQLE

Seq ID NO: 555 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1140

1 11 21 31 41 51
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CCAGGGTATC TGCTCTCTCT TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTC AAAGAATCCC AGGAGTTGAT 180
CCTGAAACGG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCCACAGT TACCTTTACT 240
TGCCCTTTAT CTTGTACCG AAATATAGCA AAGCTTGGA AGGTCTCCCT CATCTCTACA 300
GGTTTAAACA CTCGTATTCT TGGAAATGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
ATACCAAAAA CAGAAGACGC TTGGGTATT GCAAGCCCA ATGCCATTCA AGCGTCCGG 420
GTATGTCTT TTGCATTAT TTGCCACCAT AACTCCTTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
ATCTGTATAT TCITTGCTAC ATGTGGATAC TTGACATTA CTGGCTTCAC CCAAGGGGAC 600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACTGTGA TTTTGACATA CCTATGGA TGTCTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTGTG GTGGGAATCT TTCATCGGT TTCCAATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTTGTGTC ATTGCTGATT GATTGCCCTG GGTAGTCTT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTCCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAAGACACA CTCGATAAG ATTATGTCT GTGTCTATG TCCCATTTGGT 960
CTGTGGTGA TGGTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTTCTACTG CTTTCTGAC AATTTCTCT TCACAAATAC CTCAGAGTCT 1080
CATGTTCCAG AGACAACACA ACTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

Seq ID NO: 556 Protein sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
MGYQRQEPVI PPQVNTKFGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIQVVD 60
PENVFIGRHF IIGLSTVTFP LPLSLYRNI KLKRVSLIST GLTTLILGIV MARAISLQPH 120
IPKTEDAMVF AKPNAIQAVG VMSFAPICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
ICIPFATCGY LTFTGFTQGD LFNENYCRND LVTGPRFCY VIVILTYPME CPVTREVIAN 240
VFFGGNLSSV FHVIVVTVMV TVATLVSLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
SEEPRTSDK IMSCVMLPIG AVVMVGFVMA AITNTQDCTH GQEMFYCFPD NFSLNTSES 360
HVQQTQLGST LNISIFQLE

Seq ID NO: 557 DNA sequence
Nucleic Acid Accession #: XM_057188.1
Coding sequence: 769..4269

1 11 21 31 41 51
| | | | |
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CTGCCCTTCC CCAATCTCTT TGGTTTTTGC ATCCCCCTCT GCGCCCTGCC TCAGTCAAGT 180
CTCCCTGTG TGTCTCTCTC CCCCCTGCCC GGAACCTCTG ACCCCCCAGG TCGCTGTCCC 240
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AAGACTCCCC GCCCCCAGA CCTCGCCCGC CCGCAGGCTA GGTCTGGAAG TGGAGGATCC 360
GGTTTGTCTT GGGCGGCTCT GGAAGCAGAG CCGCGGAGG GAGCGCCGGG GCCTTGGGCT 420
GCAGGAGGTT GCGCGGCGCG CGGCGAGCAT GTGTGTCGGG AGAAGGAGCA GAGCTGGATC 480
CCCAAGATCT TCAAGAAGAA GACCTGCACG AGTTTCATAG TTGACTCCAC AGATCCGGGG 540
GATGCGGTCT CGCTCTATTG CCCAGGCTGT TCTCAAACCT CTGGGCTCAA GCAGTCCCTC 600
TGCTTGACCC TCCCAAGATG CTGTGATTGT GCGCAGCGGT CCTTGAAGTT TTGCTCAGAA 660
GAGCAAACTT TCTGGGAAGT AGCTGCAGGT GTTGAAGTA GCTGCAGGGG AACTAGGGGA 720

TTCAAGGATG GAGCTGAAAT GGGTGAACGG ACAAAGTCGG TAAACTGAAT GGAGGATGCC 780
 TTCCGGGCGAG CCGTGGTGAC CGTGTGGGAC AGCGATGCAC ACACCAAGCA GAAGCCCAACC 840
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 CTCTCTGACC GAAACGGATCC AGCTGCAGTT TATAGTCTGG TCACACGCAC ATGGGGGCTTC 960
 5 CGTGCCCGGA ACCTGGTGGT GTCACTGCTG GGGGATCGG GGGGCCCGT CCTCCAGACC 1020
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 10 GTGGTCCGGA ATAGAGACAC CCTCATCAAC CCCAAGGGCT CGTTCCTGTC GAGGTACCGG 1260
 TGGGCGGGTG ACCCGGAGGA CGGGGTCCAG TTTCCTCTGG ACTACAACCTA CTGCGCCTTC 1320
 TTCTGTGAGG ACAGCGCTGC ACACGGCTGC CTGGGGGGCG AGAACCGCTT CCGCTTGGGC 1380
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 15 CAGGCTCAGC TCCCATGTCT CCTCGTGGCT GGCTCAGGGG GAGCTGCGGA CTGCTGGGG 1560
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 20 TACCTGGATG AGCTGCGTTT GGCTGTGGCT TGGAAACCGG TGGACATTGC CCAGAGTGAA 1860
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 CTGCTGAATG ACCGCGCTGA GTTGTGGGC TTGCTCATTT CCCAGCGCTT CAGCCTGGGC 1980
 CACTTCTGTA CCGGATGCG CCTGGCCCAA CTCTACAGCG CCGCGCCCTC CAACTGCTC 2040
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 25 GGGGGAGCTG CGAGACTCCG GCGGCTGAC GTGGGGCATG TGCTGAGGAT GCTGCTGGGG 2160
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 TTCCGGGAGA GCGGTATCT GTCTCGGAC AAGGCCACCT CCGCGCTCTC GCTGGATGCT 2280
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 30 CAGATGGCCA TGTACTCTG GGAGATGGT TCCAATGCAG TTTCCTCAGC TCTTGGGGCC 2400
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 35 CAGTCTCTGC TGACACGAA GTGGTGGGA GATATGCCA GCACTACACC CATCTGGGCC 2700
 CTGTTCTGCG CCGTCTTTG CCGTCCACTC ATCTACACCC GCCTCATCAC CTTCAGGAAA 2760
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 GAAGGGCTG TGCGGACGCG GAGCCAGCC GAGAAGAAGC CGTGGGGGT CCGCGCCAGC 2880
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 40 TTCCACTTCT GGGGCGGCC GGTGACATC TTCATGGGA ACGTGTGCTG CTACCTGCTG 3000
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 45 ACCTGCTTCC TCGTGGCGT GGGTGGCGG CTGACCCCG GTTGTACCA CCTGGGCGCC 3300
 ACTGCTCTC CCGTCTGCT CATGTTTTC ACGGTGCGG TGCTTACAT CTTCAGGTC 3360
 AACAAACAGG TGCGGCGCA GATCGTCATC GTGAGCAAGA TGATGAAGGA CGTGTCTTC 3420
 TTCTCTTCT TCCTCGGCT GTGGCTGGTA GCGTATGCG TGGCCAGGA GGGGCTCTG 3480
 AGGCCAGCGG ACAGTACTT CCAAGTATC CTGCGCGCG TCTTCTACCG TCCCTACCTG 3540
 50 CAGATCTTCC GGCAGATTCC CCAGAGGAC ATGAGCGTGG CCGTCTAGGA GCAAGCAAC 3600
 TGCTCGTGG AGCCCGGCTT CTGGGACAC CCGTCTGGG CCCAGGCGG CACCTGCGTC 3660
 TCCAGTATG CCAACTGCT GGTGGTGTG CTCTCTGCT TCTTCTGCT CCGTGGCCAC 3720
 ATCTGCTGC TCAACTTCT CATTGCCATG TTCAGTTACA CATTGGCAA AGTACAGGGC 3780
 AACAGCGATC TCTACTGAA GCGCGAGGT TACCGCTCA TCGGGAAT CCCTCTCGG 3840
 CCGCGCTGG CCGCGGCTT TATGTCATC TCCCACTGC CCGTCTGCT CAGGCAATTG 3900
 55 TGAGCGGAG CCGGAGGCC CAGCGGCTC TCCCGGCGG TGAGCATTT CCGGTTTAC 3960
 CTTTCTAAGG AAGCGGAGG GAGCTGCTA ACGTGGGAAT CCGTGCATAA GAGGAACCTT 4020
 CTGCTGCGC GCGCTAGGA CAAGCGGAG AGCGACTCG AGCGCTGTA GCGCACGTCC 4080
 CAGAAAGTGG ACTTGGCACT GAAACAGCTG GACACATCC GCGAGTACGA ACAGCGCTG 4140
 AAAGTGTGG AGCGGAGGT CCAGCAGGT AGCGCGTCC TGGGGTGGT GCGCGAGGCC 4200
 60 CTGAGCGCT CTGCTTGTG CCGCCAGGT GCGCGCGAC CCGCTGACCT GCGTGGTCC 4260
 AAAGACTGAG CCGTGTGCG GACTTCAAG GAGAAGCCCC CACAGGGGAT TTTGCTCTA 4320
 GAGTAAGGCT CATCTGGGCC TGGCGCCCG CACCTGGTGG CTTGTCTCT GAGGTGAGCC 4380
 CCATGTCCAT CTGGGCACT GTCAGGACCA CCTTGGGAG TGTCTCTCT ACAAACACA 4440
 GCATGCGCG CTCTCCAG AACCACTCC AGCCTGGGAG GATCAAGGCC TGGATCCCGG 4500
 65 CCGGTATCC ATCTGGAGG TCAGGGTCC TTGGGTAAAC AGGAGACCA GACCCCTCAC 4560
 CACTCACAGA TTCTCACAC TGGGAAATA AAGCATTTC AGAGGAAAAA AAAAAAAA 4620
 AAAAAAAA AAAAAAAA A

Seq ID NO: 558 Protein sequence
 Protein Accession #: XP_057188.1

70
 1 11 21 31 41 51
 MEDAFGAAYV TVWDSHAHT EKPTDAYGEL DFTGAGRKHS NFLRLSDRTD PAAVYSLVTR 60
 TWGFRAPNLV VSVLGGSGGP VLQTLWQDL RGLVRAAQs TGAMIVTGG L HTGIGREVG 120
 75 AVREHQMAST GGTKVAMGV APWGVVRNRD TLINPKGSFP ARYRNRGDPE DGVQFPLDYN 180
 YSAFFLVDDG THGCLGGENR PRLRLESYIS QKGTGVGGTG IDIPVLLLLL DGEKMLTRI 240
 ENATQAQLPC LLVAGSGGAA DCLAETLED L APGSGGARQ GEARDRIRR FPKGDLVLQ 300
 AQVERIMTRK ELLTVYSSE GSEEFETIV L KALVKACGS EASAYLDEL LAVAMNRVDI 360
 80 AQSELFRGDI QWRSPHEAS LMDALLNDRP EPVRLLSHG LSLGHFLTPM RLAQLYSAAP 420
 SNSLIRNLID QASHSAGTKA PALKGGAEL RPPDVGVHLR MLLGDMCAPR YPSGGAMPDPH 480
 PGQGFESMY LLSKATSP LSLDAGLQAP WSDLLWALL LNRAQMAMYF WEMGSNAVSS 540
 ALGACLLLRV MARLEPDAE AARRKDLAFK FEGMGVDLFG ECVRSSEVRA ARLLLRRCPL 600
 WGDATCLQLA MQADARAPFA QDGVQSLLTQ KMGDMASST PIWALVLAFF CPPLIYTRLI 660
 TFRKSEEPET REELEFDMDS VINGEGPVGT ADPAEKTPLG VPRQSGRPGC CGGCGGRRRC 720

LRRWFHFWGA PVTIFMGNV SYLLFLLLF RVLLVDFQPA PPGSLELLLY FWAFTLLCEB 780
 LRQGLSGGGG SLASGGPGPG HASLSQRLRL YLADSWNQCD LVALTCPLL GVCRLTPGLY 840
 HLGRTVLICID FMVPTVRLLE IPTVNRQLGP KIVIVSKMK DVFFPLPFLG VMLVAYGVAT 900
 5 BGLLRPRDSF PFSILRRVFP RPYLQIFQOI PQEDMDVALM EHSNCSSEFG FWAHPGGAQA 960
 GTCVSYANW LVVILLVIFL LVANILLVNL LIAMPSYTFG KVQNSDLYW KAQRVRLIRE 1020
 FHSRPAIAPP FIVISHLRL LRQLCRRPRS PQSPSPALEH FRVYLSKEAB RKLLTWESVH 1080
 KENFLARAR DKRSDSERL KRTSQKVDLA LKQLGHIREY EQRLKVLERE VQCCSRVLGW 1140
 VAEALSRSAL LPPGGPPPPD LPSKSD

10 Seq ID NO: 559 DNA sequence
 Nucleic Acid Accession #: NM_006853.1
 Coding sequence: 26..874

15 1 11 21 31 41 51
 AGGAATCTGC GCTCGGGTTC CGCAGATGCA GAGGTTGAGG TGGCTCGGG ACTGGAAGTC 60
 ATCGGGGAGA GGTCTCACAG CAGCCAAGGA ACCTGGGGCC CGCTCTCTCC CCTCCAGGC 120
 CATGAGGATT TGCAGTTAA TCCTGCTTGC TCTGGCAACA GGGCTTGTAG GGGAGAGAG 180
 20 CAGGATCATC AAGGGGTTGG AGTGCAAGCC TCACTCCAG CCTGGCAGG CAGCCCTGTT 240
 CGAGAAGACG CGGTACTCT GTGGGGCGAC GCTCATGCCC CCCAGATGGC TCTGACAGC 300
 AGCCCATGTC CTCAGGCCCC GCTACATAGT TCACCTGGGG CAGCACAACC TCCAGAGGA 360
 GGAGGGCTGT GAGCAGACCC GGACAGCCAC TGAGTCTCTC CCCCACCCCG GCTTCAACAA 420
 CAGCCTCCCC AACAAAGACC AOCGCAATGA CATCATGCTG GTGAAGATGG CATGCCAGT 480
 25 CTCCATCACC TGGGCTGTGC GACCCCTCAC CCTCTCTCA CGCTGTGTCA CTGCTGGCAC 540
 CAGCTGCCTC ATTTCCGGCT GGGGCGAGC GTCCAGCCCC CAGTTACGCC TGCCTCACAC 600
 CTTCGGATGC GCCAACATCA CCATCATTGA GCACCAAGAG TGTGAGAACG CCTACCCCG 660
 CAACATCACA GACACCATGG TGTGTGCCAG CGTGCAAGAA GGGGGCAAGG ACTCCTGCCA 720
 GGGTGACTCC GGGGGCCCTC TGGTCTGTAA CCACTCTCTT CAAGGCATTA TCTCTGGGG 780
 30 CCAGGATCCG TGTGCGATCA CCGAAAGCC TGGTGTCTAC ACGAAAGTCT GCAATATATG 840
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 ACCCTCATGT TCCACTTGGT GTTGTGTTCC TGTCTACTCT GTTAATAAGA AACCTTAAGC 960
 CAGAGCCCTC TAGCAACATT CTTTGGGCCCT CCTGGACTAC AGGAGATGCT GTCACTTAAT 1020
 AATCAACCTG GGGTTCGAAA TCAGTGAGAC CTGGATTCAA ATTCTGCTTT GAAATATTGT 1080
 35 GACTCTGGGA ATGACAACAC CTGGTTTGT CTCTGTGTGA TCCCAGCCCC CAAAGACAGC 1140
 TCTTGCCAT ATATCAAGGT TTCAATAAT ATTTGCTAAA TGAGTG

Seq ID NO: 560 Protein sequence
 Protein Accession #: NP_006844.1

40 1 11 21 31 41 51
 MRILQLILLA LATGLVGGET RIIGKFECKP HSQPWQAALF EKTRLLCGAT LIAPRWLLTA 60
 AHCLKPRYIV HLGQHNLOKE EGCEQTRTAT ESPFHPGPN SLPNKDHRND IMLVKMASPV 120
 45 SITNAVRPLT LSSRCVTAGT SCLISGWGST SSPQLRLPHT LRCANITIIIE HQKCEWAYPG 180
 NITDTMVCAS VQEGGKDSQ GDSGGPLVCN QSLQGIISWG QDPCAITRKP GVTYKVCXYV 240
 DWIQETMKN

50 Seq ID NO: 561 DNA sequence
 Nucleic Acid Accession #: AY046419.1
 Coding sequence: 1..1743

1 11 21 31 41 51
 55 ATGTTTACCT TCCTGTATC TGTCAGTCT GCTGTCTAGT GCCTCCTGGT GGGTTATGAA 60
 CTGCGGATCA TCTCTGGGGC TCTTCTTCAG ATCAAAACCT TATTAGCCCT GAGCTGCCAT 120
 GAGCAGGAAA TGGTTGTGAG CTCCTCTGTC ATTGGAGCCC TCCTTGCTCT ACTCACGGA 180
 GGGGCTCTGA TAGACAGATA TGAAGAAGG ACAGCAATCA TCTTGTATC CTGCTGCTT 240
 60 GGACTCGGAA GCTTAGTCTT GATCCTCAGT TTATCCTACA CGGTTCTTAT AGTGGGAAGC 300
 ATTGCCATAG GGGTTTCCAT CTCCTCTCTT TCCATTGCCA CTGTGTGTTA CATCGCAGAG 360
 ATTGCTCCTC AACACAGAAG AGGCCCTTCT GTGTCACTGA ATGAGCTGAT GATTGTATC 420
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 TACATGTTTG GTCTGTGAT TCCCTTGGGA GTTTTGCAAG CAATTGCAAT GTATTTTCTT 540
 65 CTTCCAAGCC CTCGGTTTCT GGTGATGAAA GACAAGAGG GAGCTGCTAG CAAGGTTCTT 600
 GGAAGGTTAA GAGCACTCTC AGATACAAC TGAAGACTCA CTGTGATCAA ATCTTCCCTG 660
 AAGATGAAT ATCAGTACAG TTTTGGGAT CTGTTTCTGT CAAAGACAA CATGCGGACC 720
 CGAATAATGA TAGGACTAAC ACTAGTATTT TTTGTACAAA TCACGGGCCA ACCAAACATA 780
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 70 CTGCTCTCCA CTGGGGTTGG AGTGTCAAG GTCATTAGCA CCATCCCTGC CACTCTTCTT 900
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 AGCCACAATT CTATCAACCA GTCCTTGGAT GAGTCTGTGA TTTATGGACC AGGAAACCTG 1080
 75 TCAACCAATC ACACTACTCT CAGAGACCC TCAAGAGGA TTTCTTCCA TAGCAGAAGC 1140
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 GGTCTAGGAC CAATGGCCCTG GCTGGTGCTC AGCGAGATCT TTCTGCTGGG GATCAGAGGA 1380
 CGAGCCATGG CTTTAACTTC TAGCATGAAC TGGGGCATCA ATCTCTCAT CTGCTGAGA 1440
 80 TTTTGTACTG TAAGTATCT TATTGGCCTG CCATGGGCTG GCTTTATATA TACAATCATG 1500
 AGTCTAGCAT CCTTGTCTTT TGTGTTATG TTTATACCTG AGACAAAGGG ATGCTCTTTG 1560
 GAAACAATAT CAATGGAGCT AGCAAAAGTG AACTATGTGA AAAACAACAT TTGTTTTATG 1620
 AGTCATCACC AAGAAGAAAT AGTGCCAAA CAGCCTCAAA AAAGAAAACC CCAGGAGCAG 1680
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 TAA

Seq ID NO: 562 Protein sequence
Protein Accession #: AAL02327.1

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5      1      11      21      31      41      51
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IAPQHRRLGL VSLNLMIVI GILSAYISNY AFANVFHGWK YMFGLVIPLG VLQAIAMYPL 180
PPSPRFLVMK QEGGAASKVL GRRLALSDTT BELTVIKSSL KDEYQYSFWD LFRSKDNMRT 240
10    RIMIGLTLVP FVQITGQPNL LPYASTVLKS VGPQSNBAAS LASTGVGVVK VISTIPATLL 300
VDHVGSKTFL CIGSSVMAAS LVTMGIVNLN IHMNPTHICR SHNSINQSLD ESVIYGPGLN 360
STNNNTLRDH FKGISHSRSL SLMLPLRNDVD KRGETTSASL LNAGLSHTEY QIVTDPGDVP 420
APLKLWLSLA LLYVVAAPSI GLGPMPLVL SEIPFGQIRG RAMALTSSMN WGINLLISLT 480
15    FLTVDLIGL PWCFIYTIM SLASLLFVVM FIPETKGCGL BQISMELAKV NYVKNNICPM 540
SHHQEELVPK QPKRKPQEQ LLECNKLCGR GQSRQLSPET

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Seq ID NO: 563 DNA sequence
Nucleic Acid Accession #: XM_059466.1
Coding sequence: 1..894

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25    GAGAGCTGG AGCGCAGCG CGCGGGCGCC GACCCCGCG ACCAGAAGAA CCGCTGATG 180
CCGCTGTGC ACCTGCGCT GCGGGACTCG CCCCGCTGG GCGCGCGCT GCTCCCGGG 240
GGCCCGGGG GCGCGACCC CGAGTCTGG CGCTCGTCC TGGGGCTCG GCGGCTGGAC 300
GCGAGTGGC GCGGGCCCT CTTCGCCAC TACTCGGCC TCTGGAGAA GTGCTACTT 360
30    TGGGGCATG ACGGGACAT CGACACCTC ATCTGAAAG GTATTGCGA CGGATGCACG 420
GCCATCAAGT ACCACTTTT TCAGCCCATC CGCTTGGAA ACATTCTTT TAATTTAACC 480
AAGACCATAC AGCAAGATGA GTGGCACCTG CTTCATTAA GAAGAATCA TGCTGGCTT 540
CTCGGCATG CGTAGCGGT CTTCTCTGC GGCTGCATT TGGCCACAGT CAGTTCTTC 600
TGGGAGGAGA GCTTGACCA GCACGTGGT GACTCTCTG TCTCATGAC AGGGATATT 660
35    TGCAACATT CCCTCTGTG TTATGCGCC AGTATCTCG ATGATTGAA CGGCTCCCA 720
AAGCTAATT ATAGCCTGCC TGCTGATGT GAACATGTT ACAGCTGGT CATCTTTTG 780
GCCTGGTGA GTTTAGGCTT TATTGTGGA GCTGGAGGT TCTGCATCG TTATCCGTT 840
ATTAGCCGGA CCAAGATTG ACAGCTAAG TCTGCCAGG ACTCCACGT ATGA

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Seq ID NO: 564 Protein sequence
Protein Accession #: XP_059466.1

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40      1      11      21      31      41      51
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45    PLSHLPLRDS PPLGRLLPFG GPRADPESW RSLGLGLD AEGCRPLFAT YSGLWRKCYF 120
LGIDRDIDL ILKGIAQRCT AIKYHFSQPI RLRLNIPNLT KTIQQDEWHL LHLRRITAGF 180
LGMVAVALLC GCIVATVSPF WEESLTQHVA GLLPLMTGIF CTISLCTYAA SISYDLNRLP 240
KLIYSLPADV EHGYSWSIFC AWCSLGFIVA AGGLCIAYPF ISRTKIAQLK SGRDSTV

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Seq ID NO: 565 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3315

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55      1      11      21      31      41      51
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TGGTGAATT TTATTCAAGC AAATTTTAAG AAACGAGAAT GTGCTTCTT TACCAAGAT 180
60    TCCAAGGCCA CCGAAGATGT GTGCAAGTGT GGCTATGCC AGAGCCAGCA CATGGAAGGC 240
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70    CTGCTCGTGG ACAATGGCTG TCATGGACAT CCACTGTGCG AAGCAAAGCT CGGGAATCAG 840
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5 TGGGAGCAGA CCAGGGGCTG CACTCTGGCA GCCCTGGGAG CCAGCAAGCT TCTGAAGACT 1800
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30 Seq ID NO: 566 Protein sequence
 Protein Accession #: Eos sequence

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 45 LAKVKNDINA AGESEELANE YETRAVELFT ECVSSDEDLA EQLLVYSCEA WGSNCLELA 660
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55 Seq ID NO: 567 DNA sequence
 Nucleic Acid Accession #: NM_006911.1
 Coding sequence: 1..558

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 65 GATGCTCCTC AGACACCTAG ACCAGTGGCA GAAATTGTAC CATCCTCAT CAACAAAGAT 240
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75 Seq ID NO: 568 Protein sequence
 Protein Accession #: NP_008842.1

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Coding sequence: 1..3978

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	GAAGATGATA	TGTATTCACT	GCTGCCAGAA	GACCGCTCAC	AGCACTCTGG	AGAGGAGTTG	180
	CAAGGGTTCT	GGGATAAAGA	AGTTTTTAAGA	GCTGAGAATG	ACGCACAGAA	GCCTCTTTTA	240
	ACAAGAGCAA	TCATAAAGTG	TACTTGGAAA	TCTTATTTAG	TTTTGGGAAT	TTTTACGTTA	300
10	ATTGAGGAAA	GTGCCAAAGT	AATCCAGCCC	ATATTTTITG	GAATAATTTAT	TAATTTATTT	360
	GAATAATTTG	ATCCCATGGA	TCTGTGGCT	TTGAACACAG	CGTACGCCTA	TGCCACGGTG	420
	CTGACTTTTT	GCACGCTCAT	TTTGGCTATA	CTGCATCACT	TATATTTTAA	TCACTGTCAG	480
	TGTGCTGGGA	TGAGGTACG	AGTAGCCATG	TGCCATATGA	TTTATCGGAA	GGCACTTGGT	540
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15	GATGTGAACA	AGTTTGATCA	GGTGACAGTG	TTCTTACACT	TCTGTGGGCG	AGGACCACATG	660
	CAGGCGATCG	CAGTCATCTG	CCTACTCTGG	ATGGAGATAG	GAATATCGTG	CCTTGTCTGGG	720
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	CAGCCCTGGG	TGTTCTCGGG	AACCTCTGAG	AGTAATATTT	TATTTGGGAA	GAATAACGAA	1500
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	TCTCAACAAT	CTTCTAGACC	CTCCTTGAAA	GATGGTGCTC	TGGAGAGCCA	AGATACAGAG	2040
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	AGCGACAAGA	TAATGGTTTT	AGATTCAAGA	AGACTGAAAG	AATATGATGA	GCCGTATGTT	3780
	TTGCTGCAAA	ATAAGAGAG	CCTATTTTAC	AAGATGGTGC	AACAACGGG	CAAGGCAGAA	3840
70	GCGGCTGCCC	TCACGTGAAC	AGCAAAACAG	GTATACCTTA	AAAGAAATTA	TCCACATATT	3900
	GGTCACACTG	ACCACATGGT	TACAAACACT	TCCAATGGAC	AGCCCTCGAC	CTTAACATATT	3960
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Seq ID NO: 570 Protein sequence
 Protein Accession #: XP_036453.1

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	LSNMAMGKTT	TGQIVNLLSN	DVNKFDQVTV	FLHFLWAGPL	QAIATVALLW	MEIGISCLAG	240
	MAVLIIILLPL	QSCFGLKPS	LRSKATFTVD	ARIRTMNEVI	TGIRIKMYA	NEKSFNSLIT	300
	NLRKKKISKI	LRSSCLRGMN	LASPPSASKI	IVFVTPTTIV	LLGSVITASR	VFVAVTLYGA	360

5 VRLTVTLFFP SAIERVSEAI VSIRRIQTFP LLDEISQRNR QLPDQKQWV HVQDFTAFWD 420
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 20 HTDEELWNAL QEVQLKETIE DLPKMDTEL AESGNSFVG QRQLVCLARA ILRNQILII 1200
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Seq ID NO: 571 DNA sequence
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 75 GTGTGAGGAA CTGTTTATG CACACAGGA TTTACATTA GAGGCTTGGT TCTTGTTTT 2940
 GACACGCTCC CGCTGGTTCC CGGTCCGTCT GGAATGCCAT TGTGCAATG TTGTCTCAT 3000
 CGTTCCTTGT GGTCCCTGA TTCTGGCAA AACTCTGAT GCGGGGAGG TTGGTTTGGC 3060
 ACTGTCTTAT GCCCTCACGC TCATGGGAT GTTTCAGTG TGTGTCTGAC AAAGTCTGA 3120
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 80 CTTGACAAAT GTGAACCTCA GTTACAGTCC AGGTGGGCT CTGGTACTGA AGCATCTGAC 3300
 AGCATCTATT AAATCAAGG AAAAGGTTGG CATGTGGGA AGAACCGGAG CTGGAAGAG 3360
 TTCCCTCATC TCAGCCCTTT TTAGATTGTC AGAACCGGAA GGTAAATTT GATTTGATA 3420
 GATCTTGACA ACTGAAATTT GACTTCACTA TTTAAGGAAG AAAATGTCAA TCATACCTCA 3480
 GGAACCTGTT TTGTTCACTG GAACATGAG GAAACACCTG GATCCCTTA AGGAGCACAC 3540
 GGATGAGGAA CTGTGAATG CCTTACAAGA GGTACAACTT AAAGAAACCA TTGAAGATCT 3600

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TCGTGGTAAA ATGGAATCAA AATTAGCAGA ATCAGGATCC AATTTTAGTG TTGACAAAG 3660
 ACAACTGGTG TGCCCTGGCA GGGCAATTCT CAGGAAAAAT CAGATATTGA TTATTGATGA 3720
 AGCGACGGCA AATGTGGATC CAAGAACTGA TGAGTTAATA CAAAAAATAA TCCGGGAGAA 3780
 ATTTGCCAC TGACCGGTGC TAACCATTCG ACACAGATTG AACACCATTG TTGACAGCGA 3840
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 GCAAAATAAA GAGAGCCTAT TTTACAAGAT GGTGCAACAA CTGGCAAGG CAGAAGCCGC 3960
 TGCCCTCACT GAAACAGCAA AACAGGTATA CTTCAAAGA AATTATCCAC ATATTGGTCA 4020
 CACTGACCAC ATGGTTACAA ACACCTCCAA TGGACAGCCC TOGACCTTAA CTATTTTCGA 4080
 GACAGCACTG TGAATCCAAC CAAAATGTCA AGTCCGTTCC GAAGGCATTG TCCACTAGTT 4140
 TTTGACTAT GTAAACCACA TTGTACTTTT TTTTACTTTG GCAACAAATA TTTATACATA 4200
 CAAGATGCTA GTTCATTGA ATATTTCTCC C

Seq ID NO: 572 Protein sequence
 Protein Accession #: AAC27076.1

1 11 21 31 41 51
 MLFVYQEVKP NPLQDANICS RVFFWNLNPL FKIGHKRRLE EDDMYSVLPE DRSQHLGEEL 60
 QGFWDKEVLR AENDAQKPSL TRAIKCYWK SYLVIGIFTL IEESAKVIQ IFLGKIINYF 120
 ENYDPMDSVA LNTAYAYATV LTPCTLILAI LHLFYFYHVQ CAGMRLRVAM CBMIYRKALR 180
 LSNMAMGTTT TGGIVNLLSN DVNKPQDQTV FLHFLWAGPL QAIJAVTALLW MEIGISCLAG 240
 MAVLIILPL QSCFGKLPSS LRSKTATFTD ARIRTMNEVI TGIRIIMYA WEKSFNLIIT 300
 NLRKKEISKI LRSSCLRGMN LASFFSASKI IVFVPTTYV LLGSVITASR VFAVATLYGA 360
 VRLTVTLFPF SAIERVSEAI VSIRRIQTFL LLDEISQRNR QLPSDGKMMV HVQDFTAFWD 420
 KASETPTLQG LSPFVRPGEI LAVVGPVGAG KSSLLSAVLG ELAPSHGLVS VHGRYAVSQ 480
 QPWFSGTLR SNILFGKYE KERYEKVKA CALKKDLQLL EDGDLTVIGD RGTLSGGQK 540
 ARVNLARAVY QDADIYLLDD PLSAVIDEVS RHLFELCICQ ILHEKITILV THQLQYLKAA 600
 SQILILKDGK MVQKGYTFEF LKSGIDFGSL LKXDNBESQ PPVPGTPTLR NRTFSESSVW 660
 SQSSRPPLK DGALESQDTE NVPVTLSEEN RSEGVGFQA YKNYFRAGAH WIVFIFLILL 720
 NTAQAQVAVY QDWMLSYWAN QKSMNLVTVN GGNVTEKLD LNWYLGIVSG LTVATVLPFI 780
 ARSLVFFYL NSSQTLHKN MFESILKAPV LFFDRNPGR ILNRFPSKIDG HLDLPLTF 840
 LDPIQTLQV VGVVSVAVAV IPWIAIPLVP LGIIFIFLRR YPLETSRDKV RLESTTRSPV 900
 FSHLSSSLQG LWTIRAYKAE ERQELPDAH QDLHSEAWFL FLTTSRWFAV RLDAICAMFV 960
 IIVAFGSLIL AKTLDAGQVG LALSIALTLM GMFQWCVRQS AEVENMMISV ERVIEYTDLE 1020
 KEAPWYQKR PPPAWPHEGV IIFDNVNFMY SPGGPLVLKH LTAIKSQEK VGIUGRTGAG 1080
 KSSLISALPR LSEPEGKINI DKILTTEIGL HDLRKMSII PQEPVLPFGT MRKNLDPFKE 1140
 HTDEELWNL QEVQLKETIE DLPKMDTEL AESGSNFSVG QRQLVCLARA ILRKNQILII 1200
 DEATANVDP TDELIQKKIR EKFAHCTVLT IAHRLNTIID SDKIMVLDG RLKYEDEPYV 1260
 LLQKESLFY KMVQQLKAE AALTTETAKQ VYFKRNYPHI GHTDHMTNT SNGQPSTLTI 1320
 FETAL

Seq ID NO: 573 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1365

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 GGCATAAATG GTATCAAGA TGCAAGGAAG GTCAGTGTAG GTGTGATTGG AAGTGGAGAT 120
 TTTGCCAATC CTTTGACCAT TCAGACTATT AGATGCGGCT ATCATGTGGT CATAGGAAGT 180
 AGAAATCTTA AGTTTGCTTC TGAATTTTTT CCTCATGTGG TAGATGTAC TCATCATGAA 240
 GATGCTCTCA CAAAACAAA TATAATATT GTTGCTATAC ACAGAGAACA TTATACCTCC 300
 CTGTGGGACC TGAGACATCT GCTTGTTGGT AAAATCCTGA TTGATGTGAG CAATAACATG 360
 AGGATAAACC ATGACCCAGA ATCCAATGCT GAATATTTGG CTTATTATT CCCAGATTCT 420
 TTGATTGTCA AAGGATTAA TGTGTCTCA GCTTGGGCAC TTCAGTTAGG ACCTAAGGAT 480
 GCCAGCCGGC AGGTTTATAT ATGCAGCAAC AATATTCAAG OGGACAACA GGTATTGAA 540
 CTTGCCCGCC AGTTGAATTT CATTCCCAT GACTTGGGAT CTTATCATC AGCCAGAGAG 600
 ATTGAAAAAT TACCCTTACG ACTCTTTACT CTCTGGAGAG GGCCAGTGGT GGTAGCTATA 660
 AGCTTGGCCA CATTTTTTTT CCTTATTCC TTTGTAGAG ATGTGATTCA TCCATATGCT 720
 AGAAACCAAC AGAGTGACTT TTACAAATT CCTATAGAGA TTGTGAATAA AACCTTACCT 780
 ATAGTTGCCA TTACTTTGCT CTCCCTAGTA TACCTGCAG GTCTTCTGGC AGCTGCTTAT 840
 CAACCTTATT ACGGCACCAA GTATAGGAGA TTTCCACCTT GGTGGAAAC CTGGTTACAG 900
 TGTAGAAAAC AGCTTGGATT ACTAAGTTT TTCTTGCTA TGGTCCATGT TGCCATACAG 960
 CTCTGCTTAC CGATGAGAAG GTCAGAGAGA TATTGTGTT TCAACATGCG TTTATCAGCAG 1020
 GTTCATGCAA ATATTGAAAA CTCTTGGGAT GAGGAAGAAG TTTGGAGAA TGAATGTAT 1080
 ATCTCCCTTG GCATAATGAG CTTTGGCTTA CTTTCCCTCC TGGCAGTCAC TTCTATCCCT 1140
 TCAGTGAGCA ATGCTTTAAA CTGGAGAGAA TTCAGTTTAA TTCAGTCTAC ACTTGGATAT 1200
 GTGCGCTGCG TCATAAGTAC TTTCCATGTT TTAATTATG GATGGAAAG AGCTTTTGAG 1260
 GAAGAGTACT ACAGATTTTA TACACCACCA AACTTGTTC TTGCTCTGT TTTGCCCTCA 1320
 ATTGTAATTC TGGATCTTTT GCAGCTTTGC AGATACCCAG ACTGA

Seq ID NO: 574 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MESISMGGSP KSLSETCLPN GINGIKDARK VTVGVIGSGD FAKSLTIRLI RGYRVVIGS 60
 RNPKPASEFF PHVVDVTHE DALTKTNIIF VAIHREHYTS LMDLRHLLVG KILIDVSNM 120
 RINQYFESNA EYLASLPDS LIVKGFNVVS AWALQLCPKD ASRQVYICSN MIQARQQVIE 180
 LARQLNFIPI DLGSLSSARE IENLPLRLFT LWRGPPVVVAI SLATPFFLYS FVRDVIHPYA 240
 RNQQSDFYKI PIEIVNKTLP IVAITLLSLV YLAGLLAARY QLYYGTKYRR PPMLETWLG 300
 CRQLQLLSP FPMVHVAYS LCLPMRRESR YLFLMAYQQ VHANIENSWN EEEVWRIEM 360
 ISFGLMSLGL LSLAVTSIP SVSNALAWRE PSFIQSTLGY VALLISTFHV LIYGWKRAFE 420
 BEYFRPYTPP NFVLAIVLPS IVILDLLQLC RYPD

Seq ID NO: 575 DNA sequence
Nucleic Acid Accession #: NM_001873.1
Coding sequence: 3..1721

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AAATGGCGTG CCGTCTCTCT CGCGGGCCCC CTGCCTCGCA GTGGTTTCTC CTGCAGCTCC 60
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GTGGCCCCAG TGGCGGGGCT GACACTCAIT CAGCCGGGGA AGGTAGAGCG AGTAGAGGCT 180
GGTGCAGAAC TTGCCGCCCC CAGCAGCGCC GGCGGGCTAA GCCAGGGGCC GGGCAGACAA 240
AAGAGGCCGC CCGCGTAGGA AGGCACGGCC GGCGGGCGCG GAGCGCAGCG ATGCGCCGGC 300
GAGGGGGCAG CGCGCTGCTG GCTCTGTGCG GGGCACTGGC TGCCCTGCGG TGGCTCTCTG 360
GCGCCGAAGC CCAGGAGCCC GGGGCGCCCG CGGCGGGCAT GAGGCGGGC CGGCGGCTGC 420
AGCAAGAGGA CGGCATCTCC TTGAGTAGCC ACCGCTACCC CGAGCTGCGC GAGGCGCTCG 480
TGTCCTGTG GCTCAGTAGC ACCGCCATCA GCAGGATTTA CACGGTGGGG CGCAGCTTCG 540
AGGGCCGGGA GCTCCTGGTC ATCGAGCTGT CCGACAACCC TGGCGTCCAT GAGCCTGGTG 600
AGCCTGAATT TAAATATCAT GGAATATGCG ATGGGAATGA GGCTGTGGGA CGAGAACTGC 660
TCATTGTCTT GGGCCAGTAC CTATGCAACG AATACAGAA GGGGAACGAG ACAATTGTCA 720
ACCTGATCCA CAGTACCCGC ATTCACTCA TGCCCTCCCT GAACCCAGAT GGCCTTTGAGA 780
AGGCAGGCTC TCAGCCTGGT GAACCTCAAG ACTGGTTTGT GGGTCAAGC AATGCCAGG 840
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AAGTGTGTCC AAATAATCAT CTGTGAAAA ATATGAAGAA AATTGTGGAT CAAACACAA 960
AGCTTGTCTC GCGCCCAAGC GCTGTCTTTC ATTGATTAT GGATATTCCT TTTGTGCTTT 1020
CTGCCAATCT CCATGAGGGA GACCTTGTGG CCAATTATCC ATATGATGAG ACGCGGAGTG 1080
GTAGTGCTCA CGAATACAG TCCTCCCGAG ATGACGCCAT TTCCCAAAGC TTGGCCCGGG 1140
CATACTCTTC TTCAACCCCG GCCATGTCTG ACCCCAAATCG GCCACCATGT CGCAGAAATG 1200
ATGATGACAG CAGCTTTGTA GATGGAACCA CCAACGGTGG TGCTTGTGAT AGCGTACCTG 1260
GAGGGATGCA AGACTTCAAT TACCTTAGCA GCAACTGTTT TGAGATCACC GTGGAGCTTA 1320
GCTGTGAGAA GTTCCACCT GAAGAGACTC TGAAGACCTA CTGGGAGGAT AACAAAACT 1380
CCCTCATTAG CTACCTTGA CAGATACACC GAGGAGTTAA AGGATTGTGC CGAGACCTTC 1440
AAGGTAACCC AATTGCGAAT GCCACCATCT CGGTGGAAGG AATAGACCAC GATGTATCAT 1500
CCGCAAGGGA TGGTGATTAC TGGAGATGCG TTATACCTGG AAACATATAA CTTACAGCCT 1560
CAGCTCCAGG CTCTTAGGT AATAACAAAG AAGTGGCAGT TCCTTACAGC CCTGCTGCTG 1620
GGGTGATATT TGAATCGGAG TCATTTTCTG AAAGGAAAGA AGAGGAGAAG GAAGAATTGA 1680
TGGAAATGGT GAAATATGAT TCAGAACTT TAAATTTTAA AAAAGCTTTC TAGTTAGCTG 1740
CTTTAAATCT ATCTATATAA TGTAGTATGA TGTAATGTGG TCTTTTTTTT AGATTTTGTG 1800
CAGTTAATAC TTAACATTGA TTTATTTTTT AATCATTTAA ATATTATACA ACTTTCCCTA 1860
AAATAAATAG CCTCTTAGGT AAAAATATAA GAACCTGATA TATTTCAATC TCTTATATAG 1920
TATTCATTTT CTACCTATA TTACACAAA AAGTATAGAA AAGATTTAAG TAATTTTGCC 1980
ATCTAGGCT TAAATGCAAT ATTCTGCTA TTATTTACAA TGCAGAAATT TTTGAGTAAT 2040
TCTAGCTTTC AAAAATTAGT GAAGTTCTTT TACTGTAAAT GGTGACAATG TCACATAATG 2100
AATGCTATTG AAAAGGTTAA CAGATACAGC TCGAGTTTGT GAGCACTCTA CTGCAAGACT 2160
TAAATAGTTC AGATATAAAT GTCGTTTTTT TCTTGTGCTG ACTAATCTATA AGCATGATCT 2220
TGTTAATGCA TTTTGTATGG GAAGAAAAGG TACATGTTTA CAAAGAGGTT TTATGAAAG 2280
AATAAAAAAT GACTTCTTGC TTGTACATAT AGGAGCAATA CTATTATATT ATGTAGTCCG 2340
TTAACACTAC TTAAAGGTTT AGGGTTTTCT CTTGGTTGTA GAGTGGCCCA GAATTGCATT 2400
CTGAATGAAT AAAGGTTAAA AAAAATCCCG CAGTGAAAAA AAA

Seq ID NO: 576 Protein sequence
Protein Accession #: NP_001864.1

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MAGRGSALL ALCCALAACG WLLGABAEQEP GAPAAGMRRR RRLQQEDGIS FEYHRYPELR 60
EALVSVMLQC TAISRIYTVG RSFEGRELLV IELSDNPGVH EPGEPEPKYI GNMENEAAG 120
RELLIFLAQY LCNEYQKQNE TIVNLHSTR IHIMPBLNPD GPEKAASQPG ELKDWFPVGRS 180
NAQGDIDLNRN FPDLDRIYVY NEKEGGPNNH LLKNMKIYD QNTKLAPETK AVIHIMDIP 240
FVLSANLHGG DLVANYPYDE TRSGSAHEYS SSPDDAIFQS LARAYSSPNP AMSDPNRPFC 300
RKNDDSSSFV DGTITNGAWY SVPGMQDFN YLSSNCFBIT VELSCFKPPP EETLKTYWED 360
NKNLSLYSLA QIHRGVKGFV RDLQGNPIAN ATISVBIIDH DVTSARDGDY WRLLIPGNYK 420
LTASAPGYLA ITKKAVVPYS PAAGVDFFELE SPSEKEREK EELMEWWMKM SETLNF

Seq ID NO: 577 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..933

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TTCCCTCTGT CCAGCGGCAT CCATTGCATC ATTGTGCGCT TCCGGTGCAA TGGGTTTGGAG 180
GACTGTCCCG ATGGCAGCGA TGAAGAGAAC TGCACAGCAA ACCCTCTGCT TTGCTCCACC 240
GCCCGCTACC ACTGCAAGAA CGGCTCTGT ATTGACAAGA GCTTCATCTG CGATGGACAG 300
AATAACTGTC AAGACAACAG TGATGAGGAA AGCTGTGAAA GTTCTCAAGA ACCCGGCAGT 360
GGGCAGGGTG TTGTGACTTC AGAGAACCAA CTTGTGTATT ACCCCAGCAT CACCTATGCC 420
ATCATCGGCA GCTCGGTCAAT TTTTGTGCTG GTGGTGGCCC TGCTGGCACT GGTCTTGAC 480
CACACGGGGA AGCGGAACAA CCTCATGACG CTGCGCGTGC ACCGGCTGCA GCACCTGTG 540
CTGCTGTCCC CGCTGGTGGT OCTGGACCA CCCCACCACT GCACGCTCAC CTACAACGTC 600
AATAATGGCA TCCAGTATGT GGCCAGCCAG GCGGAGCAGA ATGCGTCSGA AGTAGGCTCC 660
CCACCCCTCT ACTCCGAGGC CTTGCTGAC CAGAGGCTTG GGTGGTATGA CCTTCTTCCA 720
CCGCCCTACT CTCTGACAC GGAATCTCTG AACCAAGCCG ACCTGCCCCC CTACCGCTCC 780
CGGTCCGGGA GTGCCAACAG TGCCAGCTCC CAGGCAGCCA GCAGCTCTCT GAGCGTGGAA 840
GACACCAGCC ACAGCCCGGG GCAGCCTGGC CCCAGGAGG GCACCTGCTGA GCCCAGGGAC 900

TCTGAGCCCA GCCAGGGCAC TGAAGAAGTA TAA

Seq ID NO: 578 Protein sequence
Protein Accession #: Eos sequence

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1	11	21	31	41	51	
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DCPDGSDDEEN	CTANPLLCST	ARYHCKRNLG	IDKSFICDGQ	MNQDNDSEB	SCSSSQEPGS	120
GGVFTTSENQ	LVYYPSTIYA	IIGSSVIFVL	VVALLALVLH	HQRKRNLMAT	LPVHRLQHPV	180
LLSRLVLDH	PHRCNVYVNV	NNGIQYVASQ	AEQNASEVGS	PPSYSEALLD	QRPAWYDLPP	240
PPYSSDTESL	NQADLPFYRS	RSGSANSASS	QAASSLLSVE	DTSHSPQPG	PQEGTAEPRD	300
SEPSQGTREV						

Seq ID NO: 579 DNA sequence
Nucleic Acid Accession #: AP179274.1
Coding sequence: 1..1125

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TGGCTGCTGC	TGCTGCCCCG	CATGCTACTC	ATCGTAGCCC	GCCCGGTGAA	GCTGCTGCT	120
TTCCCTACCT	CCTTAAGTGA	CTGCCAAACG	CCCACCGGCT	GGAATTGCTC	TGTTTATGAT	180
GACAGAGAAA	ATGATCTCTT	CCTCTGTGAC	ACCAACACCT	GTAATTTTGA	TGGGGAATGT	240
TTAAGAATTG	GAGACACTGT	GACTTGCCTC	TGTCAATTCA	AGTGCACAA	TGACTATGTG	300
CCTGTGTGTG	GCTCCAATGG	GGAGAGCTAC	CAGAATGAGT	GTTACCTGCG	ACAGGCTGCA	360
TGCAACACAG	AGAGTGAGAT	ACTTGTGCTG	TCAGAAGGAT	CATGTGCCAC	AGATGCAGGA	420
TCAGGATCTG	GAGATGGAGT	CCATGAAGGC	TCTGGAGAAA	CTAGTCAAAA	GGAGACATCC	480
ACCTGTGATA	TTTGCCAGTT	TGGTGACGAA	TGTGAACGAG	ATGCCGAGGA	TGTCTGTGTG	540
GTGTGTATA	TTGACTGTTT	TCAAAACCAAC	TTCAATCCCC	TCTGCGCTTC	TGATGGGAAA	600
TCATTATGATA	ATGCATGCCA	AATCAAAGAA	GCATCGTGTG	AGAAACAGGA	GAAATTTGAA	660
GTCTATGCTT	TGGGTGCGATG	TCAAGATAAC	ACAACATCAA	CTACTAAGTC	TGAAGATGGG	720
CATTATGCAA	GAACAGATTA	TGCAGAGAAT	GCTAACAAAT	TAGAAGAAAG	TGCCAGAGAA	780
CACCACATAC	CTTGTCCGGA	ACATTACAAT	GGCTTCTGCA	TGCATGGGAA	GTGTGAGCAT	840
TCTATCAATA	TGCAGAGGCC	ATCTTGCAAG	TGTGATGCTG	GTTATACTGG	ACAACACTGT	900
GAAAAAAGG	ACTACAGTGT	TCTATACGTT	GTTCCCGGTC	CTGTACGATT	TCAGTATGTC	960
TTAATGCGAG	CTGTGATTGG	AACAAATTCAG	ATTGCTGTCA	TCTGTGTGTT	GGTCTCTGTC	1020
ATCACAAGGA	AATGCCCCAG	AAGCAACAGA	ATTCACAGAC	AGAAAGCAAA	TACAGGGCAC	1080
TACAGTTTAC	ACAAATCAAC	AAGAGCGTCC	ACGAGGTTAA	TCTGA		

Seq ID NO: 580 Protein sequence
Protein Accession #: NP_057276.2

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1	11	21	31	41	51	
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DRENDLFLCD	TNTCKFDGEC	LRIGDTVTCV	CQFKQNDYV	FVCGSNGESY	QNECYLRQAA	120
CKQQSEILVV	SEGSCTADAG	SGSGDGVHEG	SGETGQKETS	TCDIQPGAE	CDADAEDVWC	180
VCNIDCSQTN	FNPLCASDGG	SYDNACQIKE	ASCCQKQKIE	VMSLGRCDQN	TTTTTKSDDG	240
HYARTDYAEN	ANKLEBSARE	HHIPCPEHYN	GFCMHGKCEH	SINMQSPSCR	CDAGYTGQHC	300
EKKDYSVLHV	VPGFVRPQYV	LIAAVIGTIQ	IAVICVVVLC	ITRKCPRSNR	IHRQKQNTGH	360
YSSDNTTRAS	TRLI					

Seq ID NO: 581 DNA sequence
Nucleic Acid Accession #: S78203.1
Coding sequence: 1..2190

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GAGGTACCAC	CTGACCAACC	TAGCCCTCCA	AAGAAGCCAT	CTCCGACAA	CTGTGGCTCC	120
AACTATCCAC	TGAGCATTGC	CTTCATTGTG	GTGAATGAAT	TCTGGGAGCG	CTTTTCTTAT	180
TATGGAATGA	AAGCTGTGCT	GATCCTGTAT	TTCTGTATT	TCTGTCACTG	GAATGAAGAT	240
ACCTCCACAT	CTATATACCA	TGCCCTTCAGC	AGCCTCTGTT	ATTTTACTCC	CATCCTGGGA	300
GCAGCCATTG	CTGACTCGTG	GTGGGAAAAA	TTCAAGACAA	TCACTATCT	CTCCTTGGTG	360
TATGTGCTTG	GCCATGTGAT	CAAGTCTTTG	GGTGCTTAC	CAATACTGGG	AGGACAAGTG	420
GTACACACAG	TGCTATCATT	GATCGGCCTG	AGTCTAATAG	CTTTGGGAGC	AGGAGGCATC	480
AAACCTGTGT	TGGCAGCTTT	TGGTGGAGAC	CAGTTTGAAG	AAAAACATGC	AGAGGAACGG	540
ACTAGATACT	TCTCAGTCTT	CTACCTGTCC	ATCAATGCAG	GGAGCTTGAT	TTCTACATTT	600
ATCACACCCA	TGCTGAGAGG	AGATGTGCAA	TGTTTGGGAG	AAGACTGCTA	TGCATTGGCT	660
TTTGAGTTTC	CAGGACTGCT	CATGTGAATT	GCACTTGTG	TGTTTGCAAT	GGGAAGCAAA	720
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CTAGACTGGG	CAGCTGAGAA	ATATCCAAAG	CAGCTCATT	TGGATGTAAA	GGCACTGACC	900
AGGGTACTAT	TGCTTTATAT	CCCATTTGCC	ATGTTCTGGG	CTCTTTTGG	TCAGCAGGGT	960
TCACGATGGA	CTTTGCAAGC	CATCAGGATG	AATAGGAATT	TGGGGTTTTT	TGTGCTTCAG	1020
COGACACAGA	TGCAGGTTCT	AAATCCCTTT	CTGGTTCTTA	TCTTCATCCC	GTGTTTGTAG	1080
TTTGCTATTT	ATCGTCTGGT	CTCCAAGTGT	GGAATTAAT	TCTCATCACT	TAGGAAAAATG	1140
GCTGTGTGGT	TGATCCTAGC	GTGCCTGGCA	TTTGCAAGTG	OGGCACTGT	AGAGATAAAA	1200
ATAAATGAAA	TGGCCCCAGC	CCAGTCAGGT	CCCCAGGAGG	TTTTCTTACA	AGTCTTGAAT	1260
CTGGCAGATG	ATGAGGTGAA	GGTGACAGTG	GTGGGAAATG	AAAACAATTC	TCTGTTGATA	1320
GAGTCCATCA	AATCCTTTCA	GAAAAACCCA	CACATTTCCA	AACTGCACCT	GAAAAACAAA	1380
AGCCAGGATT	TTCACTTCCA	CCTGAAATAT	CACAATTTGT	CTCTCTACAC	TGAGCATTTCT	1440
GTGCAGGAGA	AGAACTGGTA	CAGTCTTGTG	ATTGCTGAAG	ATGGGAACAG	TATCTCCAGC	1500

5 ATGATGGTAA AGGATACAGA AAGCAAAACA ACCAATGGGA TGACAACCGT GAGGTTTGTG 1560
 AACACTTTGC ATAAAGATGT CAACATCTCC CTGAGTACAG ATACCTCTCT CAATGTTGGT 1620
 GAAGACTATG GTGTGTCTGC TTATAGAACT GTGCAAGAG GAGAATACCC TGCAGTGCAC 1680
 TGTAGAACAG AAGATAAGAA CTTTCTCTG AATTGGGGTC TTCTAGACTT TGGTGCAGCA 1740
 TATCTGTTTG TTATTACTAA TAACACCAAT CAGGGTCTTC AGGCCTCGAA GATTGAAGAC 1800
 ATTCAGCCCA ACAAATGTCT CATTGCGTGG CAGCTACCAC AATATGCCCT GGTACAGCT 1860
 GGGGAGGTCA TGTTCTCTGT CACAGGTCTT GAGTTTCTT ATTCTCAGGC TCCTCTAGC 1920
 10 ATGAAATCTG TGCTCCAGGC AGCTTGGCTA TTGACAATTG CAGTTGGGAA TATCATCGTG 1980
 CTGTGTTGGG CACAGTTCAG TGGCCTGGTA CAGTGGGCGG AATTCAATTT GTTTTCTGTC 2040
 CTCTGCTGCT TGATCTGCCT GATCTTCTCC ATCATGGGCT ACTACTATGT TCCTGTAAAG 2100
 ACAGAGGATA TGCGGGGTCC AGCAGATAAG CACATTCTCT ACATCCAGGG GAACATGATC 2160
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15 Seq ID NO: 582 Protein sequence
 Protein Accession #: AAB34388.1

1 11 21 31 41 51
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 YVLGHVIXSL GALPILGGQV VHTVLSLIGL SLIALGTGGI KPCVAAFAGD QFEKHABER 180
 TRYPSVYFSL INAGSLISTF ITPMLRGDVG CPGEDCYALA FGVPGLLMVI ALVVPFAMGSK 240
 IYNKPPPEGN IVAQVFKCIW FAISNRFRNR SGDIPKQHM LDWAAEKYPK QLIMDVKALT 300
 25 RVLFYLIPLP MFWALLDQGG SRWTLQAIMR NRNLGFFVLQ PDQMQLVLPF LVLIFLPLFD 360
 FVIYRLVSKC GINPSSLRKM AVGMILACLA FAVAAAVEIK INEMAPAQSG PQEVFLQVLN 420
 LADDEVKVTY VGNENNSLLI ESIKSPQKTP HYSKLHLKTK SQDPHFHLKY HNLSTLYEHS 480
 VQERNWYSLV IREDGNSISS MMVKDTSBKT TNGMTTVRFV NTLHKDVNIS LSTDTSLNVG 540
 EDYGVPSAYRT VQRGEYPAHV CRTEDKNFSL NLGLLDFGAA YLPVITNNTN OGLQANKIED 600
 30 IPANKMSIAN QLPQYALVTA GEVMPSTVGL EFSYSQAPSS MKSVLQAAWL LTIAGVNIIV 660
 LVVAQPSFLV QWAEFPLPSC LLLVICLIFS IMGYIYVPVK TEDMRGPADK HIPHIQGNMI 720
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35 Seq ID NO: 583 DNA sequence
 Nucleic Acid Accession #: NM_032642.1
 Coding sequence: 184..1263

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 ACCATGCCCA GCCTGCTGCT GCTGTTTACG GCTGCTCTGC TGTCCAGCTG GGTCTAGCTT 240
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 55 AAGGTGCGGG ACCGCTGAA GGAGAAGTAC GACAGCGCG CCGCATGCG CGTCAACCCG 960
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80 Seq ID NO: 584 Protein sequence
 Protein Accession #: NP_116031.1

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 VGDRLEKEVD SAAAMRVTRK GRLELVNSRP TQPTPEDLVY VDPSPDYCLR NESTGSLGTQ 300
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Seq ID NO: 585 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..1479

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Seq ID NO: 586 Protein sequence
 Protein Accession #: Eos sequence

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 45 DSSGTCINPS NWCQGVSHCP GGEDENRCVR LYGPNFILQV YSSQRKSWHP VQDDWNWENY 180
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 CIACGVNLNS SRQSRIVGGE SALPGAWFWQ VSLHVQNVHV CGGSIITPEW IVTAACHVEK 300
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 50 VKPVCLPNPG MMLQPEQLCW ISGWGATEEK GRTSEVLNAA KVLLIETQRC NSRYVYDNL 420
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Seq ID NO: 587 DNA sequence
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57..1535

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 75 GAGGCTCCAT CATCAACCCC GAGTGGATCG TGACAGCGCG CCACTGCGTG GAAAAACCTC 960
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 AGAACAAATG CATTCGCGCTG ATGAAGCTGC AGAAGCCTCT GACTTTCAAC GACCTAGTGA 1140
 80 AACCAAGTGT TCTGCCCAAC CCAGGCATGA TGTGCAAGC AGAACAGCTC TGTGGAATTT 1200
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 TCCTAGCACC CTGGAGAGTG AATGCCCCCTT GGTCCCTGGC AGGGGCGCAA GTTTGGCACC 2340
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Seq ID NO: 588 Protein sequence
 Protein Accession #: NP_005647.1

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 DSSSGTCINPS NWCDDGVSHCP GGEDEVRCVR LYGFNFILQM YSSQRKSWHP VCQDDWNENY 180
 GRAACRDHGY KQNFYSSQGI VDDSGSTFSM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWFWQ VSLHVQNVHV CGGSIITPEW IVTAHCHVEK 300
 PLNNPWHWTA FAGILRQSFM FYGAGYQVQK VISHPNYDSK TKNDIALMK LQKPLTFNDL 360
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Seq ID NO: 589 DNA sequence
 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 1..2301

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 CCAAGTTTACA GAATCACATG GACGGGGAAA GAAGATATAA TATATAATGG AATAACTGAC 600
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 GGATCGGAA GTGGCGTGT TCAAGTGTGA ATAGCGTGG GCGCTGTATC CCGGTGGGAG 1980
 TACTATGACT CAGGTATCAC AGAACGTTAC ATGGGTCTCC CAATCCAGA AGACAACCTT 2040
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Seq ID NO: 590 Protein sequence
 Protein Accession #: NP_001926.1

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 MKTPWKILLG LIGAAALVTI ITVPVVLNKK GTDDATADSR KTYTLTDYLK NTRYLKLKLYSL 60

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RWISDREYLY KQENNLVFN AEYGNSSVFL ENSTFDEFHG SINDYSISPD GQPILLENYN 120
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PSYRITWTKG EDIITYNGITD WYEEZEVFSA YSALWNSPNG TFLAYAQFND TEVPLIEYSF 240
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CDVTWATQER ISLQWLRRQI NYSVMDICDY DESSGRWNCL VARQHIE MST TGMVGRFRPS 360
EPHFTLDGNS FYKIIISNEEG YRHICYFOID KKDCTPITKG TWEVIGIEAL TSDYLYYISN 420
EYKMPGGRN LYKIQLSDYT KVTCLSCSLN PERQYYSVS PSKEAKVYQL RSCSGFLPLY 480
TLHSSVNDKG LRVLEDNSAL DRMLQNVQMP SKKLDPIILN ETKEFWYQML PPHFDKSKKY 540
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Seq ID NO: 591 DNA sequence
Nucleic Acid Accession #: NM_016077.1
Coding sequence: 128..667

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Seq ID NO: 592 Protein sequence
Protein Accession #: NP_057161.1

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Seq ID NO: 593 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1896

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Seq ID NO: 594 Protein sequence
Protein Accession #: FGENESH predicted


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VPPPFILID LPARCSGRPD GGIRPGKTCF PAWWHPVESM SAATWGVKDW TWKPSGCVGV 240
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10 LNLMEKLDSS ALRRNTRAPS ARCLPLVLAE MAAESDLFN PWWHPSATGS PIKTLTYQTM 360
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Seq ID NO: 595 DNA sequence
Nucleic Acid Accession #: NM_021614.1
Coding sequence: 1..1740

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70 NAAANVLRRT WLIIYKNTKLV KKIDHAKVRK HQRKFLQAIR QLRSVKMEQR KLNDQANTLV 480
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Seq ID NO: 598 Protein sequence
 Protein Accession #: NP_057113.1

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25 Seq ID NO: 599 DNA sequence
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Seq ID NO: 600 Protein sequence
Protein Accession #: NP_000784.2

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Coding sequence: 101..3052

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CCAAATTCGA TCCGGGACAG CCGCTGGATA TGGGACGAAC AGCCGCAAGT TTGAGTTTGA 1680
AACTAGTCCA GACTCTTTCT CCACTCTCTG TGAAGTAGC CAAGTGGTCA TGATCGCCAT 1740
TTCAGCGCA GTAGCAATTA TTCTCTCTAC TGTGTCTATC TATGTTTTGA TTGGGAGGTT 1800
CTGTGGTAGT AAGTCAAAAC ATGGGGCAGA TGA AAAAAGA CTTCATTTTG GCAATGGGCA 1860
TTTAAACTT CCAGGTCTCA GGCATTATGT TGACCCACAT ACATATGAAG ACCCTACCCA 1920
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TGGAGCAGGT GAATTTGGAG AGGTGTGCAG TGGTCGCTTA AAACCTCCTT CAAAAAAGA 2040
GATTTCACTG GCCATTA AAA CCCTGAAAGT TGGCTACACA GAAAGCAGA GGAGAGACTT 2100
CTTGGGAGAA GCAAGCATT TGGGACAGTT TGACCAACCC AATATCATTC GACTGGAAGG 2160
AGTTGTATCC AAAAGTAAGC CAGTTATGAT TGTACAGAA TACATGGAGA ATGGTTCTCT 2220
GGATAGTTTC CTACGTAAC ACATGCCCCA GTTACTGTCT ATTCACTGAT TGGGGATGCT 2280
TGAGGGGATA GCATCTGGCA TGAAGTACCT GTACAGCATG GGTATGTGTC ACCGAGACCT 2340
CGCTGCTCGG AACATCTTGA TCAACAGTAA CTTGGTGTGT AAGGTTTCTG ATTTGCGGAT 2400
TTGGGCTGTC CTGGAGGATG ACCCAGAAAGC TGCTTATACA ACAAGAGGAG GGAAGATGCC 2460
AATCAGGTGG ACATCACCAG AAGCTATAGC CTACCGCAAG TTACGTCAG CCAGCGATGT 2520
ATGGAGTTAT GGGATTGTTCT TCTGGGAGGT GATGTCTTAT GGAGAGAGAC CATACTGGGA 2580
GATGTCCAAT CAGATGTAA TTAAGCTGT AGATGAGGCG TATCGATGTC CACCCCCCAT 2640
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CAGACCCAAAG TTGAGCAGA TTGTTAGTAT TCTGGACAAG CTTATCCGGA ATCCCGGAG 2760
CCTGAAGATC ATCACCAGTG CAGCCGCAAG GCCATCAAC CTTCTCTGTC ACCAAAGCAA 2820
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CTGCAAGGAA ATCTTCAAGC GCGTGGAGTA CAGTTCTTGT GACACAATAG CCAAGATTTC 2940
CAGAGATGAC ATGAAAAAGG TTGGTGTGAC CGTGGTTGGG CCACAGAAGA AGATCATCAG 3000
TAGCATTAAG GCTCTAGAAA CGCAATCAAA GAATGGCCCA GTTCCCGTGT AAAGCACGAC 3060
GGAAGTGCTT CTGACGCGAA GTGGTGGCTG TGAAGGCGT CAAGTCATCC TGCAGACAGA 3120
CAATAATTCT GGAGATACTG GTGGAAGTT

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Seq ID NO: 602 Protein sequence

Protein Accession #: NP_005224.1

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1 11 21 31 41 51
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HYTPRTYQV CNVMDHSQNN WLRTNWVPRN SAQKIYVELK FTLRDCNSIP LVLGTCKETF 120
NLYYMESDD HGVIKFRHQF TKIDTIAADE SFTQMDLADR ILKLNTAIRE VGPVNNKGFY 180
LAFQDVGACV ALVSVRVYFK KCPFTVKILA MFPDTPVPMDS QSLVEVRGSC VNNSKEEDFP 240
RMYCSTEGEW LVPIGKCSQV AGYBERGFMC QACRPGPYKA LDGWNKCAKC PPHSSTQEDG 300
SMNCRCENNY PRADKPPPM ACTRPPSSPR NVISINETS VILDWSWFLD TGGKRDVTFN 360
IICKKCGWNI KQCEPCSEFN RFLPRQFGLT NTTVTVDLL ARTNYTFRID AVNGVSELSS 420
PPRQFAAVSI TTNQAPSPFV LTIKKDRTER NSISLSWQEP EHPNGIILDY EVKYEKQEQ 480
ETSTILRAR GNTVTISLKL PDTIYVQIR ARTAAGVGTN SRKFEPTSP DSFSISGESS 540
QVVMIAISAA VAIILLTVVI VVLIGRFCGY KSKHGADEKR LHPNGHLKL PGLRTVVDPH 600
TYEDPTQAVH EFAKELDATN IISDKVVGAG EPGEVCSGRL KLPKKEISV AIKTLKVGYT 660
EKQRDPFGE ASIMQPDHP NIIRLEGVVT KSKFVMIVTE YMENGSLDSP LRKHDAQPTV 720
IQLVGLMRLGI ASGMKYLSDM GYVHRDLAAR NILINSNLVC KVSDFGLSER LEDDPEAATY 780
TRGGKIPIRW TSPALAYRK FTSASDVVSY GIVLNEVMSY GERPYWEMSN QDVIKAVDEG 840
YRLPPPMDCP AALYQLMLDC WQXDRNNRPK FEQIVSILDK LIRNPGSLKI ITSAAARPSN 900
LLLDQSNVDI STFRITGDWL NGVRTAHCKE IFTGVEYSSC DTIAKISTDD MKKVGVTUVG 960
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Seq ID NO: 603 DNA sequence

Nucleic Acid Accession #: NM_005727.1

Coding sequence: 122..847

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CATGCAGTGC CTCAGCTTCA TTAAGACCAT GATGATCCTC TTCAATTTCG TCATCTTTCT 180
GTGTGTGTGA CGCCTGTGTG CAGTGGGCAT CTGGGTGTCA ATCGATGGGG CATCCTTTCT 240
GAAGATCTTC GGGCCACTGT CGTCCAGTGC CATGCAGTTT GTCAACGTGG GCTACTTCTC 300
CATCGCAGCC GGCCTTGTGG TCTTTGCTCT TGGTTTCTGT GCGTCTATG TGCTAAGAC 360
TGAGAGCAAG TGTGCGCTCG TGACGTTCTT CTTTCATCTC CTCTCATCT TCATTGCTGA 420
GGTTGCACT GCTGTGGTGG CCTTGGGTGA CAACCAATG GCTGAGCACT TCCTGACGTT 480
GCTGTGAGTG CCTGCCATCA AGAAAGATTA TGGTTCACAG GAAGACTTCA CTCAGTGTG 540
GAACACCAAC ATGAAAGGGC TCAAGTGCTG TGGCTTCACC AACTATACGG ATTTTGAGGA 600
CTCACCTTAC TTCAAAGAGA ACAGTGCTCT TCCCCATTC TGTGCAATG ACAACGTCAC 660
CAACACAGCC AATGAAACCT GCACCAAGCA AAAGGCTCAC GACCAAAAAG TAGAGGTTG 720
CTTCAATCAG CTTTGTGTAT ACATCCGAAC TAATGCAGTC ACCGTGGGTG GTGTGGCAGC 780

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TGGAATTGGG GGCCTGAGC TGGCTGCCAT GATTGTGTCC ATGTATCTGT ACTGCAATCT 840
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 CCTGGCAAG CAGCAGTGAT TGGGGGAGGG GACAGGATCT AACATGTCA CTTGGGCCAG 960
 AATGGACCTG CCTTTCTGC TCCAGACTTG GGGCTAGATA GGGACCACTC CTTTTAGGCG 1020
 ATGCCCTGACT TTCTTCCAT TGGTGGGTGG ATGGGTGGGG GGCATTCCAG AGCCTCTAAG 1080
 GTAGCCAGTT CTGTTGCCCA TTCCCCCAGT CTATTAAACC CTTGATATGC CCCCTAGGCC 1140
 TAGTGTGTAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTTATA GCCTGGGCAT 1200
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 TGTTACAATG TTAATAAAA

Seq ID NO: 604 Protein sequence
 Protein Accession #: NP_005718.1

1 11 21 31 41 51
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 IAAGVVVFAL GFLGCTYGAKE ESKCALVTFF FILLILPIAE VAAAVVALVY TMAEHFLTL 120
 LVVPAIKKDY GSEDFTQVW NTKMKGLKCC GFTNYTDFED SPYFKENSAP PPFCCNDNVT 180
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Seq ID NO: 605 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence:

1 11 21 31 41 51
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 GCCCGGTAGG CAGCTGAGGG TATGCGAGAG AACGGATGGC GAGTCCCGAG CGCACTGGGG 240
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 CTGGATGGAT TTTGGCGGTG GCAGTGCCTG GGAGTATGAG TACCCCTCCT AGAGGACCCA 420
 GCGCCATCA GCCCAACGGA AGCAACCTCC CAACCCAGAG GAGGCAGAAAT AAGACAACAA 480
 TCACACTCAT AACTCATTTG CTGTGGAGTT TGACATTGAA TGTATCTATT TATTAAGTTC 540
 TCAATGTGAA AATTGTGTCT GTAAGATGTT CCACTGCAAC CACACACGCT CACCAGAAAT 600
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Seq ID NO: 606 Protein sequence
 Protein Accession #: NP_000720.1

1 11 21 31 41 51
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 LLARYIQAR KAPSGRMSIV KNLQNLDPFH RISDRDYMGW MDPGRRSABE YEYPS

Seq ID NO: 607 DNA sequence
 Nucleic Acid Accession #: NM_001423.1
 Coding sequence: 219..692

1 11 21 31 41 51
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 CAGGCGTGTCT GCCAGCAGCT GCCACTCAGA GCGCCTCTGT CGCTGGGACC CTTCAGAACT 180
 CTCTTTTGCTC ACAAGTTACC AAAAAAATA GAGCCAACAT GTTGGTATTG CTGGCTGGTA 240
 TCTTTTGTGT CCACATCGCT ACTGTTATTA TGCTATTTGT TAGCACCATT GCGAATGTCT 300
 GGTGGTTTC CAATACGGTA GATGCATCAG TAGGTCTTTG GAAAAACTGT ACCAACATTA 360
 GCTGCAGTGA CAGCCTGTCA TATGCCAGTG AAGATGCCCT CAAGACAGTG CAGGCTTTCA 420
 TGATCTCTCT TATCATCTTC TGTGTCTATG CCTCTCTGT CTTCTGTGTC CAGCTCTTCA 480
 CCATGGAGAA GGGAAACCGG TTCTCTCTCT CAGGGGCCAC CACACTGGTG TGCTGGCTGT 540
 GCATTCTTGT GGGGGTGTCC ATCTACACTA GTCATTTATG GAATCGTGAT GGAAOCGAGT 600
 ATCACCACGG CTATTCTTAC ATCCTGGGCT GGATCTGCTT CTGCTTCAGC TTCTATCATG 660
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 GGTGGGGAGG AGGAAGCCGT TGAATCTGGG AGGGAAGTGG AGGTTGCTGT ACAGGAAAAA 780
 COGAGATAGG GGAGGGGGGA GGGGGAAGCA AAGGGGGGAG GTCAAATCCC AAACCAATTAC 840
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 TCTGACCCAA AGCAAAACAT CACATTCCAG TCTGAAGTGC CTACTGGGGG GCTTTGGCCT 1200
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 GCTCTTCTGG AGTTTCTCTA AAGTCACTAG TGAACAATTC GGTGGTAAAA GTACCAACA 1500
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 GAGTGATCAC CTCTTGGGGA CCTTGCTTAT CCCACTTCAC AGGTGAGGCA TGGCAATTCT 1800

5 GGAAGCTGAT TAAACACAC ATAAACCAA ACCAAACAAC AGGCCCTTGG GTGAAAGGTG 1860
 CTATATAATT GTGAAGTATT AAGCCTACCG TATTTCAGCC ATGATAAGAA CAGAGTGCCT 1920
 GCATTCCCGA GAAATACGA AAATCCCATG AGATAAATAA AAATATAGGT GATGGGCAGA 1980
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 10 TCCTTTGTGG GGAGTTGTTA TGCCATGATT TTTGGTATT ATGTAAAAGG ATTATTACTA 2340
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 CTAGGCTGAG GTTAGAGAGA TTGGCCAGCA AAACTGTGG GAAGATGAAC TTTGTCAATTA 2460
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 15 ACCATGTATT CCTTATCTT TTACTTTTT TCTGTGACAT TTATGTCTCA TGTAAATTTG 2640
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Seq ID NO: 608 Protein sequence
 Protein Accession #: NP_001414.1

20 1 11 21 31 41 51
 25 MLVLLAGIFV VHIAIVIMLF VSTIANVWL V SNTVDASVGL WKNCTNISC S DLSYASEDA 60
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Seq ID NO: 609 DNA sequence
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 Coding sequence: 55..1575

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 CAGCCTCTGG AAAATCAGCT CCTCTCTGAG GAAACAAAGT CAACTAGAGC TGAGACTGGG 240
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 40 GACCACAAAC TGCGCCCTGG CATTGGAGAG AAGCCCACTG TGGTCACTGT TGAGATCGCC 360
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 45 CCAATGGATT CTCACTCTTG CCTCTATCT TTCTTAGCT TTTCTATCC TGAGAATGAG 720
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 70 CACTGGCATT ATCCCTTTAG GAAGAGGGGG GGGCAGCAAG AGAGCCTATT TGGGACAGCA 2220
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 75 ACTTTCCAG TGACTCTCTT TAGCCCTGAC CCAGGCACTA GGCCTTGGT ACTTCTGGG 2460
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 GAATGAATTT GGACATGCC CAATGCTTCT ATATGCTAAG TGAATCTGT GTCTGTAAAT 3060

TGTTGGGGGG TGGATAGGGT GGGGTCTCCA TCTACTTTTT GTCAACATCA TCTGAAATGG 3120
GGAAATATGT AAATAAATAT ATCAGCAAAG CAAAAAGAAA AAAAAAAA

Seq ID NO: 610 Protein sequence
Protein Accession #: NP_004952.1

1 11 21 31 41 51
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10 MLKVLVFLLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60
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IPQTYWYDER LCYNDYFBSL VLNQNVVSQL WIPDTFFRNS KRTHEBITM PNQMVRIYKD 180
GKVLVYTRMT IDAGCSLHML RPPMDSHSCP LSPSSFSYPE NEMIVKWNF KLEINEKNSW 240
KLPQFDFTGV SNKTEIITTP VGDPMVMITIP FNVSRFPYV AFQNYVPSSV TTMLSNVSWF 300
15 IKTESAPART SLGITSVLTM TILGTFPSRKN FPRVSYITAL DFYIAICPVF CFCALLEFAV 360
LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVQIV TTEGSDGEER 420
PSCSAQQPPS PGSPGPRSL CSKLACCEWC KRFKKYFOMV PDCEGSTWQQ GRLCIHVYRL 480
DNYSRVVPV TFPFFNVLYW LVCLNL

Seq ID NO: 611 DNA sequence
Nucleic Acid Accession #: NM_021984.1
Coding sequence: 572..1753

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30 CACTGCCCTCC CAGCAAAAGG AGCACTATCC GGACTTCTAA CACCATCGGG TCGAGGGACC 300
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CAGAGTTGGC AAAGTGCAG AAGCCTCTCG CATCCTGAAC ACTATCTGA GTAATTATGA 480
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35 CCAGACCTGG TACGACGAAC GCCTCTGTTA CAACGACACC TTGAGTCTC TTGTTCTGAA 660
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60 TTAGTGATCA GCTCCCTAAA ACCATGCCTA AGTACAGGCG GATTAGCTAT CTTCACAA 2100
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Seq ID NO: 612 Protein sequence
Protein Accession #: NP_068819.1

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 Protein Accession #: NP_068822.1

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Seq ID NO: 616 Protein sequence
Protein Accession #: NP_068830.1

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5 Seq ID NO: 617 DNA sequence
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35 Seq ID NO: 618 Protein sequence
 Protein Accession #: NP_004855.1

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45 Seq ID NO: 619 DNA sequence
 Nucleic Acid Accession #: NM_003979.2
 Coding sequence: 254..1357

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10 Seq ID NO: 620 Protein sequence
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 DDTILSSALA ANGNWFLLAY VSPEWLLTK QRNPMQPYVE DAFCKQLVK KSYGVENRAY 300
 SQEBITQGE ETQDTLYAPY STHFQLQNP PQKEFSIPRA HAMPSPKDY EVKKEGS

20 Seq ID NO: 621 DNA sequence
 Nucleic Acid Accession #: NM_002423.2
 Coding sequence: 48..851

25 1 11 21 31 41 51
 ACCAAATCAA CCATAGGTCC AAGAACAAAT GTCTCTGGAC GGCAGCTATG CGACTCACCG 60
 TGCTGTGTC TGCTGCTCTG CTGCTTGGCA GCCTGGCCCT GCCCTGCTCT CAGGAGGCGG 120
 GAGGCATGAG TAGGTCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
 ATGACTCAGA AACAAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAGAAAT 240
 TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCCGCGT CATAGAAATA ATGCAGAAAGC 300
 CCAGATGTGG AGTGCCAGAT GTTGCCAGAT ACTCATTAT TCCAAATAGC CCAAAATGGA 360
 CTTCCAAAGT GGTCACTTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
 TGGATCGATT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCC CTGCATTTC 480
 GGAAAGTTGT ATGGGGAATC GCTGACATCA TGATTGGCTT TGCCGAGGGA GCTCATGGGG 540
 ACTCTACCCC ATTGTATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCTGGGACAG 600
 GTCTGGGAGG AGATGCTCAC TCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG 660
 GGATTAACCT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT 720
 CCTCTGATCC TAATGCAGTG ATGTATCCAA CCTATGGAAA TGGAGATCCC CAAAATTTTA 780
 AACTTTCCCA GGATGATATT AAAGGCATTG AGAAACTATA TGGAAAGAGA AGTAATTC 840
 GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCTTCA TTCTATGGAT TGTATATCAT 900
 TGTTCACAAA TCAGAAATGA TAAGCACTGT TCCTCCACTC CATTAGCAA TTATGTCA 960
 CTTTTTTATT CGAGTTGGTT TTTGAATGTC TTCTACTCCT TTTATTGGTT AAACCTCTTT 1020
 ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGGCGTAG ATGTCAATAA 1080
 ATGTACATA CACAAATAAA TAAATGTTT ATTCCATGGT AAATTTA

Seq ID NO: 622 Protein sequence
 Protein Accession #: NP_002414.1

50 1 11 21 31 41 51
 MRLTVLCVAV LLPGLALPL PQEAGGMSSEL QWEQAQDYLK RFYLYDSETK NANSLEAKLK 60
 EMQKPFGLPI TGMINSRVIE IMQKPRCGVF DVAYSLFPN SPKWTISKVVT YRIVSYTRDL 120
 PHITVDRLVS KALNMMGKEI PLHFRKVVMG TADIMIGFAR GAHGDYSPFD GPGNTLAHAF 180
 APGTGLGSDA HPFEDERWTD GSSLGINFLY AATHELGHSL GMGHSSDPNA VMYPTYNGND 240
 PQNFKLSDQD IKGIQLYK RSNRKK

60 Seq ID NO: 623 DNA sequence
 Nucleic Acid Accession #: NM_031457.1
 Coding sequence: 204..956

65 1 11 21 31 41 51
 AAACAGGAAA TAAATACGAA TGAAACTGAG CTCTAAGCAG CATGTAACCT GGCCTGCATC 60
 CAGGAAATAG AGGACTTCGG ATCCTTCTAA CCTACCAACC CACTGGCCC CAGTACATTC 120
 ATTCTCTCAG GAAAAA AACAGGTCCCCA CAGCAAAGAA AAGGAATAGG ATCAAGAGAT 180
 ACGTGCTGTC TGCCAGAGCA AGCATGAATT CGATGACTTC AGCAGTTCCG GTGGCCAATT 240
 CTGTGTTGGT GGTGGCAGCC CACAATGGTT ATCCTGTGAC CCCAGGAATT ATGTCTCAGG 300
 TGCCCTCTGA TCCAAACAGC CAGCCGCAAG TCCACCTAGT TCCTGGGAAC CCACCTAGTT 360
 TGGTGTGCGA TGTGAATGGG CAGCCTGTGC AGAAGCTCT GAAAGAGGCG AAAACCTTGG 420
 GGGCCATCCA GATCATCAT TGGCCTGGCTC ACATGGGCTC CGGCTCCATC ATGGGACGG 480
 TTCTCGTAGG GGAATACCTG TCTATTTTCT TCTACGGAGG CTTTCCCTTC TGGGAGGCT 540
 TGTGTTTAT CATTCAGGA TCTCTCTCCG TGGCAGCAGA AAATCAGCCA TATTCTTATT 600
 GCTGTCTGTC TGGCAGTTTG GGCTTGAACA TCGTCAGTGC AATCTGCTCT GCAGTTGGAG 660
 TCATACTCTT CATCAGAT CTAAGTATTC CCCACCCATA TGCCCTACCC GACTATTATC 720
 CTTACGCTG GGTGTGAAC CCTGGAATGG CGATTTCTGG GGTGCTGCTG GTCTTCTGCC 780
 TCCTGGAGTT TGGCATCGCA TGGCATCTT CCCACTTTGG CTGCCAGTTG GTCTGCTGTC 840
 AATCAAGCAA TGTGAGTGT ATCTATCCAA ACATCTATGC AGCAAAACCA GTGATCACCC 900
 CAGAACCGGT GACCTCACCA CCAAGTTATT CCAGTGAGAT CCAAGCAAA AAGTAAGGCT 960
 ACAGATTCTG GAAGCATCTT TCACTGGGAC CAAAGAGAGT CCTCTCCCT TTCTGGGCTT 1020
 CCATAACCCA GGTGTTCTCT GTTCTGACAG CTGAGGAAAC GTCTCTCCCA CTGTTTGTAC 1080
 TCTCACCTTC ATTCTTCAAT TCAGTCTAGG AAACCATGCT GTTCTCTAT CAAGAAAG 1140
 ACAGAGATT TAAACAGATG TTAACCAAGA GGGACTCCCT AGGGCACATG CATCAGCACA 1200
 TATGTGGGCA TCCAGCCTCT GGGGCCCTTG CACACACACA TTGCTGTGCT CTGCTGCATG 1260

TGAGCTTGTG GGTAGAGGA ACAAATATCT AGACATTCAA TCTTCACTCT TTCAATTGTG 1320
CATTCAATTA ATAAATAGAT ACTGAGCATT CAAAAA AAAA

Seq ID NO: 624 Protein sequence
Protein Accession #: NP_113645.1

1 11 21 31 41 51
MNSMTSAVPV ANSVLVVAPH NGYPVTPGIM SHVPLYPNQ PQVHLVPGNP PSLVSNVNGQ 60
10 PVQKALKESK TLGAIQIIIG LAHIGLGSIM ATVLVGEYLS ISPYGGFFPW GGLWFIISGS 120
LSVAENQPY SYCLLSGSLG LNIIVSAICSA VGVILPITDL SIPHPYAYPD YYPYAWGVNP 180
GMAISGVLLV FCLLEFGIAC ASSHFGCQLV CQSSNVSVI YFNIYAANPV ITPEPVTSP 240
SYSSBIQANK

Seq ID NO: 625 DNA sequence
Nucleic Acid Accession #: NM_005221.3
Coding sequence: 1..870

1 11 21 31 41 51
20 ATGACAGGAG TGTTTGACAG AAGGGTCCCC AGCATCCGAT CGGGCGACTT CCAAGCTCCG 60
TTCCAGACGT CGGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACCTT GCCCGAGTCT 120
TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCGCGACGG CTACTGCTGT 180
25 CTACCTCGG CTCTCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG 240
AACGGCTCGG CGGGGAGCTA CCCAGCCAAA GCTTATGCGG ACTATAGCTA CGTAGCTCC 300
TACCACAGT ACGGCGGCGC CTACAACCGG GTCCCAAGCG CCACCAACCA GCCAGAGAAA 360
GAAGTGACCG AGCCGAGGT GAGAAATGGT AATGCCAAAC CAAAGAAAGT TCGTAAACCC 420
AGGACTATTT ATTCAGCTT TCAGCTGGCC GCATTACAGA GAAGTTTCA GAAGACTCAG 480
TACCTCGCT TGCGGGAACG CGCCGAGCTG GCGCCTCGG TGGGATTGAC ACAACACAG 540
30 GTGAATATCT GGTTCAGAA CAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG 600
ATGCCCCCGG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCGCAGTCT 660
CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCAC 720
CCTCOGACCT CCAACAGTC CCGACGCTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC 780
35 ACAAGTGCAG CCACTCAAT CAATTCCAC CTGCCGCGCG CGGGCTCCTT ACAGCACCCG 840
CTGCCGCTGG CCTCCGGAC ACTCTATTAG

Seq ID NO: 626 Protein sequence
Protein Accession #: NP_005212.1

1 11 21 31 41 51
40 MTGVFDRRPV SIRSGDFQAP FQTSAAHHP SQESPTLPES SATDSDYISP TGGAPHGYCS 60
PTSASYGKAL NPQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK 120
EVTPEVRMV NGKPKVRKP RTIYSSPQLA ALQRRFQRTQ YLALPERAEL AASLGLTQTQ 180
45 VKIWFNKRK KIKKIMNGE MPPEHSPSS DPMACNSPQS PAVWEPOGSS RSLSHHPHAH 240
PPTSNQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLV

Seq ID NO: 627 DNA sequence
Nucleic Acid Accession #: NM_014420
Coding sequence: 118..792

1 11 21 31 41 51
55 GCACGAGAGA CGACGTGCTG AGCTGCCAGC TTAGTGGAAG CTCTGCTCTG GGTGGAGAGC 60
AGCCTCGCTT TGGTGACGCA CAGTGCTGGG ACCCTCCAGG AGCCCCGGGA TTGAAGGATG 120
GTGGCGGCGG TCCTGCTGGG GCTGAGCTGG CTCTGCTCTC CCTGGGAGC TCTGTCTCTG 180
GACTTCAACA ACATCAGGAG CTCTGCTGAC CTGCATGGGG CCCGGAAGGG CTCACAGTGC 240
CTGTCTGACA CGGACTGCAA TACCAGAAAG TTCTGCCTCC AGCCCCGCGA TGAGAAGCCG 300
TTCTGTGCTA CATGCTGTGG GTTGGGAGG AGGTGCCAGC GAGATGCCAT GTGCTGCCCT 360
60 GGGACACTCT GTGTGAACGA TGTTTGACT ACGATGGAAG ATGCAACCCC AATATTAGAA 420
AGGCAGCTTG ATGAGCAAGA TGGCACACAT GCAGAAGGAA CAACTGGGCA OCCAGTCCAG 480
GAAAACCAAC CAAAAGGAA GCCAAGTATT AAGAAATCAC AAGGCAGGAA GGGACAAGAG 540
GGAGAAAGTT GTCTGAGAAC TTTTGACTGT GGCCCTGGAC TTGTCTGTGC TCGTCATTTT 600
TGGACGAAAA TTTGTAAGCC AGTCCTTTT GAGGGACAGG TCTGCTCCAG AAGAGGGCAT 660
65 AAAGACACTG CTCAGCTCC AGAAATCTTC CAGCGTTGCG ACTGTGGCCC TGGACTACTG 720
TGTGGAAGCC AATTGACCAG CAATCGGCAG CATGCTCGAT TAAGAGTATG CCAAAAAATA 780
GAAAAGCTAT AAATATTTCA AAATAAGAA GAATCCACAT TGCAAAAAA AAAAAAATA 840
A

Seq ID NO: 628 Protein sequence
Protein Accession #: NP_055235

1 11 21 31 41 51
75 MVAAVLLGLS WLCSPLGALV LDFNNIRSSA DLEGARKGSO CLSDTDCNTR KFCIQPRDEK 60
PFCATCRGLR RRCQRDMCC PGTLCVNDVC TTMEATPIL ERQLDEQDGT HAEQTTGHPV 120
QENQPKRKPS IKKSQGRKGQ EGESCLRTFD CGPGLCCARH FWTICKPVL LEGQVCSRRG 180
HKDTAQAPBI FQRCDGPGI LCRSQTLSNR QHARLRVOQK IEKL

Seq ID NO: 629 DNA sequence
Nucleic Acid Accession #: NM_002448.1
Coding sequence: 241..1134

1 11 21 31 41 51

	GGCGAGTGC	TCCCGGGAAC	TCTGCTGCG	CGGCGGCAGC	GACCGGAGGC	CAGGCCCAGC	60
	ACGCCCGGAGC	TGGCTCTGCTG	GGGAGGGGCG	GGAGGCGGCG	GCGGGAGGGT	CCGCCCGGCG	120
	AGGCCCGCGG	CCCTCGCAGA	GGCGGCGCG	GCTCCAGCC	CGCCCGGAGC	CCATGCCCGG	180
5	CGGCTGCGCA	GTGCTGCGCG	AGAAGGGGGG	GCCCGGCTCT	GCAATGGCCCC	GGCTGCTGAC	240
	ATGACTTCTT	TGCCACTCGG	TGTCAAAGTG	GAGGACTCG	CCTTCGGCAA	GCGGCGGGG	300
	GGAGGGCGCG	GCCAGGCCCC	CAGCGCCGCG	GCGGCCACGG	CAGCGCCCAT	GGGCGCGGAC	360
	GAGGAGGGGG	CAAAGCCCAA	AGTGTCCCTT	TGCTCTCTGC	CCTTCAGCGT	GGAGGGCGTC	420
	ATGGCCGACC	ACAGGAAGCC	GGGGGCCAAG	GAGAGCGGCC	TGGCGCCCTC	CGAGGGCGTG	480
10	CAGGCGGCGG	GTGCTCGCG	GCAGCCACTG	GGGCTCCGCG	CGGGTGGCT	GGGAGCCCGG	540
	GACGCGCCCT	CTTGGCGCGG	GCCGCTCGGC	CATTCTCGG	TGGGGGGAAT	CCTCAAGCTG	600
	CCAGAAGATG	CGCTCGTCAA	AGCCGAGAGC	CCGAGAGAGC	CCGAGAGGAC	CCCGTGGATG	660
	CAGAGCCCCC	GCTTCTCCCC	GCGCGCGGCC	AGCGGGCTGA	GCCCCCAGC	CTGCACCCCT	720
	CGCAACACAC	AGAGCAACCG	TAAGCGCGG	AGCCCTTCA	CCACCGCGCA	GCTGCTGGCG	780
15	CTGGAGCGCA	AGTTCGCCA	GAAGCAGTAC	CTGTCCATCG	CCGAGCGCGC	GGAGTCTCTC	840
	AGCTCGCTCA	GCCTCACTGA	GACGCGAGTG	AAGATATGCT	TCCAGAACCG	CCGCGCCAA	900
	GCAAGAGAGC	TACAGAGAGC	AGAGCTGGAG	AAGCTGAAGA	TGGCGGCCAA	GCCCATGCTG	960
	CCACCGGCTG	CCTTCGGGCT	CTCCTCCCT	CTCGCGGCGC	CCGACGCTGT	AGCGCGCGCG	1020
	GGGGTGGCT	CGCTCTACGG	TGCTCTGGC	CCCTTCCAGC	GCGCGCGGCT	GCCTGTGGCG	1080
20	CCCGTGGGAC	TCTACAGCGC	CCATGTGGGC	TACAGCATGT	ACCACCTGAC	ATAGAGGGTC	1140
	CCAGGTCCCC	ACCTGTGGGC	CAGCGGATTC	CTCCAGCCCT	GGTGTGTGAC	CCCCGACGTC	1200
	CTCCCGTGGT	CGGCAACCGC	AGCCGCGCTT	CCCTTAAACC	TCACTACTGT	CCAGTTTCAC	1260
	CTCTTTGCTC	CCTGAGTTCA	CTCTCCGAAG	TCTGATCCCT	GCCAAAGAGT	GGCTGGGAAG	1320
	GTCCCTTAGT	ACTCTTCTAG	CATTAGATC	TACACTCTCG	AGTTAAAGAT	GGGGAAGCTG	1380
25	AGGGCAGAGA	GGTTAACAGA	TTTATCTAGG	GTCCCGCAGA	GAATTGACAG	TTGAACAGAG	1440
	CTAGAGGCCA	TGCTCTCTGC	ATAGCTTTTC	CCTGTCTCTG	CACAGGCGAA	GAAAGCGCA	1500
	GAGAAATCGG	TGCTGACAGA	TTTGGGAAAT	GAGAACATCT	TCAAAAAAAA	AAAAAAAATA	1560
	AAAAAATAAA	GAAAGAGGAA	AAAAAGACT	AGCCAGCCAG	GAAGATGAAT	CCTAGCTTCT	1620
30	TCCATTGGAA	AATTTAAGAC	AAGTTCAACA	ACAAACATT	TGCTCTGGGG	GCGAGGAAAA	1680
	ACACAGATGT	GTTCGAAAGG	TAGGTTGAAG	GGA			

Seq ID NO: 630 Protein sequence
Protein Accession #: NP_002439.1

	1	11	21	31	41	51	
	MTSLPLGVKV	EDSAFGKPG	GGAGQAPSAA	AATAAAMGAD	EEGAKPKVSP	SLLPFSVEAL	60
	MADHRKPKAK	ESALAPSBGV	QAAGGSAQPL	GVPPGSLGAP	DAPSSPRPLG	HPSVGGLLKL	120
	PEDAIVKAES	PEKPERTPMW	QSPRPSPPFA	RRLSPFPACT	RKEKTNKPR	TPFTTAQLLA	180
40	LERKPRQKQY	LSIAERAEPF	SSLSLTETQV	KINPQNRRAK	AKRLQAELE	KLKMAAKPML	240
	PPAAGPLSFP	LGGPAVAAA	AGASLYGASG	PFQRAALFVA	PVGLYTAHVQ	YSMYHLT	

Seq ID NO: 631 DNA sequence
Nucleic Acid Accession #: NM_002557.1
Coding sequence: 13..2049

	1	11	21	31	41	51	
	CAGACCATG	AGATGTGGAA	GCTGTGCTG	TGGGTGGGG	TGGTCTTGT	GCTGAAACAC	60
50	CAGATGGTG	CTGCCCATAA	ACTCGTGTGT	TATTTACCA	ACTGGGCACA	CAGTCGCCCA	120
	GGCCCTGCTC	CGATCTTGCC	CCATGACCTG	GACCCCTTTC	TCTGCACCCA	CCTGATATTT	180
	GCCTTTGCTC	CAATGAACAA	CAATCAGATT	GTGCTAAGG	ATCTCCAGGA	TGAGAAAAAT	240
	CTCTACCCAG	AGTTCAACAA	ACTAAAGGAG	AGGAACAGAG	AGCTGAAACAC	ACTACTGTCC	300
	ATCGGCGGGT	GGAACTTTGG	CACCTCAAGA	ITCACCCTA	TGTTGTCCAC	ATTGCGCAAC	360
55	CGTGAAGAGT	TTATTTGCTT	AGTTATATCC	CTTCTGAGGA	CACATGACTT	TGATGTCTTT	420
	GACCTTTTCT	TCTTATATCC	TGGACTAAGA	GGCAGCCCCA	TGCTGACCGG	GTGGACTTTT	480
	CTCTTCTTAA	TGGAAGAGCT	CCTGTTTGCC	TTCGGAAGG	AGGCACTGCT	CACCATGGCG	540
	CCGAGGCTCG	TGCTGTCTGC	TGCTGTTTCT	GGGGTCCAC	ACATCGTCCA	AACATCCCTAT	600
	GATGTGCGCT	TCTAGGAAG	ACTCTGGAT	TTCATCAATG	TCTGTCTTAA	TGACTTACAT	660
60	GGAAGTTGGG	AAAGGTTTAC	AGGACATAAT	AGCCCGCTCT	TCTCTCTGCC	TGAAGACCCC	720
	AAATCTTGGG	CATATGCTAT	GAATATATGG	AGAAAGCTTG	GGGCACCCCT	AGAGAAGCTC	780
	ATCATGGGGA	TCCCCACCTA	TGGACGTACC	TTTCCCTTCC	TCAAAGCCTC	TAAGAATGGG	840
	TTGCAGGCCA	GAGCGATCGG	ACCAGCATCT	CCAGGGAAGT	ACACCAAGCA	AGAAGGCTTC	900
	TTGGCTTATT	TTGAGATTGG	TTCTTTTGTG	TGGGGAGGGA	AGAAGCACTG	GATTGATTAC	960
65	CAGTATGTCC	CGATATGCCAA	CAAGGGGAAA	GAGTGGGTTG	GCTATGACAA	TGCCATCAGC	1020
	TTCAATTACA	AGGCATGGTT	TATAAGGCGA	GAGCATTTTG	GGGGGGCCAT	GGTGTGGACA	1080
	TTGGACATGG	ATGACGTCAG	GGGCACTTTC	TGTGGCACTG	GCCCTTTCCC	CCTGTCTTAC	1140
	GTATTGAATG	ATATCCTGGT	GCGGGCTGAG	TTCAATTCAA	CTTCTTTACC	ACAATTTTGG	1200
	CTGTATCTCG	CTGTGAATTC	TTCAAGCACT	GACCTGAAA	GGCTGGCTGT	GACCAAGGCA	1260
70	TGGACCACTG	ATAGTAAGAT	TTTGCCCCCA	GGAGGAGAGG	CTGGGGTCAC	TGAGATCCAC	1320
	GGAAAGTGTG	AAATATGAC	TATAACCCCT	AGAGGTACAA	CTGTGACCCC	TACAAAGGAA	1380
	ACTGTATCCC	TTGGAAGGCA	CACGTGAGCT	CTAGGAGAGA	AGACTGAGAT	CCTGGGGGCA	1440
	ATGACCATGA	CTTCTGTGGG	TCACTAGTCC	ATGACCCCTG	GAGAGAAAGC	CCTGACCCCT	1500
	GTGGGTCATC	AATCTGTGAC	CACGTGACAG	AAGACCCCTG	CCTCTGTGGG	TTATCAGTGT	1560
75	GTGACCCCTG	GGGAAAAGAC	CCTGACCCCT	GTGGGTGATC	AGTCTGTGAC	CCCTGTGAGT	1620
	CATCAGTCTG	TGAGCCCTGG	AGGAACGACT	ATGACCCCTG	TCCATTTTCA	GACTGAGACC	1680
	CTTAGACAGA	ATACAGTGCG	CCCTAGAAGG	AAGGCTGTGG	CCCGTGAAGA	GCTGACTGTC	1740
	CCCTCCAGAA	ACATATCAGT	CACCCCTGAA	GGGCAGACTA	TGCTTTTAA	AGGGGAGAGT	1800
	TGTACTTCTG	AGGTGGGCAC	TCAACCCAGG	ATGGGTAAT	TGGGCTCTCA	GATGGAAGCT	1860
80	GAAACACAGG	TGATGCTGTC	CTCCAGCCCC	GTCATCCAGC	TCCCGGAACA	AACTCCTCTA	1920
	GCTTTTGACA	ACCGCTTTGT	TCCATCTAT	GGAAACCAAT	CCTCTGTCAA	CTCAGTAACC	1980
	CCTCAACAAA	GCTCTCTTTC	TCTAAAAAAA	GAAATCCCA	AAACTCTGCG	TGTGGATGAA	2040
	GAAGCCTAAG	CCCTCTGGT	GTCAGAAACC	AGGGAACACC	CTTGTCTTTT	CTTCTAAGTG	2100
	ACATGTTGGA	AGCCTTCTCA	TCCCGGGGCA	AAGCAGGCAT	CAAAACCA	ATAGGCCAAT	2160

CTCTTTTCCA TTAAATAAAC TGTAACACA AGAACCCA

Seq ID NO: 632 Protein sequence
Protein Accession #: NP_002548.1

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1	11	21	31	41	51	
MMKLLLVVGL	VLVLKHHGDA	AHKLVCYPTN	WAHSRPGPAS	ILPHDLDPFL	CTHLIPAPAS	60
MNNNQIVAKD	LQDEKILYPE	FNKLKERNRE	LKTLLSIGGN	NFGTSRFTTM	LSTFANREKF	120
IASVISLLRT	HDFTGLDLFP	LYPGLRGSPM	HDRTWFLFLI	EELLFAPRKE	ALLTMRPRL	180
LSAAVSGVPH	IVQTSYDVRF	LGRLLDPINV	LSYDLHGWSW	RPTGHNSPLF	SLPEDPKSSA	240
YAMNYWRKLG	AFSEKLIMGI	PTYGRTFRL	KASKNGLQAR	AIGPASPGKY	TKQEGFLAYF	300
EICSPVWGAK	KHWIDYQYVP	YANKGKEWVG	YDNAISPSYK	ANFIRREHFG	GAMVWTLDM	360
DVRGTFPGTG	PPFLVYVLND	ILVRAEFSST	SLPQFWLSSA	VNSSSTDPER	LAVTTAWTTD	420
SKILPPGGEA	GVTEIHGKCE	NMTITPRGTT	VTPTKETVSL	GKHTVALGEK	TEITGAMTMT	480
SVGHQSMTPG	EKALTYPVGHQ	SVTTGQKTLT	SVGYQSVTPG	EKTLTFVGHQ	SVTPVSHQSV	540
SPGGTMTTPV	HFQTEILRQN	TVAPRRKAVA	REKVTVPSPN	ISVTPGQTM	PLRGNLTSE	600
VGTHPRMGNL	GLQMEAEENR	MLSSSPVIQL	PEQTPFLADN	RFVPIYGNHS	SVNSVTPQTS	660
PLSLKKEIPE	NSAVDEEA					

Seq ID NO: 633 DNA sequence
Nucleic Acid Accession #: NM_003885.1
Coding sequence: 98..1021

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1	11	21	31	41	51	
AAACTCAGAA	TTTTCGGGGG	CTCGGTGAGC	GGTTTATCC	CTCCGGCCGG	CAGGCTGGGC	60
GCAGGGGGCG	AGCCCCCGCC	CGCGCGCAG	CAGCACCATG	GGCAGCGTGC	TGTCCCTGTC	120
TCCAGCTAC	CGGAAGGCCA	CGCTGTTTGA	GGATGGCGCG	GCCACCGTGG	GCCACTATAC	180
GGCGGTACAG	AACAGCAAGA	ACGCCAAGGA	CAAGAACTCT	AAGCGCCACT	CCATCATCTC	240
CGTGCTGCCT	TGGAAGAGAA	TGCTGGCCGT	GTCGGCCAAG	AAGAAGAACT	CCAAGAAGGT	300
GCAGCCTAAC	AGCAGCTACC	AGAACAACAT	CACGCACCTC	AACAATGAGA	ACCTGAAGAA	360
GTCGCTGTCT	TGCGCCAACC	TGTCCACATT	CGCCAGCCCC	CCACCGGCCC	AGCCGCTGTC	420
ACCCCGGGCC	AGCCAGCTCT	CGGGTTCCCA	GACCGGGGGC	TCCTCCTCAG	TCAAGAAAGC	480
CCCTCACCT	GCCGTCACT	CCGCAGGGAC	GCCCAACCGG	GTCATCGTCC	AGCGGTCCAC	540
CAGTGAGCTG	CTTCGCTGCC	TGGGTGAGTT	TCTCTGCCGC	CGGTGCTACC	GCCTGAAGCA	600
CCTGTCCCCC	ACGGAACCCG	TGCTCTGGCT	GCGCAGCGTG	GACCGCTCGC	TGCTTCTGCA	660
GGGCTGGCAG	GACCAGGGCT	TCATCAAGCC	GGCCAACGTG	GTCTTCCTCT	ACATGCTCTG	720
CAGGATGTT	ATCTCCTCCG	AGGTGGGCTC	GGATCAAGAG	CTCCAGGCGG	TCCTGCTGAC	780
ATGCCTGTAC	CTCTCCTACT	CCTACATGGG	CAACGAGATC	TCCTACCGCG	TCAAGCCCTT	840
CCTGGTGGAG	AGCTGCAAGG	AGGCCTTTTG	GGACCGTTGC	CTCTCTGTCA	TCAACCTCAT	900
GAGCTCAAAG	ATGCTGCAGA	TAAATGCCGA	CCCACTACT	TTCAACACAG	TCTTCTCCGA	960
CCTGAAGAAC	GAGAGCGGCC	AGGAGGACAA	GAAGCGGCTC	CTCCTAGGCC	TGGATCGGTG	1020
AGCACTGTAG	CCTGCGTCAT	GGCTCAAGGA	TTCAATGCAT	TTTTAAGAAT	TTATTATTAA	1080
ATCAGTTTGT	TGTACAG					

Seq ID NO: 634 Protein sequence
Protein Accession #: NP_003876.1

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1	11	21	31	41	51	
MGTVLSLSPS	YRKATLPEDG	AATVGHYTA	QNSKNADKN	LKRHSIISVL	PWKRIYAVSA	60
KKQNSKKVQP	NSSYQNNITH	LNNENLKKSL	SCANLSTFAQ	PPPAQPPAPP	ASQLSGSQTG	120
GSSSVKKAPH	PAVTSAGTPK	RVIVQASTSE	LLRCLGEPLC	RRCYRLKHL	PTDFVLWLR	180
VDRSLLQGW	QDQGFITPAN	VVFLYMLCRD	VISSEVGS DH	ELQAVLLTCL	YLSYSYMGNE	240
ISYPLKPLV	ESCKEAFWDR	CLSVINLMSS	KMLQINADPH	YPTQVPSDLK	NBSGQEDKKR	300
LLGLDR						

TABLE 79A:

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	Seq ID No.:	Sequence identification number linking information in Table 79A to sequences in Table 80			
10	Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
15	424212	NM_005814	Hs.143131	glycoprotein A33 (transmembrane)	Seq ID No. C1 & C217
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID No. C2 & C218
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C3 & C219
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID No. C4 & C220
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID No. C5 & C221
20	443646	AI085198	Hs.164226	Thrombospondin 1	Seq ID No. C6 & C222
	409556	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	Seq ID No. C7 & C223
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	Seq ID No. C8 & C224
	444381	BE387335	Hs.283713	hypothetical protein BC014245	Seq ID No. C9 & C225
	421582	AI910275	Hs.350470	trifol factor 1 (breast cancer, estroge	Seq ID No. C10 & C226
25	411789	AF245505	Hs.72157	Adiccan	Seq ID No. C11 & C227
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	Seq ID No. C12
	428698	AA852773	Hs.334838	KIAA1866 protein	Seq ID No. C13 & C228
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	Seq ID No. C14 & C229
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	Seq ID No. C15 & C230
30	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	Seq ID No. C16 & C231
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	Seq ID No. C17 & C232
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	Seq ID No. C18 & C233
	418888	AU078801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	Seq ID No. C19 & C234
	432179	X75208	Hs.2913	EphB3	Seq ID No. C20 & C235
35	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	Seq ID No. C21 & C236
	409889	AW630041	Hs.56937	suppression of tumorigenicity 14 (colon	Seq ID No. C22 & C237
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C23 & C238
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	Seq ID No. C24 & C239
	411975	AI916058	Hs.144583	3'UTR of: dead ringer (Drosophila)-like	Seq ID No. C25 & C240
40	434206	AW136973	Hs.362915	ESTs, Weakly similar to S69890 mitogen I	Seq ID No. C26 & C241
	423936	U77629	Hs.135639	achaeta-scute complex (Drosophila) homol	Seq ID No. C27 & C242
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	Seq ID No. C28 & C243
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	Seq ID No. C29 & C244
	415214	AA455236	Hs.125124	EphB2	Seq ID No. C30 & C245
45	443247	BE614387	Hs.333893	c-Myc target JPO1	Seq ID No. C31 & C246
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	Seq ID No. C32 & C247
	410418	D31382	Hs.63325	transmembrane protease, serine 4	Seq ID No. C33 & C248
	446342	BE296665	Hs.14846	solute carrier family 7 (cationic amino	Seq ID No. C34 & C249
	411274	NM_002776	Hs.69423	kallikrein 10	Seq ID No. C35 & C250
50	104978	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	Seq ID No. C36 & C251
	422260	AA315993	Hs.105484	regenerating gene type IV	Seq ID No. C37 & C252
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KAA119	Seq ID No. C38 & C253
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	Seq ID No. C39 & C254
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	Seq ID No. C40 & C255
55	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	Seq ID No. C41 & C256
	422330	D30783	Hs.115263	epiregulin	Seq ID No. C42 & C257
	408908	BE296227	Hs.250822	serine/threonine kinase 15	Seq ID No. C43 & C258
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	Seq ID No. C44 & C259
	437852	BE001836	Hs.256897	putative GPCR	Seq ID No. C45 & C260
60	408243	Y00787	Hs.624	interleukin 8	Seq ID No. C46 & C261
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	Seq ID No. C47 & C262
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (fg,	Seq ID No. C48 & C263
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	Seq ID No. C49 & C264
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	Seq ID No. C50 & C265
65	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazarus	Seq ID No. C51 & C266
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	Seq ID No. C52 & C267
	442006	AW975183	Hs.372210	ESTs, Weakly similar to S72482 hypotheti	Seq ID No. C53 & C268
	413048	M93221	Hs.75182	mannose receptor, C type 1	Seq ID No. C54 & C269
	443324	R44013	Hs.164225	ESTs	Seq ID No. C55 & C270
70	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C56 & C271
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	Seq ID No. C57 & C272
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	Seq ID No. C58 & C273
	442652	AI005163	Hs.201378	Homo sapiens cDNA FLJ40427 fis	Seq ID No. C59 & C274
	450726	AW204600	Hs.355462	HUMPSPBA Human pulmonary surfactant-asso	Seq ID No. C60 & C275
75	416965	N26223	Hs.160436	MDAC1	Seq ID No. C61 & C276
	442275	AW449467	Hs.64795	Homo sapiens secretoglobulin, family 3A, m	Seq ID No. C62 & C277
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C63 & C278
	431745	AW972448	Hs.163425	Novel FGENESH predicted cadherin repeat	Seq ID No. C64 & C279
	453142	AA033648	Hs.7473	Homo sapiens gap junction protein, alpha	Seq ID No. C65 & C280
80	421659	NM_014459	Hs.106511	protocadherin 17	Seq ID No. C66 & C281
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	Seq ID No. C67 & C282
	421563	NM_006433	Hs.105806	granulysin	Seq ID No. C68 & C283
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	Seq ID No. C69 & C284
	414991	C17898		Homo sapiens up-regulated by BCG-CWS (LO	Seq ID No. C70 & C285
	419833	AA251131	Hs.220697	Homo sapiens tryptophanyl-tRNA synthetas	Seq ID No. C71 & C286
	424943	AU077260	Hs.153924	death-associated protein kinase 1	Seq ID No. C72 & C287

	430890	X54232	Hs.2699	glypican 1	Seq ID No. C73 & C288
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	Seq ID No. C74 & C289
	439180	AJ393742	Hs.199057	v-erb-b2 avian erythroblastic leukemia v	Seq ID No. C75 & C290
5	410407	X66839	Hs.63287	carbonic anhydrase IX	Seq ID No. C76 & C291
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	Seq ID No. C77 & C292
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	Seq ID No. C78 & C293
	430466	BE062109	Hs.241551	chloride channel, calcium activated, fam	Seq ID No. C79 & C294
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C80 & C295
10	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	Seq ID No. C81 & C296
	431846	BE019924	Hs.271580	uropod 1B	Seq ID No. C82 & C297
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	Seq ID No. C83 & C298
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter	Seq ID No. C84 & C299
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	Seq ID No. C85 & C300
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. C86 & C301
15	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. C87 & C302
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	Seq ID No. C88 & C303
	457819	AA057484	Hs.35406	FLJ20522 Hypothetical protein FLJ20522	Seq ID No. C89 & C304
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	Seq ID No. C90 & C305
	418462	BE001596	Hs.85266	integrin, beta 4	Seq ID No. C91 & C306
20	439606	W79123	Hs.58561	G protein-coupled receptor 87	Seq ID No. C92 & C307
	407720	AB037776	Hs.38002	immunoglobulin superfamily, member 9	Seq ID No. C93 & C308
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	Seq ID No. C94 & C309
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	Seq ID No. C95 & C310
25	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C96 & C311
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C97 & C312
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C98 & C313
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C99 & C314
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C100 & C315
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C101 & C316
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C102 & C317
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	Seq ID No. C103 & C318
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C104 & C319
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C105 & C320
35	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalini	Seq ID No. C106 & C321
	440659	AF134160	Hs.7327	claudin 1	Seq ID No. C107 & C322
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C108 & C323
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C109 & C324
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	Seq ID No. C110 & C325
40	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	Seq ID No. C111 & C326
	414774	X02419	Hs.77274	plasminogen activator, urokinase	Seq ID No. C112 & C327
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	Seq ID No. C113 & C328
	453857	AL080235	Hs.35861	Ras-Induced senescence 1 (RIS1)	Seq ID No. C114 & C329
	449101	AA205847	Hs.23016	G protein-coupled receptor	Seq ID No. C115 & C330
45	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	Seq ID No. C116 & C331
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	Seq ID No. C117 & C332
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	Seq ID No. C118 & C333
	408482	NM_000676	Hs.45743	adenosine A2b receptor	Seq ID No. C119 & C334
	426761	AI015709	Hs.172089	PORIMIN Pro-oncogene receptor inducing me	Seq ID No. C120 & C335
50	429736	AF125304	Hs.212680	tumor necrosis factor receptor superfam	Seq ID No. C121 & C336
	430985	AA490232	Hs.27323	ESTs, Weakly similar to I78885 serine/th	Seq ID No. C122 & C337
	431890	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID No. C123 & C338
	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	Seq ID No. C124 & C339
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	Seq ID No. C125 & C340
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	Seq ID No. C126 & C341
	428513	BE220806	Hs.184697	plexin C1	Seq ID No. C127 & C342
	430280	AA361258	Hs.237858	Interleukin 7 receptor	Seq ID No. C128 & C343
	428486	AW583497	Hs.184604	pancreatic polypeptide	Seq ID No. C129 & C344
	457489	AI693815	Hs.127179	cryptic gene	Seq ID No. C130 & C345
60	432874	W94322	Hs.279651	melanoma inhibitory activity	Seq ID No. C131 & C346
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C132 & C347
	445891	AW391342	Hs.199460	DPCR1 protein	Seq ID No. C133 & C348
	404682			ortholog of mouse polydomain protein	Seq ID No. C134 & C349
65	429547	AW009166	Hs.99376	FGENESH predicted novel secreted protein	Seq ID No. C135 & C350
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C136 & C351
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C137 & C352
	404287			FGENESH predicted novel CUB-domain conta	Seq ID No. C138 & C353
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	Seq ID No. C139 & C354
70	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	Seq ID No. C140 & C355
	432596	AJ224741	Hs.278461	matrilin 3	Seq ID No. C141 & C356
	444006	BE395085	Hs.334762	type I transmembrane protein Fn14	Seq ID No. C142 & C357
	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	Seq ID No. C143 & C358
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C144 & C359
	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	Seq ID No. C145 & C360
75	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	Seq ID No. C146 & C361
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	Seq ID No. C147 & C362
	422109	S73265	Hs.1473	gastrin-releasing peptide	Seq ID No. C148 & C363
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	Seq ID No. C149 & C364
	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	Seq ID No. C150 & C365
80	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	Seq ID No. C151 & C366
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	Seq ID No. C152 & C367
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	Seq ID No. C153 & C368
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	Seq ID No. C154 & C369
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	Seq ID No. C155 & C370

5	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	Seq ID No. C156 & C371
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	Seq ID No. C157 & C372
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	Seq ID No. C158 & C373
	413095	AA494359	Hs.30715	potassium voltage-gated channel, Isk-rel	Seq ID No. C159 & C374
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	Seq ID No. C160 & C375
	436729	BE621807	Hs.351316	transmembrane 4 superfamily member 1	Seq ID No. C161 & C376
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	Seq ID No. C162 & C377
	451820	AW058357	Hs.199248	ESTs	Seq ID No. C163 & C378
10	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	Seq ID No. C164 & C379
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	Seq ID No. C165 & C380
	421340	F07783	Hs.1369	decay accelerating factor for complement	Seq ID No. C166 & C381
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C167 & C382
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	Seq ID No. C168 & C383
15	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	Seq ID No. C169 & C384
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	Seq ID No. C170 & C385
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	Seq ID No. C171 & C386
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	Seq ID No. C172 & C387
	439659	AW970780	Hs.59483	leucine-rich repeat-containing G protein	Seq ID No. C173 & C388
20	411825	AK000334	Hs.352415	solute carrier family 39 (zinc transport	Seq ID No. C174 & C389
	412314	AA825247	Hs.356084	G protein-coupled receptor 27 (GPR27) (S	Seq ID No. C175 & C390
	429150	AF120103	Hs.197366	smoothed (Drosophila) homolog	Seq ID No. C176 & C391
	419073	AW372170	Hs.183918	transmembrane receptor Unc5H2 mRNA	Seq ID No. C177 & C392
	411828	AW181449	Hs.72290	wingless-type MMTV integration site fami	Seq ID No. C178 & C393
25	419508	AW997938	Hs.90786	ATP-binding cassette, sub-family C (CFTR	Seq ID No. C179 & C394
	421779	AI879159	Hs.108219	wingless-type MMTV integration site fami	Seq ID No. C180 & C395
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	Seq ID No. C181 & C396
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2 (str	Seq ID No. C182 & C397
	436972	AA284679	Hs.25640	claudin 3	Seq ID No. C183 & C398
30	410268	AA316181	Hs.61635	slx transmembrane epithelial antigen of	Seq ID No. C184 & C399
	416370	N90470	Hs.203697	CD38 antigen (p45)	Seq ID No. C185 & C400
	437052	AA861697	Hs.120591	ESTs	Seq ID No. C186 & C401
	421481	AW391972	Hs.104696	KIAA1324 protein	Seq ID No. C187 & C402
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	Seq ID No. C188 & C403
35	426174	AA547959	Hs.115838	Homo sapiens similar to Echinoidin (LOC1	Seq ID No. C189 & C404
	410037	AB020725	Hs.58009	KIAA0918 protein	Seq ID No. C190 & C405
	425071	NM_013989	Hs.154424	delodinsase, iodolthyronine, type II	Seq ID No. C191 & C406
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kn	Seq ID No. C192 & C407
	418576	AW968159	Hs.302740	Epithelial calcium channel 2, Cat-like A	Seq ID No. C193 & C408
40	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	Seq ID No. C194 & C409
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	Seq ID No. C195 & C410
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C196 & C411
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C197 & C412
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C198 & C413
45	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	Seq ID No. C199 & C414
	430144	AI732722	Hs.98927	ERGL protein; ERGIC-53-like protein	Seq ID No. C200 & C415
	408833	AW612232	Hs.254835	ESTs	Seq ID No. C201 & C416
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	Seq ID No. C202 & C417
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C203 & C418
50	415992	C05837	Hs.145807	hypothetical protein FLJ13593	Seq ID No. C204 & C419
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	Seq ID No. C205 & C420
	425976	C75094	Hs.334514	NG22 protein	Seq ID No. C206 & C421
	432800	BE391046	Hs.278962	AIM-1 protein	Seq ID No. C207 & C422
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	Seq ID No. C208 & C423
55	424339	BE257148	Hs.145416	endoglycan	Seq ID No. C209 & C424
	425283	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	Seq ID No. C210 & C425
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	Seq ID No. C211 & C426
	434293	NM_004445	Hs.3796	EphB6	Seq ID No. C212 & C427
	427715	BE245274	Hs.180428	KIAA1181 protein	Seq ID No. C213 & C428
60	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	Seq ID No. C214 & C429
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	Seq ID No. C215 & C430
	422424	AI186431	Hs.296638	prostate differentiation factor	Seq ID No. C216 & C431
	432378	AI493046	Hs.146133	ESTs	Seq ID No. C432 & C433
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	Seq ID No. C434 & C435

65 TABLE 79B

Pkey: Unique Eos probe set Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

70

Pkey CAT Number Accession
 414991 1785136_1 D78831 C17898 D78863

75 TABLE 79C

Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey Ref Strand NL_position

5

404682	9797231	Minus	40977-41150
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281
404287	2326514	Plus	53134-53281

Table 80:

Seq ID NO: C1 DNA Sequence
Nucleic Acid Accession #: NM_005814
Coding sequence: 345..1304

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	AGTAGGTGAC	ACATAGAGCC	AGCCCCAGCT	CACCTGCCAA	TCCAGCTGAG	GAGCTCACCT	180
	GCCAATCCAG	CTGAGGCTGG	GCAGAGGTGG	GTGAGAAGAG	GGAAAAATTGC	AGGGACCTCC	240
	AGTTGGGCCA	GGCCAGAAGC	TGCTGTAGCT	TTAACACAGC	AGCTCAGACC	TGCTCGGAGG	300
15	CTGCCAGTGA	CAGGTATAGT	TTAGGGCAGA	GAAGAAGCAA	GACCATGGTG	GGGAAGATGT	360
	GGCCTGTGTT	GTGGACACTC	TGTGAGTCA	GGGTGACCGT	CGATGCCATC	TCTGTGGAAG	420
	CTCCGACAGA	CGTTCTTGGG	GCTTGGCAGG	GAAGAGAGTG	CACCTGGCCC	TGCACTTACC	480
	ACACTTCCAC	CTCCAGTCCG	GAGGGACTTA	TTCAATGGGA	TAAGCTCCTC	CTCACTCATA	540
	CGAAAGGGGT	GGTCACTGAG	CGTCTTTCAA	ACAAAACTA	CATCCATGGT	GAGCTTTATA	600
20	AGAATTCGGT	CAGCATATCC	AACAATGCTG	AGCAGTCCGA	TGCCCTCATC	ACCAATTGATC	660
	AGCTGACCAT	GGCTGACAA	GGCAGCTACG	AGTGTTCGTG	CTCGCTGATG	TCAGACCTGG	720
	AGGGCAACAC	CAAGTCAAGT	GTCCGGCTGT	TGGTCTCGTG	GCCACCTCCC	AAACCAGAAT	780
	GCGGCATCGA	GGGAGAGACC	ATAATTGGGA	ACAACATCCA	GCTGACCTGC	CAATCAAAGG	840
	AGGGCTCACC	AACCCCTCAG	TACAGCTGGA	AGAGGTACAA	CATCCTGAAT	CAGGAGCAGC	900
25	CCCTGGCCCA	GGCAGCCTCA	GGTCAGCCTG	TCTCCCTGAA	GAATATCTCC	ACAGACACAT	960
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	TGGCCGTGAG	ATCTCCCTCC	ATGAACGTGG	CCCTGTATGT	GGGCATCGCG	GTGGGCGTGG	1080
	TTGCAGCCCT	CATTATCATT	GGCATCATCA	TCTACTGCTG	CTGCTGCCGA	GGGAAGGACG	1140
	ACAACACTGA	AGACAAGGAG	GATGCAAGGC	CGAACCGGGA	AGCCTATGAG	GAGCCACCAAG	1200
30	AGCAGCTAAG	AGAACTTTCC	AGAGAGAGGG	AGGAGGAGGA	TGACTACAGG	CAAGAAGAGC	1260
	AGAGAGAGC	TGGGCGTGAA	TCCCGGACCC	ACCTCGACCA	GTGACAGGCC	AGCAGCAGAG	1320
	GGCGGCGGAG	GAAGGGTTAG	GGGTTCAATC	TCCCGCTTCC	TGGCCTCCCT	TCTCCTTTCT	1380
	AAGCCCTGTT	CTCCTGTCCC	TCCATCCCAG	ACATTGATGG	GGACATTTCT	TCCCAGTGTG	1440
	CAGCTGTGGG	GAACATGGCT	GGCCTGGTAA	GGGGGTCCCT	GTGCTGATCC	TGCTGACCTC	1500
35	ACTGTCCGTG	GAAGTAACCC	CTCCTGGCTG	TGACACCTGG	TGCGGGCCTG	GCCCTCACTC	1560
	AAGACCAAGC	TGCAGCCTCC	ACTTCCCTCG	TAGTTGGCAG	GAGCTCCTGG	AAGCAGACGG	1620
	CTGAGCATGG	GGCGCTCCCA	CTCAGAACTC	TCCAGGGAGG	CGATGCCACG	CTTGGGGGGT	1680
	GGGGGCTGTC	CTGCTCACCT	GTGTGCCCCG	CACCTGGAGG	GGCACCAGGT	GGAGGGTTTG	1740
	CACCTCCAC	ATCTTTCTTG	AATGAATGAA	AGAATAAGTG	AGTATGCTTG	GGCCCTGCAT	1800
40	TGGCCTGAAC	TCCAGCTCCC	ACTCCCTTTC	CAACCTCACT	TCCCGTAGCT	GCCAGTATGT	1860
	TCCAAACCTC	CTTGGGAAGG	CCACCTCCCA	CTCCTGCTGC	ACAGGCCCTG	GGGAGCTTTT	1920
	GCCACACAC	TTTCCATCTC	TGCCCTGTCA	TATCGTACCT	GTCCCTCCAG	GCCCATCTCA	1980
	AATCACAGGG	ATTTCTCTAA	CCCTATCCCTA	ATTGTCCACA	TACGTGGAAA	CAATCCTGTT	2040
	ACTCTGTCCC	ACGTCCAATC	ATGGGCCACA	AGGCACAGTC	TTCTGAGCGA	GTGCTCTCAC	2100
45	TGTATTAGAG	CGCCAGCTCC	TTGGGGCAGG	GCCTGGGCTC	CATGGCTTTT	GCTTTCCCTG	2160
	AAGCCCTAGT	AGCTGGCGCC	CATCCTAGTG	GGCACAATAA	CTTAATTGGG	GAAACTGCTT	2220
	TGATTGGTTG	TGCCCTCCCT	TCTCTGGTCT	CCTTGAGATG	ATCGTAGACA	CAGGGATGAT	2280
	TCCACCCCAA	ACCCAGGTAT	TCATTCACTG	AGTTAAACAC	GAATTGATTT	AAAGTGAACA	2340
	CACACAAGGG	AGCTTGCTTG	CAGATGGTCT	GAGTCTCTGT	GTCTTGATTA	TTCTCTCCCA	2400
50	GGCCAGAATA	ATTGGCATGT	CTCCTCAACC	CACATGGGGT	TCCTGGTTGT	TCCTGCATCC	2460
	CGATACCTCA	GCCTGGGCCC	TGCCAGCCCC	ATTGGGGCTC	TGGTTTCTTG	GTGGGGCTGT	2520
	CCTGTGCCCC	TCCCAAGGCC	TCCTTCTGTT	TGTGAGGCAT	TTCTTCTACT	CTTGAGAGCT	2580
	CAGGGATGTT	TAGGGCTGCT	TAGGTCTCAT	GGACCAAGTG	CTGGTCTCAC	CCAAGTGCAG	2640
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55	TTGCCAATTT	TTAAAAAATG	TATATTTTGA	TATATATTGT	TAAATCCTTT	GCTTCAATCC	2760
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Seq ID NO: C2 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..3150

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	GGCTTCMACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGGAGTTTFA	CCGGCCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACCAGCCA	GCCAGGAGTG	CTGCAGGGTG	GTGCTGTCTA	CCTCTGTCTC	300
	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAAGG	CTCTCGGCTC	360
70	CTGGAGTCCT	CACGTGCCAG	CTCAGAGGGA	GAGGAGCCTG	TGGAGTACAA	GTCTTGCAG	420
	TGGTTCGGGG	CAACAGTTCC	AGCCCATGGC	TCCTCCATCT	TGGCATGGGC	TCCACTGTAC	480
	AGCTGGCGCA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCGGCT	CAGATTTTCA	CTGGGACGCA	600
	GGACAGGGTT	ACTGCCAAGG	AGGCTTCAGT	GCGGAGTTCA	CCAAGACTGG	CGGTGTGGTT	660
75	TTAGGTGGAC	CAGGAAGCTA	TTTCTGGCAA	GGCCAGATCC	TGCTGCGCAC	TACAGGACAG	720
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	CGCCAGGCCA	GTTCATCTTA	TGATGACAGC	TACCTAGGAT	ACTCTGTGGC	TGTTGGTGAA	840
	TTCAAGTGTG	ATGACACAGA	AGACTTTGTT	GCTGGTGTGC	CCAAGGGGAA	CCTCACTTAC	900
	GGCTATGTCA	CCATCTCTAA	TGGCTCAGAC	ATTGATTCCT	TCTACAACTT	CTCAGGGGAA	960
80	CAGATGGCCT	CCTACTTTGG	CTATGCAGTG	GCCGCCACAG	AGTCAATAGG	GGAGCGGCTG	1020
	GATGACTTGC	TGGTGGGGGC	ACCCCTGCTC	ATGGATCGGA	CCCTGTACGG	GCGGCTCAG	1080
	GAGGTGGGCA	GGGTCTACGT	CTACCTGCAG	CACCCAGCCG	GCATAGAGCC	CACGCCACCC	1140
	CTTACCTCCA	CTGGCCATGA	TGAGTTTGGC	CGATTTGGCA	GCTCCTTGAC	CCCCCTGGGG	1200
	GACCTGGACC	AGGATGGCTA	CAATGATGTG	GCCATCGGGG	CTCCCTTTGG	TGGGGAGACC	1260
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GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
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CTCAAGCCTC CAGCCACCTC TGATGCCTGA 3150

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Seq ID NO: C3 DNA Sequence

Nucleic Acid Accession #: NM_002421.2

Coding sequence: 1..1410

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GTTGAAAAAT TGAAGCAATG GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCCAGT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCGTGATG GGCTCAGTTT 300
GTCCTCACTG AGGGAAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360
TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCAATCTC 420
TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
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GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGTATGA CCCTAGCTAC 720
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Seq ID NO: C4 DNA Sequence

Nucleic Acid Accession #: Bos sequence

Coding sequence: 1..1410

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TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180
GTTGAAAAAT TGAAGCAATG GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCCAGT 240
GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCGTGATG GGCTCAGTTT 300
GTCCTCACTG AGGGGAAACC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360
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TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
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CTTGCTCATG CTTTTCACAC AGGCCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGCCCTC 660
GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGTATGA CCCTAGCTAC 720
ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
GGACGTTCCC AAAATCTCTG CAGCCCATC GGCCCAACAA CCCCAAAAGC ATGTGACAGT 840
AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAAG TGATGTTCTT TAAAGACAGA 900

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5 TTCTACATGC GCACAAATCC CTTCTACCCG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTTC 960
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Seq ID NO: C5 DNA Sequence
 Nucleic Acid Accession #: NM_014331.2
 Coding sequence: 1..1506

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Seq ID NO: C6 DNA Sequence
 Nucleic Acid Accession #: NM_003246.1
 Coding sequence: 112..3624

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	AATACCTGG	GCCCATATAG	CGACCCCATG	TACCGCTGCG	AGTGAAGGCC	TGGCTACGCT	2160
30	GGCAATGGCA	TCATCTCGGG	GGAGGACACA	GACCTGGATG	GCTGGCCCAA	TGAGAACCTG	2220
	GTGTGCGTGG	CCAATGCGAC	TTACCACTGC	AAAAAGGATA	ATTGCCCCAA	CCTTCCCAAC	2280
	TCAGGGCAGG	AAGACTATGA	CAAGGATGGA	ATTGGTGATG	CCTGTGATGA	TGACGATGAC	2340
	AATGATAAAA	TTCCAGATGA	CAGGGACAAC	TGTCCATTCC	ATTACAACCC	AGCTCAGTAT	2400
35	GACTATAGCA	GAGATGATGT	GGGAGACCGC	TGTGACAAC	GTCCCTACAA	CCACAACCCA	2460
	GATCAGGCAG	ACACAGACAA	CAATGGGGAA	GGAGACGCTT	GTGCTGCAGA	CATTGATGGA	2520
	GACGGTATCC	TCAATGAAAG	GGACAACCTG	CAGTACGCTT	ACAATGTGGA	CCAGAGAGAC	2580
	ACTGATATGG	ATGGGGTTGG	AGATCAGTGT	GACAATTGCC	CCTTGGAAAC	CAATCCGGAT	2640
	CAGCTGGAGT	CTGACTCAGA	CGCATTTGGA	GATACCTGTG	ACAACAATCA	GGATATTGAT	2700
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	GACCATGACA	AAGATGCGAA	GGGAGATGCC	TGTGACCACG	ATGATGACAA	CGATGGCATT	2820
	CCTGATGACA	AGGACAACCT	CAGACTCTGT	CCCAATCCCG	ACCAGAAGGA	CTCTGACGGC	2880
	GATGGTCCAG	GTGATGCTCG	CAAAAGATGAT	TTTGACCATG	ACAGTGTGCC	AGACATCGAT	2940
	GACATCTGTC	CTGAGAATGT	TGACATCAGT	GAGACCGATT	TCCGCGGATT	CCAGATGATT	3000
45	CCTCTGGAAC	CCAAAGGGAC	ATCCCAAAAT	GACCTTAAC	GGGTGTGACG	CCATCAGGGT	3060
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	AATGCTGTGG	ACTTCAGTGG	CACCTTCTTC	ATCAACACCG	AAAGGGACGA	TGACTATGCT	3180
	GGATTTTGCT	TTGGCTACCA	GTCCAGCAGC	CGCTTTTATG	TTGTGATGTG	GAAGCAAGTC	3240
	ACCCAGTCTT	ACTGGGACAC	CAACCCACG	AGGGCTCAGG	GATACTCGGG	CCTTCTGTGT	3300
50	AAAGTTGTAA	ACTCACCAC	AGGGCCTGGC	GAGCACTGCG	GGAAACGCGT	GTGGCACACA	3360
	GGAAACACCC	CTGGCCAGGT	GCGCACCTCG	TGGCATGACC	CTGCTCACAT	AGGCTGGAAA	3420
	GATTTCACCG	CCTACAGATG	GGGTCTCAGC	CACAGGCCAA	AGACGGGTTT	CATTAGAGTG	3480
	GTGATGTATG	AAGGGAAGAA	AATCATGGCT	GACTCAGGAC	CCATCTATGA	TAAAACTAT	3540
	GCTGGTGGTA	GACTAGGGTT	GTTTGTCTTC	TCTCAAGAAA	TGGTGTCTCT	CTCTGACCTG	3600
55	AAATACGAAT	GACTAGATCC	CTAATCATCA	AATTGTGAT	TGAAAGACTG	ATCATAAACC	3660
	AATGCTGGTA	TGCACTCTTC	TGGAACATG	GGCTTGAGAA	AACCCCGCAG	ATCACTTCTC	3720
	CTTGGCTTCC	TTCTTTTCTG	TGCTTGCACT	AGTGTGGACT	CCTAGAACGT	GCGACCTGCC	3780
	TCAAGAAAAAT	GCAGTTTTCA	AAAAACAGCT	CATCAGCATT	CAGCCTCCAA	TGAATAAGAC	3840
	ATCTTCCAA	CATATAAACA	ATTGCTTTGG	TTTCTTTTGG	AAAAAGCATC	TACTTGCTTC	3900
60	AGTTGGGAAG	GTGCCCATTC	CACCTGCGCT	TTGTACACAG	GCAGGGTGCT	ATTGTGAGGC	3960
	CATCTCT						3967

Seq ID NO: C7 DNA Sequence

Nucleic Acid Accession #: NM_002192

Coding sequence: 86..1366

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70	AATCACAACA	ACTTTTGCTG	CCAGGATGCC	CTTGTCTTGG	CTGAGAGGAT	TTCTGTGGC	120
	AAGTTGCTGG	ATTATAGTGA	GGAGTTCCCC	CACCCACAGGA	TCCGAGGGGC	ACAGCGCGGC	180
	CCCCAGACTG	CGGTCTCTGG	CGCTGGCCGC	CCTCCCAAG	GATGTACCCA	ACTCTCAGCC	240
	AGAGATGGTG	GAGGCGGTCA	AGAAGCACAT	TTTAAACATG	CTGCACCTGA	AGAAGAGACC	300
	CGATGTCAAC	CAGCCGGTAC	CCAAGGCGGC	GCTTCTGAAC	GCGATCAGAA	AGCTTCATGT	360
75	GGGCAAGTGC	GGGGAGAACG	GGTATGTGGA	GATAGAGGAT	GACATTGGAA	GGAGGGCAGA	420
	AATGAATGAA	CTTATGGAGC	AGACCTGGGA	GATCATCAGG	TTTGCQAGT	CAGGAACAGC	480
	CAGGAAGACG	CTGCACTTGG	AGATTTCCAA	GGAGGCAAGT	GACCTGTCTG	TGGTGGAGCG	540
	TGCAGAAATC	TGGCTCTTCC	TAAAAAGTCCC	CAAGGCCAAC	AGGACCAAGGA	CCAAAGTCAC	600
	CATCCGCTCT	TTCAGCAGC	AGAAGCACCC	CGAGGGCAGC	TTGGACACAG	GGGAAGAGGC	660
80	CGAGGAAGTG	GGCTTAAAGG	GGGAGAGGAG	TGAACTGTTG	CTCTCTGAAA	AAGTAGTAGA	720
	CGCTGGGAAG	AGCACCTGGC	ATGTCTTCCC	TGTCTCCAGC	AGCATCCAGC	GTTTGTCTGA	780
	CCAGGGCAAG	AGCTCCCTGG	ACGTTCCGAT	TGCTCTGTAG	CAGTGCAGCG	AGAGTGGGCG	840
	CAGCTTGGTT	CTCTTGGGCA	AGAAGAAGAA	GAAAGAAGAG	GAGGGGGAAG	GGAAAAAGAA	900
	GGGCGGAGGT	GAAGGTGGGG	CAGGAGCAGA	TGAGGAAAGG	GAGCACTGCG	ACAGACCTTT	960
	CCTCATGCTG	CAGGCCCGGC	AGTCTGAAGA	CCACCTCAT	CGCGGCGCTG	GGCGGGGCTT	1020

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GGAGTGTGAT GGCAAGGTCA ACATCTGCTG TAAGAAACAG TTCTTTGTCA GTTTCAGGA 1080
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GCCCACCAAG CTGAGACCCA TGTCCATGTT GTACTATGAT GATGGTCAAA ACATCATCAA 1320
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GGGGGAAAGG GAGCAAGAGT TGTCCAGAGA AGACAGTGGC AAAATGAAGA AATTTTAAAG 1440
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AGTTGTATAA ACGGGGTATT GTCTTTTCCC CCCTTGAGGT TCCCTTGTA GCTTGAATCA 1740
ACCAATCTGA TCTGCAGTAG TGTGGACTAG AACACCCAA ATAGCATCTA GAAAGCCATG 1800
AGTTTGAAGG GGCCCATCAC AGGCACTTTC CTAGCCTAAT 1840

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Seq ID NO: C8 DNA Sequence
Nucleic Acid Accession #: NM_000095.1
Coding sequence: 26..2299

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GCGGCAGCAG GTACAGGGAGA TCACGTTCTT GAAAAACACG GTGATGGAGT GTGACGCGTG 240
CGGGATGCAG CAGTCAGTAC GCACCGGCTT ACCCAGCGTG CGGCCCTTGC TCCACTGCGC 300
GCCCGGCTTC TGCTTCCCCG GCGTGGCGTG CATCCAGACG GAGAGCGGCG GCCCTGCGG 360
CCCTGTCCCC AAGTAAATTA CGGGCAACGG CTGCACTGTC ACCGACGTCA ACGAGTGCAA 420
CGCCCACCCC TGCTTCCCCG GAGTCCGCTG TATCAACACC AGCCCGGGGT TCCGCTGCGA 480
GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCAACAGGGC GTGGGCTGCG CTTCGCCCAA 540
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CCCCAATCTC GTGTGCATCA ACACCGGGGG CTCTTCCAG TGCGGCCGCT GCCAGCCCGG 660
CTTCGTGGGC GACCAGCGGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGACGG 720
CTGCGCCAGC GAGTGCCACG AGCATGCAGA CTGCGTCTTA GAGCGCGATG GCTCGCGGTC 780
GTGCGTGTGT CCGGTGGCTT GGGCCGCGAA CCGGATCCTC TGTGTGCGC ACACTGACCT 840
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CGTGACTGTG CCCAATCTAG GGCAGGAGGA TGTGGACCGC GATGCGATCG GAGACGCTG 960
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CGATCAAGAC CAGGATGGAG ACGGACATCA GGAATCTCGG GACAACTGTC CCACTGGTCC 1380
TAACAGTGCC CAGGAGGACT CAGACCAAGA TGGCCAGGGT GATGCTGCGC ACGACGAGA 1440
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CATGTGGAAG CAGATGGAGC AAACGTATTG GCAGGCGAAC CCCTTCCGTG TGTGGCGGA 1920
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CGCTCTGTGG CATAAGGAG ACACAGAGTC CCAAGTGCGG CTGCTGTGGA AGGACCGCG 2040
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AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG 2439

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Seq ID NO: C9 DNA Sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

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CGCTGCCCGG CAGCCGGGAG CCATGCGACC CCAGGCCCCC GCGGCTTCCC CGCAGCGGT 180
CGCGGGCTTC CTGCTGCTCC TGCTGCTGCA GCTGCGCGCG CGGTGAGGCG CCTCTGAGT 240
CCCCAAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATG 300
AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTGCAGAC GGGAGCCCTG GGGCCAAATG 360
CAITCCGGGT ACACCTGGGA TCCAGGTGCG GGATGGATTG AAAGGAGAAA AGGGGGAATG 420
TCTGAGGAAA AGCTTTGAGG AGTCTCTGAC ACCCACTAC AAGCAGTGT CATGAGTTT 480
ATTGAATTAT GGCATAGATC TTGGGAAAAA TGCGGAGTGT ACATTTACAA AGATGOGTT 540
AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAAAAAGCA GAAATGCGAT 600
CTGTGACGCT TGTATTTTCA CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTG 660
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TTCTCGCATC ATTATTGAAG AACTACCCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
TTTTTTTATT ATGCCTTGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
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TTTAAATCTA GCATTATTTA TTTTGTCTCA ATCAAAAGTG GTTTCATATAT TTTTCTTAGT 1080
TGGTGTAGAT ACTTCTCTCA TAGTCACATT CTCTCAACCT ATAATTTTGA ATATTGTTGT 1140
GGTCTTTTGT TTTTCTCTCT AGTATAGCAT TTTTAAAAAA ATATAAAAGC TACCAATCTT 1200
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CAACCTTAAA AAAAAAAAAA AAAA 1284

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Seq ID NO: C10 DNA Sequence
Nucleic Acid Accession #: NM_003225
Coding sequence: 41..295

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GACAGAGACG TGTACAGTGG CCCCCCTGGA AAGACAGAAT TGTGTTTTC CTGGTGTAC 180
GCCTCTCCAG TGTGCAAAAT AGGGCTGCTG TTTGAGCAGC ACCGTTCTGT GGGTCCCTCG 240
GTGCTTCTAT CCTAATACCA TCGACGTCCC TCCAGAAAGG GAGTGTGAAT TTTAGACACT 300
TCTGACGGGA TCTGCTGCA TCCTGACGGG GTGCCGTCCC CAGCACGGTG ATTAGTCCCA 360
GAGCTCGGCT GCCACCTCCA CCGGACACCT CAGACAGGCT TCTGCAGCTG TGCCTCGGCT 420
CACACACAGC ATTGACTGCT CTGACTTTGA CTACTCAAAA TTGGCCTAAA AATTAAAAAG 480
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Seq ID NO: C11 DNA Sequence
Nucleic Acid Accession #: NM_015419.1
Coding sequence: 1..8487

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AATTGGGGGT TTAATAGCAT ACAGGCCCTG TCAGAAACCT CATTGTCAGG ACTGACCAAG 240
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30 Seq ID NO: C12 DNA Sequence
Nucleic Acid Accession #: AK001903
Coding sequence: none

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Nucleic Acid Accession #: Kos sequence
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 25 GCGCCCATTT GCACCCCTGA GTTCTCTGAC GACCCTATCA AGCGGTGCAA GTCGGTGTGC 540
 CAACGCGCGC GCGACGACTG CGAGCCCTCT ATGAAGATGT ACAACCCAG CTGCGCCGAA 600
 AGCTCGGCTC GCGACGAGCT GCCTGTCTAT GACCGTGGCG TGTGCAATTC GCCTGAAGCC 660
 ATCGTCAACG ACCTCCCGAG GGATGTTAAG TGGATAGACA TCACACCAGA CATGATGGTA 720
 CAGGAAGGCG CTCTTGATGT TGACTGTAAA CGCCTAAGCC CGCATCGGTG CAAGTGTAAA 780
 30 AAGGTGAAGC CAACCTTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTCAATGC 840
 AAAATAAAG CTGTGCAAGG GAGTGGCTGC AATGAGGTCA CAACGGTGGT GGATGTAAAA 900
 GAGATCTTCA AGTCCCTCAT ACCCATCCCT CGAACTCAAG TCCCGCTCAT TACAAATTC 960
 TCTTGCCAGT TCCACACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTACGAGTGG 1020
 CGTTCAAGGA TGATGCTTCT TGAAAATTGC TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 35 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAA 1140
 AAGAAACAG CCGGGCGCAC CAGTCTAGT AATCCCCCA AACCAAGGG AAAGCCTCCT 1200
 GCTCCCAAC CAGCAGTCC CAAGAAGAAC ATTAACCTA GAGATGCCCA GAAGAGACA 1260
 AACCCGAAA GAGGTGAGC TAACTAGTTT CCAAGCGGA GACTTCCAG TTCCTTACAG 1320
 GATGAGGCTG GGCATTGCTT GGGACAGCCT ATGTAAGGCC ATGTCGCCCT TGCCCTAACA 1380
 40 ACTCATGCA GTGCTCTTCA TAGACACATC TTGAGCAATT TTTCTTAAG CTATGCTTCA 1440
 GTTTTCTTGT GTAAGCCATC ACAAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAAGT 1500
 GAGTTAAGC TGGTGGAAA GGCCTATTGC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560
 CTAGAAGAGT AGGGAATAA ATGCTTGTTA CAATTGCGAC TAATATGTGC ATTGTAAAA 1620
 45 AAATGCCATA TTTCAACAA AACACGTAAT TTTTTCAG TATGTTTTAT TACCTTTTGA 1680
 TATCTGTGTG TGCAATGTTA GTGATGTTT AAAATGTGAT GAAATATAA TGTTTTAA 1740
 AAGGAACAGT AGTGAATGA ATGTTAAAG ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800
 TTTTGTGAT GAAAGGGGAT TTTTGAAGA ATTAGAGAAG TAGCATATGG AAAATTATA 1860
 TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTATGCT AGAAACTTAA AAACAAAAAT 1920
 50 AATAATTAAG AAAATAAAT AAAAAGGAGA GGCAGACAAT GTCTGGATTC CTGTTTTTTG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC OCTCTTAAG AGCACCAGAA 2040
 ACAGTGAGTT TGTCTGTACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100
 ATTTTATACC CACAAGAGAG GTATGTCACT CATCTTACTT CCCAGGACAT CCACCTGAG 2160
 AATAATTTGA CAAGCTTAAA AATGSCCTTC ATGTGAGTGC CAAATTTTGT TTTTCTTACT 2220
 TAAATATTT TCTTTGCCCTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
 55 AAAGTTGAGT TCCACTCTG AAATGAGAAT TACTTGACAG TTGGGATAC TTAATCAGAA 2340
 AAAAAGAACT TATTGCAAGC ATTTTATCAA CAAATTTTCA AATTGTGGAC AATTGGAGGC 2400
 ATTTATTTTA AAAACAATTT TTTTGGCCT TTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 AGGCATTCAA TAAATGCACA ACGCCCAAAG GAAATAAAT OCTACTAAT CCTACTCTCC 2520
 ACTACACAGA GGTAACTACT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 60 GCACCTATTA TCAATTTGA ACAATAAATA CTAGGAACCT GTATACATGT GTTTTATAAC 2640
 CTGCTCCTTT TGCTTGGCCC TTTATTGAGA TAAATTTTCC TGTCAAGAAA GCAGAAACCA 2700
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 TATTGGATAC TTAGTGGTT TCTTCACTGA CAATACTGAA TAAACATCTC ACCGGAATTC 2820

65 Seq ID NO: C15 DNA Sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

70 1 11 21 31 41 51
 AAGCCAGCA GCGCCGGGCG GATGCTCTCC GCGCGCTCG CTCCGACGCG CGGCGCGCG 60
 CGCCTCTCTG CCGCCGATGC TGCTGCTGCT GCTCCAGCG CGCGCGCTGC TGGCCCGGGC 120
 TCTGCGCGCG GAGCTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCGGCAATGC 180
 AGCCTGCGCC AGTAGCCCGG CACCTGCCCC TGCCACGCG GAGCCCGCCC GGCCTGCCAG 240
 75 CAGCTCGAG CTCCCGCT GTGGGCTGCC GACCCATCT GATGGCTGA GTGCCCGCA 300
 CCGACAGAAG AGGTCTGTGC TTTCTGGCG GCGCTGGAG AAGACGGACC TCACCTACAG 360
 GATCCTTGG TTCCATGGC AGTTGGTGCA GGAGCAGGT CGGCAGACGA TGGCAGAGGC 420
 CCTAAAGGTA TGGAGCGATG TGACGCACT CACCTTACT GAGGTGCAOG AGGGCCGTGC 480
 TGACATCATG ATGACTTTCG CCAGGTAAGT GCATGGGAC GACCTGCGGT TTGATGGGCG 540
 80 TGGGGGATC CTGGCCATG CTTCTTCCC CAAGACTCAC CGAGAAGGG ATGTCCACT 600
 CGACTATGAT GAGACCTGGA CTATCGGGA TGACCAGGC ACAGACCTGC TGCAGGTGCG 660
 AGCCCATGAA TTTGGCCACG TGCTGGGCT GCAGCACACA ACAGCAGCA AGGCCCTGAT 720
 GTGCGCGTAC TACACCTTTC GCTACCACT GAGTCTCAG CCAGATGACT GCAGGGGCGT 780
 TCAACACTTA TATGGCCAGC CTGGCCAC TGTCACTTCC AGGACCCAG CCTGGGCC 840
 CCAGGCTGGG ATAGACACCA ATGAGATTGC ACCGCTGGAG CCGAAGCCCG CGCCAGATGC 900

5 CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCOGAGGC GAGCTCTTTT TCTTCAAAGC 960
 GGGCTTTGTG TGGGCGCTCC GTGGGGGCCA GCTGCAGCCC GGCTACCCAG CATTGGCCCTC 1020
 TCGCCACTGG CAGGGAAGTG CCAGCCCTGT GGAAGCTGCC TTGAGGATG CCCAGGGGCA 1080
 CATTGTGTTT TTCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCCCTGG 1140
 CCCCACACCC CTCACCGAGC TGGGCTGGT GAGGTTCCCG GTCCATGCTG CCTTGGTCTG 1200
 GGGTCCCGAG AAGAACAAGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACACC 1260
 CAGCACCCGG CGTGTAGACA GTCCCGTGCC CCGCAGGGCC ACTGACTGGA GAGGGGTGCC 1320
 CTCTGAGATC GACGCTGCCT TCCAGGATGC TGATGGCTAT GCCTACTTCC TGGCGGGCCG 1380
 CCTCTACTGG AATCTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGTCTCGT 1440
 10 GGGTCTCTGAC TTCTTTGGCT GTGCCGAGCC TGCCAACACT TTCTCTGAC CATGGCTTGG 1500
 ATGCCCTCAG GGGTGTGAC CCCTGCCAGG CCACGAATAT CAGGCTAGAG ACCCATGGCC 1560
 ATCTTTGTGG CTGTGGGCAC CAGGCATGGG ACTGAGCCCA TGTCTCCTGC AGGGGGATGG 1620
 GGTGGGGTAC AACCAACATG ACAACTGCCG GGAGGGCCAC GCAGGTCTGT GTCACTGCC 1680
 AGCGACTGTC TCAGACTGGG CAGGGAGGCT TTGGCATGAC TTAAGAGGAA GGCAGTCTT 1740
 15 GGGACCCGCT ATGCAAGTCC TGGCAAACTT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800
 GTAGCACCAT GGCAGGACTG GGGGAACATG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860
 TCCTTCCAGG GCTTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCCTT CAGCCCTGGC 1920
 TGAGCAACTG GCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTGTC 1980
 20 ATCTGTCTGC TTCTGGCTG ACAATCCTGG AAATCTGTTT TCCAGAATCC AGGCCAAAAA 2040
 GTTCACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGAGGGCTG 2100
 CAACATACCT CAATCTGTCT CCAGGCCGGA TCCTCCTGAA GCCTTTTTCG CAGCACTGCT 2160
 ATCCTCCAAA GCCATTGTAA ATGTGTATAC AGTGTGTATA AACCTTCTTC TTCTTTTTTT 2220
 TTTTAAACT GAGGATTGTC ATTAAACACA GTTGTTTTCT 2260

Seq ID NO: C16 DNA Sequence
 Nucleic Acid Accession #: NM_024022
 Coding sequence: 202..1563

30 1 11 21 31 41 51
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 ACCGGGCACC GAGCGGCTCG GGTACTTTGG TTCTTAATTA GGTCAATGCC GTGTGAGCCA 60
 GGAAGGGCT GTGTTTATGG GAAGCCAGTA ACACTGTGGC CTACTATCTC TTCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATAT GAGGTAGAGG TGGAGGCGGA GCGGATGTCT 180
 35 AGAGGTCTCG AAATAGTCAC CATGCGGGA AATGATCCGC CTGCTGTGA AGCCCCCTTC 240
 TCAATCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATGTGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTGG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 40 GAGGTCTCGG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT AGCAGAAATGT TGCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 45 TGTGCTCTG GCCAGTGGT TACCTTGACG TGCCACAGCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG CAGGGCCAGC 900
 CTTCAGTTCC AGGCTACCA CCTGTGCGGG GGTCTGTGCA TCACGCCCCT GTGGATCATC 960
 ACTGCTGAC ACTGTGTTTA TGACTGTGAC CTCCCAAGT CATGACCAT CCAGTGGGT 1020
 CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080
 50 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGGCGGGCCA 1140
 CTCAGTTCA ATGAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACCTTCCC 1200
 GATGAAAAG TGTCTGGAC GTCAAGATGG GGGGCCACAG AGGATGAGG TGACGCTCC 1260
 CCTGTCTGA ACCACGCGG CGTCCCTTTG ATTTCCAACA AGATCTGCAA CCACAGGAC 1320
 GTGTACGGTG GCATCATCTC CCGCTCCATG CTCTGCGCG GCTAOCCTGAC GGTGCGCTG 1380
 55 GACAGCTGCC AGGGGACAG CGGGGGGCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440
 TTATGTGGAG CGACAGCTT TGGCATCGGC TGGCAGAGG TGAACAAGCC TGGGGTGTAC 1500
 ACCCGTGTCA CTCTCTTCT GGAAGTGGAT CACAGACAGA TGGAGAGAGA CTTAAAAACC 1560
 TGAAGAGCAA GGGGACAAGT AGCCACCTGA GTTCTGAGG TGATGAAGAC AGCCGATCC 1620
 TCCCTGGAG TCCGTTGTAG GAACCTGCAC ACGAGCAGAC ACCCTTGGAG CTCTGAGTTC 1680
 60 CGGCACCAAT AGCAGGCCCG AAAGAGGCAC CCTTCCATCT GATTCCAGCA CAACCTTCAA 1740
 GCTGCTTTT GTTTTTTGT TTTTGTAGGT GAGTCTGCG TCTGTTGCC AGGCTGGAGT 1800
 GCAGTGGGGA AATCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTT 1860
 CCTCAGCTTC CCCAGTAGCT GGGACCAAG GTGCCGCGCA CCACACCCAA CTAATTTTGT 1920
 TATTTTATGT AGAGACAGGG TTTCACCATG TTGCCAGGC TGCTCTCAA CCCCTGACCT 1980
 65 CAATGATGT GCCTGCTTCA GCCTCCCAAG GTGCTGGGAT TACAGGCATG GGCACCAAG 2040
 CCTAGCCTCA CGCTCTTTC TGATCTTAC TAAGAACAAA AGAAGCAGCA ACTTGCAAG 2100
 GCGGCTTTC CCACTGGTCC ATCTGTTT CTCTCCAGGG GTCTTGCAA ATTCTGAGC 2160
 AGATAAGCAG TTATGTGACC TCAGTGCAA AGCCACCAAC AGCCACTCAG AAAAGACGCA 2220
 CCAGCCAGA AGTGAGAAC TGCACTCACT GCACGTTTC ATCTCTAGGG ACCAGAACCA 2280
 70 AACCCACCTT TTCTACTTCC AAGACTTAT TTCAATGTG GGGAGGTTAA TCTAGGAATG 2340
 ACTGTTTAA GGCCTATTT CATGATTTCT TTGTAGCAT TGGTCTTGA CGTATTATG 2400
 TCCTTGATT CCAATAATA TGTTCCTTC CCTCAAAAAA AAAAAAAA AAAAAAAA 2460
 AAAAA 2465

Seq ID NO: C17 DNA Sequence
 Nucleic Acid Accession #: NM_003220
 Coding sequence: 63..1376

80 1 11 21 31 41 51
 | | | | |
 GAATTCGGC TCTCTGGGTG AGAGACCGAG AGGGGCATAT CGTTCAAGC CGATCCATGA 60
 AAATGCTTTG GAAATGACG GATAATATCA AGTACGAGGA CTGCGAGGAC CGTCAAGGAG 120
 GCACACCAA CGGAGCGGCA CGGTGCCCC AGCTGGGCAC TGTAGGTTCA TCTCCCTACA 180
 CGAGCGCCCC GCGCTGTGCC CACACCCCA ATGCCGACTT CCAGCCCCCA TACTTCCCCC 240
 CACCTACCA GCCTATCTAC CCCAGTCCG AAGATCCTTA CTCCACGTC AACGACCCCT 300

5 ACAGCCTGAA CCCCCGAC GCCCAGCCGC AGCCGCAGCA CCCAGGCTGG CCGGCCAGA 360
 GGAGAGGCA GGAGTCTGGG CTCTGCACA CGCACCGGG GCTGCCTCAC CAGCTGTGG 420
 GCCTGGATCC TCCAGGGGAC TACAGGCGGC ACGAGGACCT CCTGCAOGGC CCACACGCGC 480
 TCAGCTCAGG ACTCGGAGAC CTCTCGATCC ACTCCTTACC TCACGCCATC GAGGAGGTCC 540
 CGCATGTAGA AGACCCGGGT ATTAACATCC CAGATCAAAC TGTAAATTAAG AAAGGCCCCG 600
 TGTCCCTGTC CAAGTCCAAAC AGCAATGCCG TCTCCGCCAT CCCTATTAAAC AAGGACRAAC 660
 TCTTGGCGGG CGTGGTGAAC CCCAACGAAG TCTTCTGTTT AGTTCCGGGT CGCCTCTCGC 720
 TCCTCAGCTC CACCTGGAAG TACAAGGTCA CGGTGGCGGA AGTGCAGCGG CGGCTCTCAC 780
 10 CACCGAGTG TCTCAACGGG TCGCTGCTGG GCGGAGTGCT CCGGAGGGCG AAGTCTAAAA 840
 ATGGAGGAAG ATCTTTAAGA GAAAAACTGG AAAAAATAGG ATTAATCTG CCTGCAGGGA 900
 GACGTAAGC TGCCAAACGTT ACCCTGTCTA CATCACTAGT AGAGGGAGAA GCTGTCCACC 960
 TAGCCAGGGA CTTTGGGTAC GTGTGCGAAA CCGAATTTC TGCCAAAGCA GTAGCTGAAT 1020
 TTCTCAACCG ACAACATTCC GATCCCAATG AGCAAGTGAC AAAAAAATC ATGCTCTCTG 1080
 15 CTACAAAAA GATATGCAAA GAGTTCACCG ACCTGCTGGC TCAGGACCGA TCTCCCCCTG 1140
 GGAATCTACG GCCCAACCCC ATCTTGGAGC CCGCATCCA GAGCTGCTTG ACCCACTTCA 1200
 ACCTCATCTC CCAGCGCTTC GGCAGCCCGG CGGTGTGTGC CGCGGTCAOG GCCCTGCAGA 1260
 ACTATCTCAC CGAGGCCCTC AAGGCCATGG AAAAAATGTA CCTCAGCAAC AACCCCAACA 1320
 GCCACAOGGA CAACAACGCC AAAAGCAGTG ACAAAGAGGA GAAGCAGAGA AAGTGAGGCT 1380
 20 CTCTCCCGC CCGCCCTCTC CACGCGCTCA CAGCCCGCCC GCGCGCCAC CCTCGGCGG 1440
 GTGACAGCTC CGGGATCAGC AACCCCTTCT GCTGTGCTGA CTGTGCTGCT TGCTGCGGCC 1500
 CGCCGCGCGC CGCTGCGCCT TGGGTCCCC CGAGTCTCCG GAGTGCCTT CTGACTGTC 1560
 AGTGGGGCAG CCTCTCGAC TCTGCACCCG CCTCGACCTC CCCACCCGT CCCACACCC 1620
 TGTGCCCCG GAATTC 1636

25 Seq ID NO: C18 DNA Sequence
 Nucleic Acid Accession #: NM_002988
 Coding sequence: 71..340

30 1 11 21 31 41 51
 CCGGCACGAG AGGAGTTGTG AGTTTCCAAG CCCAGCTCA CTCTGACCAC TTCTCTGCCT 60
 GCCCAGCATC ATGAAGGGCC TTGCAGCTGC CCTCCTGTGC CTGCTCTGCA CCATGGCCCT 120
 CTGCTCTGTG GCACAGTTG GTACCAACAA AGAGCTCTGC TGCCCTGTCT ATACCTCTCTG 180
 35 GCAGATTCCA CAAAAGTTCA TAGTTGACTA TTCTGAAACC AGCCCCCAGT GCCCAAGGCC 240
 AGGTGTATCC CTCTAAACCA AGAGAGGCCG GCAGATCTGT GCTGACCCCA ATAAGAAAGTG 300
 GGTCCAGAAA TACATCAGCG ACCTGAAGCT GAATGCCTGA GGGGCTTGA AGCTGCGAGG 360
 GCCCAGTGAA CTTGGTGGGC CCAGGAGGGA ACAGGAGCCT GAGCCAGGGC AATGGCCCTG 420
 CCACCTTGGA GGCCACCTCT TCTAAGAGTC CCATCTGCTA TGCCAGCCA CATTAACTAA 480
 40 CTTTAATCTT AGTTATGCA TCATATTTC TTTTGAATTT GATTTCATT GTTGAGCTGC 540
 ATTAAGAAAT TTGATTTTC TCTGACATCT CATGACATTG TCTTTATCAT CCTTCCCTCT 600
 TTCCCTTCAA CTCTCTGTAC ATTCAATGCA TGGATCAATC AGTGTGATTA GCTTCTCAG 660
 GCACATTTGT GCCATATGTA TCAATGACA AATCTTTATT GAATGGTTTT GCTCAGCACC 720
 ACCTTTAAAT ATATTGGCAG TACTTATTAT ATAAAAGGTA AACCAAGCAT CTCACGTGTA 780
 45 AAAAAAAAAA AAAAAAAAAA AAA 803

Seq ID NO: C19 DNA Sequence
 Nucleic Acid Accession #: NM_004063
 Coding sequence: 121..2619

50 1 11 21 31 41 51
 AGGGAGTGT CCGGGGGGAG ATACTCCAGT CGTAGCAAGA GTCTCGACCA CTGAATGGAA 60
 GAAAGGACT TTAAACCAAC ATTTTGTGAC TTACAGAAAG GAATTTGAAT AAAGAAAAC 120
 55 ATGATACTTC AGGCCCATCT TCACTCCCTG TGCTCTCTTA TGCTTTATTT GGCAACTGGA 180
 TATGGCCAGG AGGGGAAGTT TAGTGGAGCC CTGAAACCCA TGACATTTTC TATTTATGAA 240
 GGCCAGAAAC CGAGTCAAAT TATATTCCAG TTAAAGGCCA ATCTCTCTGC TGTGACTTTT 300
 GAACATAACT GGGAGACAGA CAACATATTT GTGATAGAAC GGGAGGACT TCTGTATTAC 360
 AACAGAGCCT TGGACAGGGA AACAGATCT ACTCACAATC TCCAGGTTCG AGCCCTGGAC 420
 60 GCTAATGGAA TTATAGTGGG GGGTCCAGTC CCTATCACC TAGAAGTGAA GGACATCAAC 480
 GACAAATGAC CCACGTTTCT CCAGTCAAAG TACGAAGGCT CAGTAAGGCA GAACCTCGC 540
 CCAGGAAAGC CCTTCTTGTA TGTCAATGCC ACAGACCTGG ATGATCCGGC CACTCCCAAT 600
 GGCCAGCTTT ATTACAGAT TGTCAATCCG CTTCCCATGA TCAACAATGT CATGTACTTT 660
 CAGATCAACA ACAAAACGGG AGCCATCTCT CTTACCCGAG AGGGATCTCA GGAATTGAAT 720
 65 CCTGCTAAGA ATCTTCTTA TAATCTGGTG ATCTCAGTGA AGGACATGGG AGGCCAGAGT 780
 GAGAAATCCT TCAGTGATAC CACATCTGTG GATATCATAG TGACAGAGAA TATTTGAAA 840
 GCACCAAAAC CTGTGGAGAT GGTGGAAAAC TCAACTGATC CTCACCCCAT CAAAATCACT 900
 CAGGTGCGGT GGAATGATCC CGGTGCACAA TATTCTTAG TTGACAAAGA GAAGCTGCCA 960
 70 AGATTCCCAT TTTCAATTGA CCAGGAAGGA GATATTTACG TGACTCAGCC CTTGGACCGA 1020
 GAAGAAAAGG ATGCATATGT TTTTATGCA GTTGCAAGG ATGAGTACGG AAAACCACTT 1080
 TCATATCCGC TGGAAATTC TGTAAAAGTT AAAGATATTA ATGATAATCC ACCTACATGT 1140
 CCGTACCAGG TAAACGATTT TGAGGTCCAG GAGAATGAAC GACTGGGTAA CAGTATCGGG 1200
 ACCCTTACTG CACATGACAG GAGTGAAGAA AATACTGCCA ACAGTTTCTT AAACACAGG 1260
 75 ATTGTGAGGC AAACCTCCAA ACTTCCCATG GATGGACTCT TCCTAATCCA AACCTATGCT 1320
 GGAATGTTAC AGTTAGCTAA ACAGTCCCTG AAGAAGCAAG ATACTCTCA GTACAACCTA 1380
 ACGATAGAGG TGCTGACAA AGATTTCAG ACCCTTTGTT TTGTGCAAT CAACGTTATT 1440
 GATATCAATG ATCAGATCCC CATCTTTGAA AAATCAGATT ATGGAAAACCT GACTCTTGCT 1500
 80 GAGACACAA ACATTGGGTC CACCATCTTA ACCATCCAGG CCACTGATGC TGTAGAGCCA 1560
 TTTACTGGGA GTTCTAAAAT TCTGTATCAT ATCATAAAGG GAGACAGTGA GGGACGCGCTG 1620
 GGGGTGACA CAGATCCCCA TACCAACACC GGATATGTCA TAATTAAAAA GCCTCTTGAT 1680
 TTTGAAACAG CAGCTGTTTC CAACATTGTG TTCAAAGCAG AAAATCCTGA CCCTCTAGTG 1740
 TTTGGTGTGA AGTACAAATG AAGTCTTTT GCCAAGTTCA CGCTTATGTG GACAGATGTG 1800
 AATGAAGCAG CTCATTTTTC CCAACACGTA TTCAAAGCGA AAGTCAGTGA GGATGTAGCT 1860
 ATAGGCACTA AAGTGGGCAA TGTGACTGCC AAGGATCCAG AAGGTCTGGA CATAACTAT 1920
 TCATGAGGGG GAGACACAG AGGTTGGCTT AAAATTGACC ACGTGACTGG TGAGATCTTT 1980

5	AGTGTGGCTC	CATTGGACAG	AGAAGCCGGA	AGTCCATATC	GGGTACAAGT	GGTGGCCACA	2040
	GAAGTAGGGG	GGCTTCCTTT	GAGCTCTGTG	TCAGAGTTCC	ACCTGATCCT	TATGGATGTG	2100
	ATGACAAACC	CTCCAGGCT	AGCCAAGGAC	TACACGGGCT	TGTTCTTCTG	CCATCCCCTC	2160
	AGTGCACCTG	GAAGTCTCAT	TTTCGAGGCT	ACTGATGATG	ATCAGCACTT	ATTTGGGGT	2220
	CCCCATTTTA	CATTTTCCCT	CGGCAGTGGG	AGCTTACAAA	ACGACTGGGA	AGTTTCCAAA	2280
	ATCAATGGTA	CTCATGCCCG	ACTGTCTACC	AGGCACACAG	AGTTTGAGGA	GAGGGAGTAT	2340
	GTGCTCTTGA	TCGCGATCAA	TGATGGGGGT	CGGCCACCTT	TGGAAGGCAT	TGTTTCTTTA	2400
	CCAGTTACAT	TCTGCAGTTG	TGTGGAAGGA	AGTTGTTTCC	GGCCAGCAGG	TCACCAGACT	2460
10	GGGATACCCA	CTGTGGGCAT	GGCAGTTGGT	ATACTGCTGA	CCACCTTCTT	GGTGATTGGT	2520
	ATAATTTTAG	CAGTTGTGTT	TATCCGCATA	AAGAAGGATA	AAGGCAAGA	TAATGTTGAA	2580
	AGTGCTCAAG	CATCTGAAGT	CAAACTCTCT	AGAAGCTGAA	TTTGAAAAGG	AATGTTTGAA	2640
	TTTATATAGC	AAGTGCTATT	TCAGCAACAA	CCATCTCATC	CTATTACTTT	TCATCTAACG	2700
	TGCAATTATA	TTTTTTAAAC	AGATATTCCC	TCTGTCTCTT	TAATATTTCG	TAAATATTTC	2760
15	TTTTTTGAGG	TGGAGTCTTG	CTCTGTGCGC	CAGGCTGGAG	TACAGTGGTG	TGATCCAGC	2820
	TCACCTGCAAC	CTCCGCTCTC	TGGGTTTACA	TGATTCTCCT	GCCTCAGCTT	CCTAAGTAGC	2880
	TGGGTTTACA	GGCACCCACC	ACCATGCCCC	GCTAATTTTT	GTATTTTFAA	TAGAGACGGG	2940
	GTTTCGCCAT	TTGGCCAGGC	TGGTCTTGAA	CTCCTGACGT	CAAGTGATCT	GCCTGCCCTG	3000
	GTCTCCCAAT	ACAGGCATGA	ACCACTGCAC	CCACCTACTT	AGATAATTCA	TGTGCTATAG	3060
20	ACATTAGAGA	GATTTTTCAT	TTTTCCATGA	CATTTTTCCT	CTCTGCAAA	GGCTTAGCTA	3120
	CTTGTTGTTT	TCCCTTTTGG	GGCAAGACAG	ACTCATTAAA	TATTCTGTAC	ATTTTTTCTT	3180
	TATCAAGGAG	ATATATCAGT	GTGTCTCAT	AGAACTGCCT	GGATTCCATT	TATGTTTTTT	3240
	CTGATTCCAT	CTGTGTCTCC	CTTCATCCTT	GACTCCTTTG	TGATTTCACT	GAATTTCAAA	3300
	CATTGTCTAG	AGAAGAAAAA	CGTGAGGACT	CAGGAAAAAT	AAATAAATAA	AAGAACAGCC	3360
25	TTTTCCCTTA	GTATTAAACAG	AAATGTTTCT	GTGTCAITAA	CCATCTTTAA	TCAATGTGAC	3420
	ATGTTGCTCT	TTGGCTGAAA	TTCTTCAACT	TGGAATGAC	ACAGACCCAC	AGAAGGTGTT	3480
	CAAAACCAAC	CTACTCTGCA	AACCTTGGTA	AAGGAACCA	TCAGCTGGCC	AGATTTCCTC	3540
	ACTACCTGCC	ATGCATACAT	GCTGCGCATG	TTTTCTTCAT	TGATATGTTA	GTAAAGTTTT	3600
30	GGTTATTATA	TATTTAACAT	GTGGAAGAAA	ACAAGACATG	AAAAGAGTGG	TGACAAATCA	3660
	AGAATAAACA	CTGTTGTAG	TCAGTTTGTG	TGTITAA			3697

Seq ID NO: C20 DNA Sequence
Nucleic Acid Accession #: NM_004443
Coding sequence: 28..3024

35	1	11	21	31	41	51	
	GGCTCGGCTC	CTAGAGCTGC	CACGGCCATG	GCCAGAGGCC	GCCCGCCGCC	GCCGCGGTGG	60
40	CCGCGCGCGG	GGCTTCTGCT	GCTGCTCCCT	CCGCTGCTGC	TGCTGCCGCT	GCTGCTGCTG	120
	CCCGCGCGCT	GCCGGGGGCT	GGAAGAGACC	CTCATGGACA	CAAAATGGGT	AACATCTGAG	180
	TTGGCGTGGG	CATCTCATCC	AGAAAGTGGG	TGGGAAGAGG	TGAGTGGCTA	CGATGAGGCC	240
	ATGAATCCCA	CCCGCACATA	CCAGGTGTGT	AATGTGCGCG	AGTCAAGCCA	GAACAACTGG	300
	CTTCGCACGG	GGTTCATCTG	GCGCGGGGAT	GTGCAGCGGG	TCTACGTGGA	GCTCAAGTTC	360
45	ACTGTGCGTG	ACTGCAACAG	CATCCCCAAC	ATCCCCGGCT	CCTGCAAGGA	GACCTTCAAC	420
	CTCTTCTACT	AGAGGGCTGA	CAGCGATGTG	GCCTCAGCCT	CCTCCCCCTT	CTGGATGGAG	480
	AACCCCTAAG	TGAAGTGGG	CACCAATTGA	CCCGATGAGA	GCTTCTCGCG	GCTGGATGCC	540
	GGCGGTGTCA	ACACCAAGGT	GCGCAGCTTT	GGGCCACTTT	CCAAGGCTGG	CTTCTACCTG	600
	GCCTTCCAGG	ACCAGGGGCG	CTGCATGTGG	CTCATCTCCG	TGCGCGCCTT	CTACAAGAAG	660
50	TGTGCAITCA	CCACCGCAGG	CTTCGCACTC	TTCCCCGAGA	CCCTCACTGG	GGCGGAGCCC	720
	ACCTCGCTGG	CATTTGCTCC	TGGCACCTGC	ATCCCTAACG	CGTGGAGGT	GTGCGTGCCA	780
	CTCAGCTCTT	ACTGCAACGG	CGATGGGGAG	TGGATGGTGC	CTGTGGGTGC	CTGCACCTGT	840
	GCCACCGGCC	ATGACGAGC	TGCCAAGGAG	TCCAGTGCCG	GCCCCGTGCC	CCCTGGGAGC	900
	TACAGGCGGA	AGCAGGGAGA	GGGGCCCTGC	CTCCCATGTC	CCCCCAACAG	CCGTACCACC	960
55	TCCCCAGCCG	CCAGCATCTG	CACCTGCCAC	AATAACTTCT	ACCGTGCGAG	CTCGGACTCT	1020
	GGGACAGATG	CCCTGTACCA	CGTGCCATCT	CCACCCCGAG	GTGTGATCTC	CAATGTGAAT	1080
	GAAACCTTAC	TGATCTCTGA	GTGGAGTGAG	CCCGGGGACC	TGGGTGGCCG	GGATGACCTC	1140
	CTGTACAAAT	TCATCTGCAA	GAAGTGCCAT	GGGGCTGGAG	GGGCCTCAGC	CTGCTCAACG	1200
	TGTGATGACA	ACGTGGAGTT	TGTGCCCTCG	CAGCTGGGCC	TGACGGAGCG	CCGGTCCAC	1260
60	ATCAGCCATC	TGCTGGCCCC	CACGCGCTAC	ACCTTTGAGG	TGCAGGCGGT	CACCGGTGTC	1320
	TGGGGCAAGA	GCCCTCTGCC	GCCTCGTTAT	GCGGCCGTGA	ATATCAACAC	AAACCAAGCT	1380
	GCCCCGTCTG	AAGTGCCCTC	ACTACGCGCT	CACAGCAGCT	CAGGCAGCAG	CCTCACCTTA	1440
	TCCTGGGCAC	CCCCAGAGCG	GCCCCAACGA	GTCTCTCTGG	ACTACGAGAT	GAAGTACTTT	1500
	GAGAAGAGCG	AGGGCATCGC	CTCCACAGTG	ACCAGCCAGA	TGAACCTCGT	GCAGCTGGAC	1560
65	GGGCTTTCGG	CTGACGCCCG	CTATGTGGTC	CAGGTCCGTC	CCCGCACAGT	AGCTGGCTAT	1620
	GGGCAGTACA	GCCGCGCTGC	CGAGTTTGAG	ACCACAAGTG	AGAGAGGCTC	TGGGGCCAG	1680
	CAGCTCCAGG	AGCAGCTTCC	CCTCATCTGT	GGCTCCGCTA	CAGCTGGGCT	TGCTCTCGTG	1740
	GTGGCTGTGC	TGGTCACTGC	TATGCTCTGC	CTCAGGAAGC	AGCGACACGG	CTCTGATTGG	1800
	GAGTACACGG	AGAAGCTGCA	GCAGTACATT	GCTCTCGGAA	TGAAGGTTTA	TATTGACCTT	1860
70	TTTACCTAAG	AGGACCTTAA	TGAGGCTGTT	CGGGAGTTTG	CCAAGGAGAT	CGAAGTGTCC	1920
	TGCGTCAAGG	TOGAGGAGGT	GATCGGAGCT	GGGGAATTGG	GGGAAGTGTG	CCGTGGTCTG	1980
	CTGAAACAGC	CTGGCCGCGG	AGAGGTGTTT	GTGGCCATCA	AGACGCTGAA	GGTGGGCTAC	2040
	ACCGAGAGGC	AGCGGCGGGA	CTTCTTAAGC	GAGGCCCTCA	TCTAGGCTCA	GTTTGTATCA	2100
	CCCAATATAA	TCCGGCTCTG	GGGCGTGGTC	ACCAAAAGTC	GGCCAGTTAT	GATCTCTACT	2160
75	GAGTTTCAAT	AAAACCTGCG	CCTGGACTCC	TTCTTCCGGC	TCAACGATGG	GCAAGTCTAG	2220
	GTCAATCCAG	TGGTGGGCTG	GTGCGGGGCT	ATTGCTGCGG	GCAATGAAGTA	CTCTGTCGAG	2280
	ATGAACATAT	TGCACCGCGA	CCTGGCTGCT	CGCAACATCC	TTGTCAACAG	CAACCTGGTC	2340
	TGCAAGCTGT	CAGACTTTGG	CCTCTCCGCG	TTCTGGAGG	ATGACCCCTC	CGATCCTACC	2400
	TACACCAAGT	CCCTGGGCGG	GAAGATCCCC	ATCCGCTGGA	CTGCCCCAGA	GGCCATAGCC	2460
80	TATCGGAAGT	TCACTTCTGC	TAGTGATGTC	TGGAGCTAAG	GAATTTGTAT	GTGGGAGGTC	2520
	ATGAGCTATG	GAGAGGAGCC	CTACTGGGAC	ATGAGCAACC	AGGATGTCTA	CAATGCGGTC	2580
	GAGCAGGATAT	ACCGGCTGCC	ACCAACCATG	GACTGTCCCA	CAGCACTGCA	CCAGCTCATG	2640
	CTGAGCTGCT	GGGTGCGGGA	CGGAAACCTC	AGGCCAAAT	TCTCCAGAT	TGTCAATACC	2700
	CTGGAACAAG	TCATCCGCAA	TGCTGCCAGC	CTCAAGGTCA	TTGCCAGCGC	TCACTCTGGC	2760
	ATGTCACAGC	CCCTCCTGGA	CCGACCGGTC	CCAGATTACA	CAACCTTCC	GACAGTTGGT	2820

5	GATTGGCTGG	ATGCCATCAA	GATGGGGCGG	TACAAGGAGA	GCTTCGTGAC	TGCGGGGTTT	2880
	GCATCTTTTG	ACCTGGTGGC	CCAGATGACG	GCAGAAGACC	TGCTCCGTAT	TGGGGTCACC	2940
	CTGGCGGGCC	ACCAGAAAGAA	GATCCTGAGC	AGTATCCAGG	ACATGCGGCT	GCAGATGAAC	3000
	CAGACGCTGC	CTGTGCAAGT	CTGACACCGG	CTCCACCGGG	GACCCTGAGG	ACCGTGACGG	3060
	GATGCCAAGC	AGCGGGCTGG	ACTTTCGGAC	TCTTGGACTT	TGGGATGCGT	GGCCTTAGGC	3120
	TGTGGCCAG	AAGCTGGAAG	TTTGGGAAAG	GCCCAAGCTG	GGACTTCTCC	AGGCCTGTGT	3180
	TCCCTCCCCA	GGAAGTGGCG	CCCAAACCTC	TTCATATTGA	AGATGGATTG	GGAGAGGGGG	3240
	TGATGACCCC	TCCCAAGGCC	CCTCAGGGCC	CAGACCTTCC	TGCTCTCCAG	CAGGGGATCC	3300
10	CCACAACCTC	ACACTTGTCT	GTTCTTCAGT	GCTGGAGGTC	CTGGCAGGGT	CAGGCTGGGG	3360
	TAAGCCGGGG	TTCCACAGGG	CCCAAGCCCTG	GCAGGGGTCT	GGCCCCCAG	GTAGGCGGAG	3420
	AGCAGTCCCT	CCCTCAGGAA	CTGGAGGAGG	GGACTCCAGG	AAATGGGAAA	TGTGACACCA	3480
	CCATCCTGAA	GCCAGCTTGC	ACCTCCAGTT	TGCACAGGGA	TTTGTCTCTG	GGGCTGAGGG	3540
	CCCTGTCCCC	ACCCCGCCCC	TTGGTGCTGT	CATAAAGGG	CAGCGAGGGG	CAGGCTGAGG	3600
15	AGTTGCCCTT	TGCCCCCAG	AGACTGACTC	TCAGAGCCAG	AGATGGGATG	TGTGAGTGTG	3660
	TGTGTGTGTG	TGTGGCGCGG	CGCGCGCGTG	TGTGTGTGCA	CGCACTGGCC	TGCACAGAGA	3720
	GCATGGGTGA	GCGTGTAAAA	GCTTGGCCCT	GTGCCCCACA	ATGGGGCCAG	CTGGGGCCGAC	3780
	AGCAGAATAA	AGGCAATAAG	ATGAA				3805

20 Seq ID NO: C21 DNA Sequence
Nucleic Acid Accession #: NM_001804
Coding sequence: 82..879

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	GCGGGGGACC	CCGCGGCCAC	CATGTATGTG	GGCTATGTGC	TGGACAAGGA	TTCCGCCGTG	120
	TACCCCGGCC	CAGCCAGGCC	AGCCAGCCTC	GGCTTGGGCC	CGGCAAACTA	CGGCCCCCCG	180
30	CGCCCGCCCC	CGCGCGCCCC	GCAGTACCCC	GACTTCTCCA	GCTACTCTCA	CGTGAGACCG	240
	GGCCCGCGCG	CCCGGAGGCG	CTGGGGGGCG	CCCTTCCCTG	CGCCCAAGGA	CGACTGGGCC	300
	GGCGCTACG	GGCCGGGCCC	CGCGGGCCCT	CGCGCCAGCC	CAGCTTGGCT	GGCATTGGGG	360
	CCCCCTCCAG	ACTTTAGCCC	GGTGCGGGCG	CCCCCTGGGC	CGGCCCCGGG	CCTCTGGGG	420
	CAGCCCTTCG	GGGGCCCGGG	CACACCGTCC	TGCGCCGGAG	CGCAGAGGCC	GAOCCCTTAC	480
35	GAGTGGATCG	GGCGCAGCGT	GGCGGCCGGA	GGCGCGGGTG	GCAGCGGTAA	GACTCGGACC	540
	AAGGACAAGT	ACCGCGTGGT	CTACACCGAC	CACCAAGGCC	TGGAGCTGGA	GAAGGAGTTT	600
	CATTACAGCC	GTTACATCAC	AAATCCGGCGG	AAATCAGAGC	TGGCTGCCAA	TCTGGGGCTC	660
	ACTGAAACGG	AGGTGAAGAT	CTGGTTCCAA	AAACGGCGGG	CAAGAGAGCG	CAAAAGTGAAC	720
	AAGAAGAAAC	AGCAGCAGCA	ACAGCCCCCA	CAGCGCCGGA	TGGCCACGGA	CATCAGGGCC	780
40	ACCCAGCGCG	GGCTATCCCT	GGGGGGGCTG	TGTCCAGCA	ACACCAAGCT	CCTGGCCACC	840
	TCCTCTCCAA	TGCTGTGAA	AGAGGAGTTT	CTGCCATAGC	CCCATGCCCA	GCCTGTGCGC	900
	CGGGGACCT	GGGAGCTCGG	GTGCTGGGAG	TGTGGCTCCT	GTGGGCCCGG	GAGGTCTGGT	960
	CGAGCTTCAG	CCCTTAGACCT	TCTGGGACAT	GGTGACAGT	CACCTATCCA	CCCTCTGCAT	1020
	CCCTCTGGCC	CATTGTGTGC	AGTAAGCCTG	TGGATAAAG	ACCTTCCAGC	TCCTGTGTTT	1080
45	TAGACCTCTG	GGGGATAAGG	GAGTCCAGGG	TGGATGATCT	CAATCTCCCG	TGGGCATCTC	1140
	AAGCCCCAAA	TGGTTGGGGG	AGGGGCTTAG	ACAAGGCTCC	AGGCCCCACC	TCCTCTCTCA	1200
	TACGTTTACA	GGTGCAGCTG	GAGGCTTGTG	TGGGAGCCAC	ACTGATCCTG	GAGAAAAGGG	1260
	ATGGAGCTGA	AAAGATAGGA	ATGCTTGCA	AGCATGACCT	GAGGAGGGAG	GAAAGTGGTC	1320
	AACTCACAC	TGCTCTTCT	GCAGCCTCAC	CTCTACCTGC	CCCATCATTA	AGGGCACTGA	1380
50	GGCTTTCCTA	GGCTGGATAC	TAAGCACAAA	GCCCATAGCA	CTGGGCTCTG	ATGGCTGCTC	1440
	CAGTGGGTTA	CAGAATCACA	GCCCTCATGA	TCATTCTCAG	TGAGGGCTCT	GGATTGAGAG	1500
	GGAGGGCCCT	GGAGGAGAGA	AGGGGGCAGA	GTCTTCCCTA	CCAGGTTTCT	ACACCCCGCG	1560
	CAGGCTGCC	ATCAGGGCCC	AGGGAGCCCC	CAGAGGACTT	TATTCGGACC	AAGCAGAGCT	1620
	CACAGCTGGA	CAGGTGTGTT	ATATAGAGTG	GAATCTCTTG	GATGCAGCTT	CAAGAAATAA	1680
55	TTTTTCTTCT	CTTTTCAAA					1699

Seq ID NO: C22 DNA Sequence
Nucleic Acid Accession #: NM_021978
Coding sequence: 36..2603

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	GCGGAGGGGG	CCGGAAGGAC	TTGGGGCGGG	GACTCAAGTA	CAACTCCCGG	CACGAGAAAG	120
65	TGAATGGCTT	GGAGGAAGGC	GTGGAGTTCC	TGCCAGTCAA	CAACGTCAAG	AAGGTGGAAG	180
	AGCATGGCCC	GGGGCGCTGG	GTGGTGCTGG	CAGCCGTGCT	GATCGGCTCT	CTCTGTGTCT	240
	TGCTGGGGAT	CGGCTTCTCT	GTGTGGCATT	TGCAGTACCG	GGAGTGTGCT	GTCCAGAAAG	300
	TCTTCAATGG	CTACATGAGG	ATCACAAATG	AGAAATTTGT	GGATGCTCTC	GAGAACTCCA	360
	ACTCCACTGA	GTTTGTAAAG	CTGGCCAGCA	AGGTGAAGGA	CGCGCTGAAG	CTGCTGTACA	420
70	GCGGAGTCCC	ATTCTGGGCG	CCCTACCAAC	AGGAGTCGGC	TGTGAAGGCC	TTGAGCGAGG	480
	GCAGCTCAT	CGCTACTTAC	TGGTCTGAGT	TCAGCATCCC	GCAGCACCTG	GTGGAGGAGG	540
	CCGAGCGCGT	CATGGCGGAG	GAGCGGCTAG	TCATGCTGCC	CCCGCGGGCG	CGCTCCCTGA	600
	AGTCTTTTGT	GGTCACTCTA	GTGGTGGCTT	TCCCCACGGA	CTCCAAAAAC	GTAACAGAGG	660
	CCAGAGACAA	CAGCTGCAGC	TTTGGCCTGC	ACGCGCGCGG	TGTGGAGCTG	ATGCGCTTCA	720
75	CCAAGCGCGG	CTTCCCTGAC	AGCCCTTACC	CCGCTCATGC	CCGCTGCCAG	TGGGCCCTGC	780
	GGGGGAGCGC	CGACTCAGTG	CTGAGCCTCA	CCTTCCGCGG	CTTTGACCTT	GCGTCTTGGG	840
	ACGAGCGCGG	CAGCGACCTG	GTGAGCGGTG	ACAACACCTT	GAGCCCCATG	GAGCCCCACG	900
	CCCTGTGCA	GTGTGTGGCG	ACCTACCTTC	CCTCTACAAA	CCTGACCTTC	CACCTCTCCC	960
	AGAACTTCTT	GCTCATCACA	CTGATAACCA	ACACTGAGCG	GCGGCATCCC	GGCTTTGAGG	1020
80	CCACTTCTTT	CCAGTGCCTT	AGGATGAGCA	GCTGTGGAGG	CCGCTTACGT	AAAGCCACGG	1080
	GGACATTCAA	CAGCCCCCTAC	TACCCAGGCC	ACTACCCACC	CAACATTGAC	TGCATGAGGA	1140
	ACATTGAGGT	GCCTCAACAC	CAGCATGTGA	AGGTGCGCTT	CAAAATCTTC	TACCTGTCTG	1200
	AGCCCGGGGT	GCTGCGGGCG	ACCTGCCCCA	AGGACTACGT	GGAGATCAAT	GGGGAGAAAT	1260
	ACTGCGGAGA	GAGGTCCACG	TTGGTCTGTA	CCAGCAACAG	CAACAAGATC	ACAGTTCGCT	1320
	TCCACTCAGA	TCAGTCTTAC	ACCGACACCG	GCTTCTTAGC	TGAATACCTC	TCCTACGACT	1380

5 CCAAGTGAACCC ATGCCCGGGG CAGTTCAAGT GCCGCAACGG GCGGTGTATC CGGAAGGAGC 1440
 TGCGCTGTGA TGGCTGGGCC GACTGCACCG ACCACAGCGA TGAGCTCAAC TGCAGTTGCG 1500
 ACGCCGGGCA CCAAGTTACG TGCAAGAACA AGTTCTGCAA GCCCCTCTTC TGGGTCTGCG 1560
 ACAGTGTGAA CGACTGGCGA GACAACAGCG ACGAGCAGGG GTGCAGTTGT CCGGCCAGAA 1620
 CCTTCAGGTG TTCCAATGGG AAGTGCTCTT CGAAAAGCCA GCAGTGCAAT GGGAAAGGACG 1680
 ACTGTGGGGA CCGGTCCGAC GAGGCCCTCT GCCCAAGGT GAACTGTGTC ACTTGTACCA 1740
 AACACACCTA CCGCTCCCTC AATGGGCTCT GCTTGAGCAA GGGCAACCTT GAGTGTGACG 1800
 GGAAGGAGGA CTGTAGCGAC GGCTCAGATG AGAAGGACTG CGACTGTGGG CTGCGGTGAT 1860
 10 TCACGAGACA GGCTCGTGT GTTGGGGGCA CGGATGCGGA TGAGGGCGAG TGGCCCTGGC 1920
 AGGTAAGCCT GCATGCTCTG GGCAGGGGCC ACATCTGCGG TGCTTCCTCC ATCTCTCCCA 1980
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 CCAAGCAGTG GACGGCCTTC CTGGGCTTGC ACGACCCAGG CCAGCGCAGC GCCCCTGGGG 2100
 TGCAGGAGCG CAGGCTCAAG CGCATCATCT CCCACCCCTT CTTCAATGAC TTACCTTGG 2160
 15 ACTATGACAT CGGCTGCTG GAGCTGGAGA AACGGGAGA GTACAGCTCC ATGGTGCGCG 2220
 CCATCTGCTT GCGGAGCGCC TCCCATGTCT TCCCTGCGG CAAGGCCATC TGGGTACCGG 2280
 CTGGGGGACA CACCCAGTAT GAGGAGCACTG GCGCGCTGAT CCTGCAAAAG GGTGAGATCC 2340
 GCGTCATCAA CACGACCAAC TGCGAGAACG TCCTGCGCGA GCAGATCAAC CCGCGCATGA 2400
 TGTGCGTGGG CTCTCTCAGC GCGCGCTGG ACTCCTGCCA GGTGTATTCC GGGGAGCCCC 2460
 20 TGTCCAGCGT GGAGGCGGAT GGGCGGATCT TCCAGGCCGG TGTGTGTAGC TGGGAGACG 2520
 GCTGCGCTCA GAGGAACAAG CCGAGCGTGT ACACAAGGCT CCCTCTGTTT CGGGACTGGA 2580
 TCAAGAGGAA CACTGGGGTA TAGGGGCGCG GGCACCCCAA ATGTGTACAC CTGCGGGGCC 2640
 ACCCATGCTA CACCCAGTGT TGCAAGCTGT CAGGCTGGAG ACTGGACCGC TGACTGCACC 2700
 AGCGCCCCCA GACATACAC TGTGAACCTA ATCTCCAGGG CTCCAAATCT GCCTAGAAAA 2760
 25 CCTCTGCTT CCTCAGCCTT CAAAGTGGAG CTGGGAGGTA GAAGGGGAGG ACACTGGTGG 2820
 TTCTACTGAC CCAACTGGGG GCAAAAGGTT GAAGACACAG CCTCCCGCGC CAGCCCCAAG 2880
 CTGGGCGGAG GCGCGTTTGT GTATATCTGC CTCCCTGTCT TGTAAAGAGC AGCGGGAACG 2940
 GAGCTTCGGA GCTCTCTCAG TGAAGGTGGT GGGGCTGCGG GATCTGGGCT GTGGGGCCCT 3000
 TGGGCGACGC TCTTGAGGAA GCCCAGGCTC GAGGAGCCCT GGAAACAGA CGGGTCTGAG 3060
 30 ACTGAAATG GTTTACCAGC TCCCAAGTGA CTTCAGTGTG TGTATTGTGT AAATGAGTAA 3120
 AACATTTTAT TTCTTTTAA AAAAAAAA 3149

Seq ID NO: C23 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2268

35 1 11 21 31 41 51
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 40 TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGAAGAT TTCAGCTGCC 120
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 AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTGT CCATCAGAGT CTGTGAGCGT 240
 CTGGAGATCA GCCCCAGAGG GGTCAAGATG GGAGCATTCC AGTTCAAGTT CACTCTCAT 300
 CTGGAATTCC CCTTGGATTG ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
 45 ATGGTTTTCA AAGGAGGGCG CAAGGAGACG GAACCTGCTC TGAATATCCT TCTGCACAGA 420
 GGGTTCCTCG GAGGACAGAA TGCTTCTGTG CCCCAGATCC TCATCATCGT CACTGATGGG 480
 AAGTCCAGCG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
 TTTGTGTGGG GGGTCAGGTT TCCAGGTGG GAGGAGCTGC ATGCACTGCG CAGCGAGCCT 600
 AGAGGCGAGC ACGTGTCTGT GGCTGAGCAG GTGGAGGATG CCAACCAAGG CCTCTTCAGC 660
 50 ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
 CCTGTGAGC ACAGGACGCT GGAGATGGTC CGGAGTTGCG CTGGCAATGC CCAATGCTGG 780
 AGAGGATCGC GCGGAGCCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
 AGAGTGTGCC TAAACCAACC TGCCACCTGC TACAGGACCA CCTGCCAGG CCCCTGTGAC 900
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 55 CTCTGCCCCG TGGCCTTTGG AGGGAGGCT AACTGTGCCC TGAAGCTGAG CTGGAATGC 1020
 AGGGTCGACC TCCTCTTCTT GCTGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCTGC 1080
 CGGCGCAAGG TCTTGTGTA GCGGTTTGTG CCGGCGGTGC TGAGCGAGGA CTCTCGGGCC 1140
 CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCTGTG GGGGAGTAC 1200
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 60 CTGACGGGCA GTGCTTGGC GCAGGCGGCA GAGCGTGGCT TCGGAGCGC CACCAAGACA 1320
 GGCCAGGACC GGCCACGTAG AGTGTGTGTT TTGCTCACTG AGTCACACTC CGAGGATGAG 1380
 GTTGCAGGCC CAGGCGCTCA CGCAAGGCGC CGAGAGCTGC TCCTGCTGGG TGTAGGCAGT 1440
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 65 CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTGTGCT TCATGTTGGA CACCTCTGCC 1620
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 70 GCGCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
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 GCGCGGAGAG GCGCAGAGGA TGACGCGGTT CCTGCCAGA AGCTGAGGAA CAATGGCATA 1980
 TCTGTCTTGG TGTGGGGCTT GGGGCTGTGC CTAAGTGAGG GTCTGCGGAG GCTTGCAGTT 2040
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 75 CTCAATGAGT GGTGTGTGG AGAAGCCAAG CGGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
 TGCATGAATG AGGGCAGCTG GTCCTGCAAG AATGGGAGCT ACCGCTGCAA GTGTGCGGAT 2220
 GGTGGGAGG GCCCCACTG CGAGAACCGA TTCTTGAGAC GCCCCTGA 2268

Seq ID NO: C24 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2424

80 1 11 21 31 41 51
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5	AGCAAAATGA	TGTGGTGTCT	GGCTGCAGTG	GACATCATGT	TTCTGTTAGA	TGGGTCTAAC	180
	AGCGTGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTTG	CCATCACAGT	CTGTGACGGT	240
	CTGGACATCA	GCCCGAGAG	GGTCAGAGTG	GGAGCATTCC	AGTTCAAGTTC	CACTCCTCAT	300
	CTGGAATTC	CTTTGGAATC	ATTTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
	ATGGTTTTCA	AAGGAGGGCG	CACGGAGACG	GAACCTTGCTC	TGAAATACCT	TCTGCACAGA	420
	GGGTTCGCTG	GAGGCAGAAA	TGCTTCTGTG	CCCCAGATCC	TCATCATCGT	CACTGATGGG	480
	AAGTCCACAG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
	TTTGCTGTGG	GGGTCAAGTT	TCCCAAGGTG	GAGGAGCTGC	ATGCACTGGC	CAGCGAGCCT	600
10	AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAACGG	CCTCTTCAGC	660
	ACCCCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCAGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
	CCCTGTGAGC	ACAGGAACCT	GGAGATGGTC	CGGGAGTTCC	CTGGCAATGC	CCCATGTCTG	780
	AGAGGATCCG	GGCGAACCTT	TGCGGTGCTG	GCTGCACACT	GTCCCTTCTA	CAGCTGGAAG	840
	AGAGTGTTC	TAAACCAACC	TGCCACCTGC	TACAGGACCA	CCTGCCACAG	CCCTGTGTAC	900
15	TCGCAGCCCT	GCCAGAAATG	AGGCACATGT	GTTCAGAAAG	GACTGGACGG	CTACCACTGC	960
	CTCTGCCCGC	TGGCTTTTGG	AGGGGAGGCT	AACTGTGCC	TGAAGCTGAG	CCTGGAATGC	1020
	AGGGTCGACC	TCTCTTCTCT	GCTGGACAGC	TCTGCGGGCA	CCAATCTGGA	CGGCTTCTCT	1080
	CGGGCCAAAG	TCTTCGTGAA	GCAGTTTGTG	CGGGCGGTGC	TGAGCGAGGA	CTCTGGGGCC	1140
	CGAGTGGGTG	TGGCCACATA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCCTGT	GGGGGAGTAC	1200
20	CAGGATGTGC	CTGATCTGGT	CTGGAGCCTC	GATGGCATTC	CCTTCCGTGG	TGGCCCAACC	1260
	CTGACGGGCA	GTGCCTTGGG	GCAGGCGGCA	GAGCGTGGCT	TGGGAGCGCG	CACCAAGACA	1320
	GGCCAGGACC	GGCCACGTAG	AGTGGTGGTT	TTGCTCACTG	AGTCACACTC	CGAGGATGAG	1380
	GTTCGCGGCC	CAGCGCGTCA	CGCAAGGGCG	CGAGAGCTGC	TCTCTGTGGG	TGTAGGCAGT	1440
	GAGGCGGTGC	GGGCAGAGCT	GGAGGAGATC	ACAGGCAGCC	CAAGCATGT	GATGGTCTAC	1500
25	TCCGATCCTC	AGGATCTGTT	CAACCAATC	CCTGAGCTGC	AGGGGAAGCT	GTGCAGCCGG	1560
	CAGCGGCCAG	GGTGCCGGAC	ACAAGCCCTG	GACCTCGTCT	TCATGTTGGA	CACCTCTGCC	1620
	TCAGTAGGGC	CCGAGAAATT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
	TTTGAGGTGA	ACCTTGACCT	GACACAGGTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCAG	1740
	ACTGCCTTGG	GGCTGGACAC	CAAAACCAAC	CGGGCTGCGA	TGCTGCGGGC	CATTAGCCAG	1800
30	GCCCCCTACC	TAGGTGGGGT	GGGCTCAGCC	GGCACCGCCC	TGCTGCACAT	CTATGACAAA	1860
	GTGATGACCG	TCCAGAGGGG	TGCCCGGCTT	GGTGTCCCA	AAGCTGTGGT	GGTGTCTACA	1920
	GGCGGAGAG	GCGCAGAGGA	TGCAGCGGTT	CCTGCCCAGA	AGCTGAGGAA	CAATGGCATC	1980
	TCTGTCTTGG	TCTGGGGCGT	GGGGCCTGTC	CTAAGTGAGG	GTCTGCGGAG	GCTTGCAGGT	2040
	CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCGGACC	TGCGGTACCA	CCAGGACGTG	2100
35	CTCATTTAGT	GGCTGTGTGG	AGAAGCCAAG	CAGCCAGTCA	ACCTCTGCAA	ACCCAGCCCG	2160
	TGCATGAATG	AGGGCAGCTG	CGTCTCTGAG	AATGGGAGCT	ACCGCTGCAA	GTGTGCGGAT	2220
	GGCTGGGAGG	GCCCCCACTG	CGAGAACCGT	GAGTGGAGCT	CTTGCTCTGT	ATGTGTGAGC	2280
	CAGGATGAGA	TCTTTAGAC	GCCCCGAGG	CACATGGCTC	CGGTGCAGGA	GGGCAGCAGC	2340
	GTACCCCTCT	CCAGCAACTA	CAGAGAAGGC	CTGGGCACCT	AAATGGTGCC	TACCTTCTGG	2400
40	AATGTCTGTG	CCCCAGGTCC	TTAG				2424

Seq ID NO: C25 DNA Sequence
Nucleic Acid Accession #: XM_097386.3
Coding sequence: 142..795

45	1	11	21	31	41	51	
	CTCGCAGAAC	CACCTGGACT	CTGTCCGTGT	CTGTCCCCCG	GCCTCCAGGG	CTCCTCTCCC	60
	GGGACCCCCG	TCCACAGCCT	GGGCCCCGCG	CGGGGGGAAG	CGCTGCTGCG	CTATCTCTGT	120
50	CTACCTCAGG	TCTGACTTTT	GATGCCAATA	TCTGAGCCCC	TGGGGTGCCT	CTCCCCCGCC	180
	TCCGTGTCAC	CAGGGTCTGC	AGCAGCCACT	GGGGCTTGCG	TGCTGTCTGC	ATCTGGCGGC	240
	CCTGGACCCC	TGGGGCCCCC	GTGCACCTGC	CCACCTCGGA	GCCTGGGGAG	GGGCGGTGCA	300
	GGGTGAGGGG	CTGGGTGCTG	TCCCTGCGGC	TGCGTGTGTG	TGTGCGGAAT	CCTGCGTGTG	360
	GTGTCTGTGG	GCGATCCGGG	TCCCGGCGCG	TGGGTGGACC	TGGATTCTAA	CTCAGAGGAC	420
55	TTGAGCCCTG	TGTTAACTCC	GATGATTGTA	GGGACAGGCG	GGGTGGGTGG	GGGGTGGGCG	480
	CGAGGCTGGG	TCCCGGCCCA	GGAGAAGGAA	GTGCTGAAG	GCACTGGCCA	TGCTGGCGGT	540
	GGAAATGGGA	GGCGGTTGCA	GAGGGTCTAT	GGGGCCCGGT	CCTGGATACT	CGGCAGGAAG	600
	CCGTGTCTGC	AGAGGCTCCT	CCCTGCTTCA	GGTGGCCCCG	TTCAACCCCA	GCGTGCCCA	660
	TCTCCTGCCA	CGGCTGTGCG	GTGGGGGTTT	AAATTCGGTG	TGGCTTCTGT	GGGTGCAGCT	720
60	CAGCACCCCC	CCTTATGCAG	ACTGGGAGGG	GGTGGGGCAG	TCCCTTCAGC	CAGAGGACC	780
	CTGGATGGGT	TCTAGTTCAC	TTGGGACCGT	GGGGCCTGCG	TGCGTACTGA	GTGGGTGCCC	840
	CACAGTCAAG	GCCAACGGGG	GCTCCCCCTG	CTCTGAGATG	TTGGGAGAAA	GGCGGCTTCT	900
	GGAACTCTCC	GTGGGACCCG	TAAAGTGGCT	TCCAGAAAGG	CGGGAGGGTG	GGCAGGGGGC	960
	ACGGGGGGCA	GCTGGGGTGG	TTGTTAAGGG	TACGCATCT	GTACAGTTGA	ATTTCCTTTT	1020
65	TCTTATCATG	TTTAAACCCAC	CTTGTCCCTT	TTTTCCCAAA	TTGTGCTTTT	GCATTTTTTT	1080
	CCTTGGCAAA	TGTAACCTCA	GCCTTTTATT	CATGACGTGT	GAAATTTTCA	TTTCTCTGGA	1140
	GTTTGTGAGA	CGGCGTGGGA	ACCACGCGCT	AAACTCAGGT	AATAGGAGGA	AAAAAATAAA	1200
	AACTTAAAAA	AATTTTAAAA	AAACATAAAA	CTACTCTCTA	CCTCTGGCTG	GGCCAGCCT	1260
	GTCTGCGCCT	GGCGCGGGCA	GGGTGGCGCT	TAACAATTTT	AGTTTTCGCA	GAACATTTCAG	1320
70	GTATTAAAAA	GAAAAA					1337

Seq ID NO: C26 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 95..2128

75	1	11	21	31	41	51	
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	CTCCTGGAAG	GGAGAGACAC	CAGCATTTGC	CACAAATGCTG	TCATCCACTG	ACTTTACATT	120
80	TGCTTCTCTG	GAGCTTGTGG	TCCGCGTTGA	CCATCCCAAT	GAAGAGCAGC	AGAAAGACGT	180
	CACACTGAGA	GTATCTGGAG	ACCTTCATGT	TGGAGGAGTG	ATGCTCAAGT	TAGTAGAACA	240
	GATCAATATA	TCCCAAGACT	GGTCAGACTT	TGCTCTTTGG	TGGGAACAGA	AGCATTTGCTG	300
	GCTTCTGAAA	ACCCACTGGA	CCCTGGACAA	ATATGGGGTC	CAGGCAGATG	AAAGCTTCT	360
	CTTACCCCT	CAGCATAAAA	TGCTGCGCCT	TCGTCTGCCG	AATTTGAAGA	TGGTGAAGTT	420
	GCGAGTCAGC	TTCTCAGCTG	TGGTTTTTAA	AGCTGTCACT	GATATCTGCA	AAATCTTGAA	480

5	TATTAGAAGA	TCAGAAGAGC	TTTCCTTGTT	AAAGCCGTCT	GGTGAATAIT	TTAAGAAGAA	540
	GAAGAAAAAA	GACAAAAATA	ATAAGGAACC	CATAATTGAA	GATATTCTAA	ACCTGGAGAG	600
	TTCTCCAACA	GCTTCAGGTT	CATCAGTAAG	TCCTGGTTTA	TACAGTAAAA	CCATGACCCC	660
	TATATATGAC	CCCATCAATG	GAACACCAGC	ATCATCCACC	ATGACTTGGT	TCAGTGACAG	720
	CCCTTTGACG	GAACAAAAC	GCAGCATCCT	CGCATTCAGC	CAACCCCCC	AGTCCCCAGA	780
	AGCACTTGGC	GATATGTACC	AGCCTCGGTC	TCTGTTGAT	AAAGCCAAGC	TCAATGCAGG	840
	TTGGCTAGAC	TCCTCACGCT	CCCTTATGGA	ACAAGGCATC	CAAGAGGATG	AGCAGCTGCT	900
	CTTACGATT	AAATATTAT	CTTCTCTGGA	CTTGAATCCT	AAATATGATG	CTGTCCGAAT	960
10	AAACCAACTC	TATGAGCAAG	CCAGGTGGGC	CATTCTCTTA	GAAGAAATG	ATTGCACAGA	1020
	GGAGAAATG	TTGATCTTGG	CAGCTCTACA	GTACCAATT	AGCAAACTGT	CGTTGTCTGC	1080
	TGAAACACAG	GAATTTGCG	GCGAGTCGA	GTTGATGAA	ATAGAAGCGG	CGCTTTCTAA	1140
	TTTGGAAAGTA	ACCCTAGAAG	GTGGAAGAGC	GGACAGCCTT	TTGGAGGACA	TTACTGATAT	1200
	CCCTAAACTT	GCAGATAATC	TCAAATTAT	TAGGCCCAAG	AAGTTACTAC	CAAAAGCTTT	1260
15	CAAAACAAT	TGGTTTATCT	TTAAAGACAC	ATCCATAGCA	TACTTTAAAA	ATAAGGAAC	1320
	TGAACAAGGA	GAACCACTAG	AAAAACTAAA	TCTTAGAGGC	TGCGAAGTTG	TGCCCGATGT	1380
	AAATGTAGCA	GGAGAAAT	TTGGAATCAA	GTTACTAATC	CCTGTTGCCG	ATGGTATGAA	1440
	TGAAATGTAT	TTGAGATGTG	ACCATGAGAA	TCAATACGCC	CAATGGATGG	CTGCCCTGCAT	1500
	GTTGGCATGG	AAGGGCAAAA	CCATGGCAGA	CAGCTCCTAC	CAGCCAGAGG	TCCTCAACAT	1560
20	CTTTCAATT	CTGAGGATGA	AAAAACAGGA	CTCTGCATCT	CAGGTGGCTT	CCAGTCTCGA	1620
	AAACATGGAT	ATGAACCCAG	AATGTTTTGT	GTCAACACGG	TGTCAAAAA	GACACAAATC	1680
	CAACACAGCTG	GCCGCCCGGA	TCTTGGAGGC	GCACCAGAAC	GTGGCCCGGA	TGCCCTGGT	1740
	CGAAGCCAAG	CTGGGTTTCA	TCCAGGCGTG	GCAGTCACTG	CCTGAGTTTG	GCCTCACCTA	1800
	CTACCTTGTG	AGATTTAAAG	GAAGCAAAAA	AGATGACATT	CTGGAGATT	CATATAACAG	1860
25	GTTGATTAAG	CTGATGTCAG	CCACCGGAT	TCCAGTGACA	ACATGGAGAT	TCAAAATAT	1920
	CAACAGTGG	AATGTAAACT	GGGAAACCCG	GCAGGTGGTC	ATCGAGTTTG	ACCAAAACGT	1980
	CTTACTGCT	TTCACTGCC	TGAGTGCAGA	TTGCAAGATT	GTGCAAGAGT	ACATTGGCGG	2040
	CTACATTTTC	TTGTCCACCC	GCTCCAAGGA	CCAGAATGAA	ACACTCGATG	AGGACTTGTT	2100
	CCACAAAT	ACCGGCGGTC	AGGATTGAAA	CAAGCAACGG	TGCTCGGCTC	ACACCAACAA	2160
30	GGCAACCAAA	AGCGGCCCT	CCCCAGAGGG	ATCCCTAAGC	TGCCACAGAT	GTAGATTCTG	2220
	GACTAACAGA	CAACATACAT	TCACCGCTGG	TCACCCAGAT	CCTCATTTCA	ACCCACTGCT	2280
	GGCACATCCC	TTTCCITACT	TTGCCCTGTG	CTACCAGCCA	CGGAAGGAGC	CTCTCTTGTT	2340
	TTTTCTATAA	AATGGGTAGG	CAGGAGAAAA	GCAGGTGCC	TAAGATTGCT	CTAAGGCCCA	2400
	GCATGTGGTT	ACAGTTCTCT	GACTTGACAG	ACCTGCCAGG	TGTATGGCTA	CAAGTTATCC	2460
35	TCGTGCTGAT	CTGTCTCAT	ACTAAGTCAA	TGAGAGAGAC	AGAAAGGTAA	AAATCACGTG	2520
	TAGCAAGAAC	AATCTTTAT	TCACAAACTC	AGGTATGAAA	CGAAACGCTT	GTCTTTCATG	2580
	GAATGCTTT	TAGCTCCTGT	CTTTTCAAAA	TGGCAGAGGG	AGTTCTCTACA	CACACTTTTT	2640
	CCCTGGAGGC	CAAGGCTTAG	GGGTAGAAAG	GGGAGGGGTG	GGGCTACCCG	GTAGCAGTTG	2700
	ACAACCCAAG	GTCAAGAGAG	TGGCCCTCAG	TGTCACTCTG	CCACAGTAT	ACCTGCCAAG	2760
40	ATGACCACTG	ACCCACATCT	GCTCTTAGTC	ATTGCTCTCG	TCAGATTCTT	GGGGCCACT	2820
	GCAAGCCCCA	TTCCATTCTC	ACAGATCTCT	CAGCCACCTG	TAACTCTTTT	GTGAAGATGT	2880
	GGGTGACACA	GCGGACAGG	AAAAACCAT	TCTCAACCCA	GATCCATGTC	TCCACTGCTT	2940
	CTACTCTGGG	TTGGGATTCA	GGAGACAGG	CACAGTCTCT	TCTGTTTATA	GAACACCTTG	3000
	CCAGTGTCAA	GGATTCCAGT	CAGGTGTCTA	TCCCAACTGG	TGAGGAGAG	AAGGCGAGC	3060
45	CCATTCTCAA	AGACCAACAT	GTCCAAGGTC	TGACAGCTCC	CCACTGGCTG	CCCCACAGG	3120
	GGCTTAGGCG	TGGTCTGGGT	CATGGGGAAG	CGTCCCTCTT	ATCGCTGGTC	TGTGTTCTCC	3180
	TGGATTGGTT	ATCTATGTTG	GTACAGCTCC	TG3CCTTTTA	TCTAAAGGAC	TTTGGCTTTT	3240
	GTAAATCACA	AGCCAATAAT	AGACTTTTTT	CTCCCTCTCT	GTTTITTTGCT	GTGTCACTCT	3300
	TGCCCTTGAGA	CTGCCCTTGG	ACAGTGTCTG	CCTTGAGAGA	GTGAGCCAA	TAAACAGTGC	3360
50	CTGAATTGTC	ATTTTCCATT	TTGGTTTGTT	AGAGGTGGGA	GGGTGGGTT	TTGAGAAGGT	3420
	CAAAAGCAAT	ACCAGAAGTA	AAGGGAATA	TCAGACAATA	TTTTATTATT	TTTTCATAGA	3480
	TGTTCTGCCA	CACAAAGAAC	TTGGGGTGTA	AGGATAAGGC	AAAAGCTCCA	ATCCCATTTT	3540
	TCAGTTCTCC	TAGGATGCAC	CCCTCAGGGA	GCCTGGCCAG	AGTTCCGAGG	CCCGTGGCG	3600
	TCAGCTGTGG	CTTTATTTTC	CATCAAGGCC	CTCTGAGAA	TGAGACCTCA	GCAATTCCGG	3660
55	GAGCCACATA	GAGACAGACT	TGGCAAGGGA	CCCTCTGGTT	CTGAGCCAGT	AGCTGCCATC	3720
	TGGAAATTC	TCITTTAGCC	TCTCCTTAGA	GTTGAATGTG	AATGAAGCCT	CCAGGCCACC	3780
	CGCTGAATTT	CTGAGGCCCT	GCTTAAAGCT	CAGAAGTGGT	TTAGGCATTT	GGAAAACTGT	3840
	GTTACATCA	TAAAGAACT	GATTTGAAAT	GTTTCTATA	GAACCAAGTG	CTAAGTGTAC	3900
	CGTATTATAC	TTGATGTTGG	TCATTCTCA	GTCTTATTT	TCAGTTCTAT	TATTTTAGAA	3960
60	CCTAGTCACT	TCITTAAGAT	TATAACTGGT	CCTACATTAA	AATAATGCTT	CTCGATGTCA	4020
	GATTTTACCT	GTTTGTGCT	GAGAACATCT	CTGCCTAATT	TACCAAGGCC	AGACCTTCAG	4080
	TTCAACATGC	TTCTTAGCT	TTTCATAGTT	GTCTGACATT	TCCATGAAAA	CAAGGGAACC	4140
	AACITTTGTT	TAAACAACT	TTGTTTGGTT	ACAGTTTTCA	GGGGAGCGTT	TCTTCCATGA	4200
	CACACAGCAA	CATCCCAAG	AAATAACAA	GTGTGACAAA	AAAAAAGAAA	AACAAACCTA	4260
65	AATGCTACTG	TTCCAAAGAG	CAACTTGATG	GTTTTTTT	ATACTGAGTG	CAAAAGGTCA	4320
	CCCAATTC	TATGATGAAA	TTTTAAATTA	ATGGGCACCT	TTCAACATCA	TTTGTCTCCT	4380
	TATCTACAGT	TGATTCAGAA	ATCTGCATT	TTTATCTTT	TATATGACTT	TTAAGTAAAA	4440
	GATTATATG	GATTGAAAA	AAAAA	A			4471

Seq ID NO: C27 Protein Sequence
Protein Accession #: NP_005161.1

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MDGGTLPRSA	PPAPPVFPVGC	AARRRPASPE	LLRCSRRRRP	ATABTGGGAA	AVARRNERER	60
NRVKLVNLF	QALRQHPVPHG	GASKKLSKVE	TLRSAVEYIR	ALQRLLAHD	AVRNALAGGL	120
RPQAVRPSAP	RGPPGTTPVA	ASPSRASSSP	GRGGSSEPGS	PRSAISSDD	GCEGALSPAE	180
RELLDPSSWL	GGY					193

Seq ID NO: C28 DNA Sequence
Nucleic Acid Accession #: NM_017763
Coding sequence: 169..2520

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AAGCATAAAT GTTCTTTTCC TCCATTGTCT TGGATCTGAG AACCTGCATT TGGTATTAGC 120
TAGTGGAGAGC AGTATGTATG GTTGAAGTGC ATTGCTGCAG CTGGTAGCAT GAGTGGTGGC 180
CACCAGCTGC AGCTGGCTGC CCTTGGCCCC TGGCTGCTGA TGGCTACCTC GCAGGCAGGC 240
TTTGGACGCA CAGGACTGGT ACTGGCAGCA GCGGTGGAGT CTGAAAGATC AGCAGAACAG 300
AAAGCTGTTA TCAGAGTGAT CCCTTGAAGA ATGGACCCCA CAGGAAACTC GAATCTCACT 360
TTGGAAGGTG TGTCTGCTGG TGTGTGTGAA ATAACTCCAG CAGAAGGAAA ATTAATGCAG 420
TCCCACCCAC TGTACCTGTG CAATGCCAGT GATGACGACA ATCTGGAGCC TGGATTTCATC 480
AGCATCGTCA AGCTGGAGAG TCCTCGACGG GCCCCCGCCC CTGCGCTGTC ACTGGCTAGC 540
AAGGCTCGGA TGGCGGGTGA GCGAGGAGCC AGTGTCTGCC TCTTTGACAT CACTGAGGAT 600
CGAGCTGCTG CTGAGCAGCT GCAGCAGCCG CTGGGGCTGA CCTGGCCAGT GGTGTGTGATC 660
TGGGTAATG AGCTGAGAAA GCTGATGGAG TTTGTGTACA AGAACCAAAA GGCCCATGTG 720
AGGATTGAGC TGAAGGAGCC CCGGCTCTGG CCAGATTATG ATGTGTGGAT CCTAATGACA 780
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AGCTCAGCT AGCTGCTGCT GTGTGCCATC TGTCTGAGG AGTTCTCTGA GGGGCAGGAG 1020
CTACGGTCA TTTCTGCTCT CCATGAGTTC CATCGTAAT GTGTGGACCC CTGGTTACAT 1080
CAGCATCGA CTTGCCCTCT CTGCGTGTTC AACATCAG AGGGAGATT ATTTTCCAG 1140
TCCCTGGGAC CCTCTCGATC TTACCAAGAA CAGGTCGAA GACTCCACCT CATTGCGCAG 1200
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CTGGCAGAG CCCAGCACC CTATGCACAA GGTGGGGAA TGAGCCACCT CCAATCCACC 1440
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TCCAGCCATG TCCACTACCA CCGCCACCG CACCAACCT ACAAAGAGG GTTCCAGTGG 1860
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AGGCAGAAA GCTAGCTATG GGTAGCCAGG TGTACAAAG GTGCTGCTCC TTCTCCAACC 2880
CCTACTTGT TTCCCTCACC CCAAGCCTCA TGTTCATACC AGCCAGTGGG TTCAGCAGAA 2940
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TCCCTCAGTT AGTGGGGAGA CTAGCACCTA GGTACCCACA TGGGTATTTA TATCTGAACC 3720
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Seq ID NO: C29 Protein Sequence
 Protein Accession #: NP_004280.2

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TLPQNTLTGP LSPVDNEMRN LTSQDLLYDL DINIFDBEINL MSLATEDNFD PIDVSQLPDE 120
PDSDSLGLSLD SSSHNSTSVIK SSSHSVCDB GAIGYCTDHE SSSHDLEGA VGGYYPEPSK 180
LCHLDQSDSD PHGLDLPQHV PHNHTYHLQP TAPESTSEPP PWPQKSQKIR SRYLEDTRDN 240
LSRDEQRAKA LHIFFSVDEI VGMPVDSEFN MLRSYYLTDL QVSLIRDIRR RGNKVAQAQ 300
CRKRKLDIIL NLEDDVCNQG AKKETLRREQ AQCNKAINIM RQKLHDLVHD IFSRLRDDQG 360
RPVNPNIHYAL QCTHDGSIIL VPKELVASGH KKETQXGRKK 420
  
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Seq ID NO: C30 DNA Sequence
 Nucleic Acid Accession #: NM_004442
 Coding sequence: 19..2982

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5	TGGATGGTGC	ATCCTCCATC	AGGGTGGGAA	GAGGTGAGTG	GCTACGATGA	GAACATGAAC	180
	ACGATCCGCA	CGTACCAGGT	GTGCAACGTG	TTTGAATCAA	GCCAGAACAA	CTGGCTACGG	240
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	CGTGACTGCA	GCAGCATCCC	CAGCGTGCC	GGCTCCTGCA	AGGAGACCTT	CAACCTCTAT	360
	TACTATGAGG	CTGACTTTGA	CTCGGCCACC	AAGACCTTCC	CCAAGTGGAT	GGAGAATCCA	420
10	TGGGTGAAGG	TGGATACCAT	TGCAGCCGAC	GAGAGCTTCT	CCCAGGTGGA	CCTGGGTGAC	480
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	TACTTGGCCT	TCCAGGACTA	TGGCGGTGCG	ATGTCCCTCA	TGGCCGTGCG	TGTCTTCTAC	600
	CGCAAGTGCC	CCCGCATCAT	CCAGAAATGG	GCCATCTTCC	AGGAAACCTT	GTCGGGGGCT	660
	GAGAGCACAT	CGCTGGTGCG	TGCCCGGGGC	AGCTGCATCG	CCAATGCGGA	AGAGGTGGAT	720
15	GTACCCATCA	AGCTCTACTG	TAAAGGGGAC	GGGAGTGGC	TGGTGCCCAT	CGGGCGCTGC	780
	ATGTGCAAGG	CAGGCTTCGA	GGCCGTGAG	AATGGCACCG	TCTGCGAGG	TTGTCCATCT	840
	GGGACTTTCA	AGGCCAACA	AGGGGATGAG	GCCTGTACCC	ACTGTCCCAT	CAACAGCCGG	900
	ACCACTTGCC	AAGGGGCCAC	CAACTGTGTC	TGCCGCAATG	GCTACTACAG	AGCAGACCTG	960
	GACCCCTCGG	ACATGCCCTG	CACAACCATC	CCCTCCGGCG	CCCAGGCTGT	GATTTCCAGT	1020
20	GTCAATGAGA	CCTCCCTCAT	GCTGGAGTGG	ACCCCTCCCG	GCGACTCCCG	AGGCCGAGAG	1080
	GACCTCGTCT	ACAACATCAT	CTGCAAGAGC	TGTGGCTCGG	GCGGGGTGTC	CTGCACCCGC	1140
	TGCGGGGACA	ATGTACAGTA	CGCACCAACG	CAGCTAGGCC	TGACGAGGCC	ACGCAATTAC	1200
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	ACTGACCAAG	GCCCTTCTCT	GCCTCAGTTC	GCCTCTGTGA	ACATCAACAC	CAACCAAGCA	1320
25	GCTCCATCGG	CAGTGTCCAT	CATGCATCAG	GTGAGCCGCA	CCGTGGACAG	CATTACCCTG	1380
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	GAGAAAGGAG	TCAATGAGTA	CAACGCCACA	GCCATAAAAA	GCCCCACCAA	CACGGTCAAC	1500
	GTGCAAGGCC	TCAAAGCCCG	GCCTCATCTA	GTCTTCCAGG	TGCGGGCAAG	CACCGTGGCA	1560
	GGCTAGCGGG	GCTACAGCGG	CAAGATGTAC	TTCCAGACCA	TGACAGAAAC	CGAGTACCAAG	1620
30	ACAAGCATCC	AGGAGAAGTT	GCCACTCATC	ATCGGCTCCT	CGGCCGCTGG	CCTGGTCTTC	1680
	CTCATTTGCT	TGGTGTTCAT	CGCCATCGTG	TGTAACAGAA	GACGGGGGTT	TGAGCGTGCT	1740
	GACTCGGAGT	ACACGGACAA	GCTGCAACAC	TACACCAAGT	GCCACATGAC	CCCAGGCATG	1800
	AAGATCTACT	TGATCCTTTT	CACCTACGAG	GACCCCAACG	AGGCAGTGCG	GGAGTTTGCC	1860
	AAGGAAATTT	ACATCTCCTG	TGTCAAAATT	GAGCAGGTGA	TGCGAGCAGG	GGAGTTTGGC	1920
35	GAGGTCTGCA	GTGGCCACCT	GAAGCTGCCA	GGCAAGAGAG	AGATCTTTGT	GGCCATCAAG	1980
	ACGCTCAAGT	CGGCTACACG	GGAGAAAGCAG	CGCCGGGACT	TCTTGAGGGA	AGCTTCCATC	2040
	ATGGGGCAGT	TGACCATACC	CAACGTATCT	CACCTGGAGG	GTGTGCTGAC	CAAGAGCACA	2100
	CCTGTGATGA	TCAATCACCGA	GTTTATGGAG	AATGGCTCCC	TGGACTCCTT	TCTCCGCAAA	2160
	AAAGATGGGC	AGTTTACAGT	CATCCAGCTG	GTGGGCATGC	TTCCGGGCAT	CGCAGCTGGC	2220
40	ATGAAGTACC	TGCGAGACAT	GAATATATTT	CACCGTGACC	TGGCTGCCCG	CAACATCTCT	2280
	GTCAACAGCA	ACCTGGTCTG	CAAGGTGTG	GACTTTGGGC	TCTCACGCTT	TCTAGAGGAC	2340
	GATACCTCAG	ACCCCACTTA	CACCAAGTCC	CTGGGGGGAA	AGATCCCATC	CCGCTGGACA	2400
	GCCCGGAGAG	CAATCCAGTA	CGGAAAGTTC	ACCTCGGCCA	GTGATGTGTG	GAGCTACGGC	2460
	ATTGTCTATG	GGGAGGTGAT	GTCTTATGGG	GAGCGGCCCT	ACTGGGACAT	GACCAACCAAG	2520
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	GCCCTGCACC	GAATCATGCT	GGACTGTTGG	CAGAAAGGACC	GCAACCAACG	CGCCAAAGTT	2640
	GGCCAAATTT	TCAACAGGCT	AGACAAAGAT	ATCCGCAATC	CCAACAGCCT	CAAGGCCATG	2700
	GCGCCCTCT	CCTCTGGCAT	CAACCTGCGG	CTGCTGGACC	GCAAGTCCCG	CGACTACACC	2760
	AGCTTTAAAC	CGGTGGACGA	GTGGCTGGAG	GCCATCAAGA	TGGGGCAGTA	CAAGGAGAGC	2820
50	TTTCGCCAAT	CCGGCTTACC	CTCCTTTGAC	GTGCTGTCTC	AGATGATGAT	GGAGGACATT	2880
	CTCCGGGTGG	GGCTCACTTT	GGCTGGCCAC	CAGAAAAAAA	TCTTGAACAG	TATCCAGGTT	2940
	ATGGGGGGCG	AGATGAACCA	GATTCACTCT	GTGGAGGTTT	GACATTCAAC	TGCTCGGGCT	3000
	CACCTCTTCC	TCCAAGCCCG	GCCCTCTCTG	CCCAAGTGGC	CGGCCCTCCT	GGTCTCTAT	3060
	CCACTGCAAG	GCCAGCCACT	CGCCAGGAGG	CCACGGGCCA	CGGGAAGAAC	CAAGCGGTGC	3120
55	CAGCCAGGAG	AGTCAACCAA	GAAGCAATGC	AACTCAAAAC	ACGGAAGAAC	AAAGGGAATG	3180
	GGAAAAAAGA	AAACAGATCC	TGGAGGGGGG	CGGGAATATC	AAGGAATATT	TTTTAAAGAG	3240
	GATTCTCATA	AGGAAAGCAA	TGACTGTCTC	TGCGGGGGAT	AAAAAAGGGC	TTGGGAGATT	3300
	CATGCGATGT	GTCCAATCGG	AGACAAAGAC	AGTTTCTCTC	CAACTCCCTC	TGGGAAGGTG	3360
	ACCTGGCCAG	AGCCAAGAAA	CACCTTCAGA	AAAACAATG	TGAAGGGGAG	AGACAGGGGC	3420
60	CGCCCTTGGC	TCTGTCCCTT	GCTGTCTCTC	TAGGCTCAC	TCAACAACCA	AGCGCTTGGA	3480
	GGACGGGACA	GATGGACAGA	CAGCCACCTT	GAGAACCCCT	CTGGGAAAT	CTATTCTCTG	3540
	CACCACTGGG	CAACAGAAAG	AATTTTCTG	TCTTTGAGAG	GTATTTTAGA	AACTCCAATG	3600
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	AGGGAGAAAG	CGGGAGCCCC	AGAAAGGTCA	GCCTTCTTGA	GGATGGGCAA	CCCCAGGTCT	3720
65	CGAGCTCCAG	GTACATATCA	CGCGCACAGC	CTGGCAGCCT	GGCCCTCTCT	GTGCCCACTC	3780
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	TGAGAAAGGT	TGATCCTGCA	TCTGGGTTTG	TTTACAGCAA	TTCTTGAGCT	CGGGGGTATT	3900
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	GTTTTTTTTA	ATGACAAATGA	AGTGACACTT	TGACATTTCC	TACCTTTTGA	GGACTTGATC	4020
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	TTTATATGCA	CATTCTGGA	TTTTTTTATA	CGGTTTTCAT	TGACACTCTT	CCCTCTCTCC	4140
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	TGGAGTGAGA	TTTGGGTGTG	GAGGGGGAGG	CGCAAGGTG	GAGGAGCTTC	CCACTCAGG	4260
	ACTGTTGATG	AAAGGACAG	ATTGAGGAGG	AAATGGGCTC	TGAGGCTGCA	GGGCTGGAAG	4320
75	TCCTTGCCCA	CTTCCCACTC	TCTTGGCCCA	ATCTATCTAG	TACTTCCAGC	GCAAAATAGG	4380
	CCCTTTGAGG	TTCTTGAATG	CCCTCAGATG	GTCAAAACCC	AGTTTTCCTC	CTGGGAGCCT	4440
	AAACAGGGCT	GCATCGGAGG	CCAGGACCCG	GATCATTCAC	TGTGATACCC	TGCCCTCCAG	4500
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	ACCCAAGCAG	AGCAATCAGT	TAGTGAATTT	GAATCCCCCA	AGTCTTGTCT	ATTGTGAATA	4740
	GTGCTGCAAT	AAACATAGCT	GTGCAATGTT	CTTTATAGTA	GAATGATCTA	TAATCTCTCT	4800
	GGTATGTACC	CAGTAAATGG	ATTGCTGGGT	CAATGGTTTT	TTCTGTTTCT	AGATCCTTGA	4860
	GGAAATTCGA	CACCTGTCTT	CACAATGGTT	GAACTAATTT	ACACTCCTAC	CAACAGTGTG	4920
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Seq ID NO: C31 DNA Sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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TCCTCTGATG ACAGTGTGTA CAGCTTTGCT TCTGATAAAT TTGCAAAAC GAGGCTGCGA 300
TCAGTTCCGG AAGGCTGTAG GACCCGCGAG CAGTGCAGGC ACTCTGAGC TCTCAGGGTG 360
GCGATGAAGT TTCCAGCGCG GAGTACCAGG GGAGCAACCA ACAAAGAAC AGAGTCCCGC 420
CAGCCCTCAG AGAATCTGT GACTGATTCC AACTCCGATT CAGAAGATGA AAGTGGAAATG 480
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GACTCACAAT CAAGGAGACC GCGAAGGCGT ACATTCGCCG GTGTGTGCTC CAGGAGAAAC 660
CCTGAACGGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCTCGG GTCCCTTGAC 720
GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGTGTGAG AAGAGGGAAG 780
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CGGCAGCGAG ATGCAAGGTT TGCGACTGGG GTCCCTGTGT ATTTAGCCAA ATATCATGGC 1200
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TCAAGGCACA AAAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATG 1800
CTCTCAATCC CATGTATTGC GCTTATGTTA CAGTTGTGTT TCACAGTTGA GACTTAATTT 1860
CTCCTAATTT CTCTGCCCC AAGGGTAAGT GGTGCGTCCA GCTTACAGA TCATAATTCA 1920
AAGGTTGGTG GCAATGTAA TACTTAATTA AATAATGAT GGAAGAGCTA TCTGGAGATT 1980
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Seq ID NO: C32 DNA Sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

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GGCCCGGGGC GCGCGCTCTG GGCTTAAATA GGAGCTCCGG GCTCTGGCTG GGACCGGACC 240
GCTGCGGGCC GCGCTCCCGC TGCTCTCTGC GGTGTATGGA AAACCCAGC CGCGCGCGCG 300
CCCTGGGCAA GCGCCTCTGC GCTCTCTCTC TGGCACTCT CGCGCGCGCC GCGCAGCCTC 360
TTGGGGGAGA GTCCATCTGT TCGCCAGAG CCCCGGCCAA ATACAGCATC ACCTTCAAGG 420
GCAAGTGGAG CCAGAGGGCC TTCCCAAGC AGTACCCCT GTTCCGCCCC CCGCGCAGT 480
GGTCTTGCT GCTGGGGGCC GCGCATAGT CCGACTACAG CATGTGGAGG AAGAACCAGT 540
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ACCTGTGCGA CGGGGACCGT TGGGGGAAC AGGCGGGCGT GGACCTGTAC CCCTACGACG 840
CCGGGACCGA CAGCGGCTTC ACCTTCTCCT CCCCCAATT CGCCACCATC CCGCAGGACA 900
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CTCTCCGAGG GCGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740
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TGCTCAC                                     1807

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Seq ID NO: C33 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1314

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GACACCTGCC AGGTGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
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Seq ID NO: C34 DNA Sequence

Nucleic Acid Accession #: NM_003045.1

Coding sequence: 148..2037

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CAGATGCTGC GCGGGAAGGT GGTGGAATGT AGCCGGGAGG AGACCGGCGT GTCTGCTGTC 240
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GGATCGGTTA AAAACTGGCA GCTCAAGGAG GAGGATTTTG GGAACACATC AGGCCGCTCTC 840
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 5 TTGCTGAACG TCTATCTCAT GATGCAGCTG GACCAAGGCA CCTGGGTCGG GTTTGCTGTG 1920
 TGGATGCTGA TAGGCTTCAT CATCTACTTT GGCTATGGCC TGTGGCACAG CGAGGAGGCG 1980
 TCCTTGGATG CCGACCAAGC AAGGACTCCT GACGGCAACT TGGACCAATG CAAGTGACGC 2040
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 10 CACCCACCCC TCCCCACGAG TGCAACAGAA ACCACCTGCG TCCACACCTT CACTGCA 2157

Seq ID NO: C35 DNA Sequence
 Nucleic Acid Accession #: NM_002776.1
 Coding sequence: 82..912

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 20 GCGCTGCTCC CCAAAAACGA CACGCGCTTG GACCCCGAAG CCTATGGCGC CCCGTGGCGG 240
 CGCGGCTCGC AGCCCTGGCA GGTCTCGCTC TTCACGGGCC TCTCGTTCCA CTGCGCGGGT 300
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 25 GATGAGCAGC ATCTCATGTT GCTAAAGCTG GCCAGGCGCG TAGTGCGGGG GCCCGCGCTC 540
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 40 GTCATGTAAG GCTTAACACA GTGGGTGGTG AGTCTGACT AAAGGTTACC TGTGTCTGTG 1440
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Seq ID NO: C36 DNA Sequence
 Nucleic Acid Accession #: XM_095088
 Coding sequence: 1..4074

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 GTGCTGTAC AGGGTTTGGG GATGATGGCG CAGGGCGCGC ATTGGTACCA GCAGCAGCTG 540
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Seq ID NO: C37 DNA Sequence
 Nucleic Acid Accession #: NM_032044
 Coding sequence: 182..658

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Seq ID NO: C38 DNA Sequence
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 Coding sequence: 52..3042

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Seq ID NO: C39 DNA Sequence
Nucleic Acid Accession #: NM_014373
Coding sequence: 322.1338


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Seq ID NO: C40 DNA Sequence
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Coding sequence: 1..2571

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   CATACTGGAA GCATAAGCAG TGAATTGGAA AGTCTGAAGG TAAATCTTAA TATCTTTCTG 1800
70  TTGGGTGAG CAGGAAGAAA AAACCTTCAG GATTTTGTCT CTTGTGGAAT AGACAGAATG 1860
   AATTATGACA GCTACTTGGC TCACTCTGTT AAATCCCGCG CAGGAGTGAA TCTTTTATCA 1920
   TTTGCATATG ATCTAGAAGC AAAAGCRAAC AGTTTGGCCC CAGGAAATTT GAGGAACCTCC 1980
   CTGAAAAGAG ATGCACAAAC TATTAACAAC ATTCACAGC AACGAGTCTT TCCTATAGAA 2040
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   CCTGTGGCCA CGCTCTTAGA TACTGCTGTT GATGCTTTT TGTGTAGCTA CATTATCGAC 2340
   CCCTTGAATT TGTTTTGGTT TTGCATAGGA AAAGCTACTG TATTTTACT TCGGCTCTA 2400
80  ATTTTTCGGG TAAAGTGGC TAAGTACTAT CGTGAATGG ATTGGAAGGA OGTGTACGAT 2460
   GATGTTGAAA CTATACCCAT GAAAAATATG GAAAATGGTA ATAATGGTTA TCATAAGAT 2520
   CATGTATATG GTATTCAAA TCCTGTTATG ACAAGCCCAT CACAACATTG A 2571

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Seq ID NO: C41 DNA Sequence

Nucleic Acid Accession #: NM_033049
Coding sequence: 28..1566

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CTCCTTTCTG TAAACACAGC CACCAACCAA GGCAACTCAG CTGATGCTGT AACAAACCACA 120
GAAACTGCTA GCACACAGC AAATACACCT TCCTTCCCAC CAGCTACTTC ACCTGCTCCC 240
10 CCCATAATTA GTACACATAG TTCTCCACA ATTCTACAC CTGCTCCCCC CATAATTAGT 300
ACACATAGTT CCTCCACAAT TCCTATACCT ACTGCTGCAG ACAGTGAGTC AACCAACAAT 360
GTAAATTTCAT TAGCTACCTC TGACATAATC ACCGCTTCAT CTCCAATGTA TGGATTAAATC 420
ACAAATGGTTC CTCTGAAAC ACAAAGTAAC AATGAAATGT CCCCACCAC AGAAGACAAT 480
CAATCATCAT GGCCTCCCAC TGGCACCGCT TTATTGGAGA CCAGCACCCCT AAACAGCACA 540
15 GGTCCACAGA ATCTCTGCCA AGATGATCCC TGTGCAGATA ATTGGTTATG TGTTAAGCTG 600
CATATAACAA GTTTTTCGCT GTGTTTAGAA GGGTATTACT ACAACTCTTC TACATGTAAG 660
AAGAGAAAGG TATTCCCTGG GAAGATTTC AAGACAGTAT CAGAAACATT TGACCCAGAA 720
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20 CCAAGATCTG AAATGCGTGC TGATGACAAG TTTGTTAATG TAACAATAGT AACAAATTTG 900
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25 AGGCCTAACC CACAGAGCCC TTCTCGCGTT GCTTCCAGTC TCAAGTGTCC TGATGCGTGC 1140
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30 AAGCATATTG AAGAAGAGAA CTTGATTGAC GAAGACTTTC AAAATCTAAA ACTGCGGTGC 1440
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35 TTTTCTCTCC ATCTGACATC TGCCAGCCTC TCTGAATGGA AGTTGTGAAT GTTTGCAACG 1740
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CTTGTGAGAG AGGTGGTTTT CTTCATCAG TACAAAGTAC TGAGACAATG GTTAGGGTGT 1860
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45 TTTTGAATAT GCTAGGAGGC AAGAGGGGCA GAGAGTAAAA AACATGACCT GGTAGAAGGA 2340
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CTGGTACAGG AGGCTCAGCT GTGGCCACCA ACACACACAC AACCCACAC 2700
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ATTCTAATG CTTGTCTCTC TTAAGAATTA TTTTATTGT TATTATTAT TGTCTCTGAC 2820
TGTTAATGTG GAATGGTAAT GCAATAAAGT GCCTTTGTGA GATGGTGAAA AAAAAAAA 2880
55 AAAAAA 2887

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Seq ID NO: C42 DNA Sequence
Nucleic Acid Accession #: NM_001432.1
Coding sequence: 167..676

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TCCGACGCGC CCTCCGCGCA AGCCCCAGCG CCCGCTCCCA TCGCGATGTA CCGCGGGGAG 180
65 GAGGATGGAG ATGCTCTGTG CCGGCAGGGT CCGTGGCTGT CTGCTCTGCC TGGGTTTCCA 240
TCTCTCTAGC GCAGTCTCTA GTACAACCTG GATTCATCA TGTATCCAG GAGAGTCCAG 300
TGATAACTGC ACAGCTTTAG TTCAGACAGA AGACAATCCA CGTGTGGCTC AAGTGTCAAT 360
AACAAAGTGT AGCTCTGACA TGAATGGCTA TTGTTTGATG GGACAGTGCA TCTATCTGGT 420
GGACATGAGT CAAACTACTC GCAGGTGTGA AGTGGGTTAT ACTGGTGTCC GATGTGAACA 480
70 CTTCTTTTAA ACCGTCCACC AACCTTTAAG CAAAGAGTAT GTGGCTTTGA CCGTGATTCT 540
TATTATTATG TTTCTATCA CAGTCTGCGG TTCCACATAT TATTCTGCA GATGGTACAG 600
AAATCGAAAA AGTAAAGAAC CAAAGAAGGA ATATGAGAGA GTTACCTCAG GGGATCCAGA 660
GTTGCCGCAA GTCTGAATAG GAGAGAGTTA CCTCAGGGGA TCCAGAGTTG CCGCAAGTCT 720
GAATGGCGCC ATCAAACTTA TGGGCAGGGA TAACAGTGTG CCGTGTAAAT ATTAATATTC 780
75 CATTTTATTA ATAAATATTA TGTGGGTCA AGTGTAGGT CAATAACACT GTATTTTAAT 840
GTACTTGAAA AATGTTTTTA TTTTGTGTTT ATTTTGACA GACTATTGCG TAATGTATAA 900
TGTGCAGAAA ATATTTAATA TCAAAAGAAA ATTGATATT TATACAAAT AATTTCTGTA 960
GCTAAATGCT TCATTTAAAG CTTCAAAGTT TATATGCGTG GTGCAGAGT CTTAGAAGTA 1020
80 AGCAATTTCC AGGTCAATAG TCAAGAAATG TTAGCAAAAT ACAGATTCTC GTAAGCCTAT 1080
ATATATGACT AATTCGATTT AGTAAGTATG TTTTATATG TCCTCAAAAT AGTGATAAT 1140
GGTTTGACTG TACCATGGTT TGATATGTAG TTGGCACCAT GGTATCATAT ATTAACACAA 1200
TAATGCAATT AGAATTTGGG AGAAGCAAAAT ATAGGTCCCTG TGTAAACAC TACACATTG 1260
AAACAAGCTA ACCCTGGGGA GTCTATGGTC TCTCACTCA GGTCTCAGCT ATAATTCTGT 1320
TATATGAGGG GCAGTGGACA GTTCCCTATG CCAACTCAG ACTCCTACAG GTACTAGTCA 1380

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	ATGTGAGGTA	ATTATTGTCT	AACAGACAAAT	TAGAAAAAAG	TCCACACTTG	AAGCCTAAAT	1560
5	TTGTGCTTTT	TAAGAAATATT	TTTAGACTAT	TTCTTTTAT	AGGGGCTTTG	CTGAATTCTA	1620
	ACATTAAATC	ACAGCCCAAA	ATTGTATGGA	CTAATTATTA	TTTTAAAAAT	TATGAAGACA	1680
	ATAATTCTAC	ATGTTGTCTT	AAGATGGAAT	TACAGTTATT	TCATCTTTTA	TTCAAGGAAG	1740
	TTTTAACTTT	AATACAGCTC	AGTAAATGGC	TTCTTCTAGA	ATGTAAGATT	ATGTATTATA	1800
	AGTTGTATCT	TGACACAGGA	AATGGGAAAA	AACCTTAAAA	TAAATATGGT	GTATTTTTC	1860
10	AAATGAAAAA	TCTCAATTGA	AAGCTTTTAA	AATGTAGAAA	CTTAAACACA	CCTTCTGTG	1920
	GAGGCTGAGA	TGAAAACTAG	GGCTCATTTT	CCTGACATTT	GTTTATTTT	TGGAAGAGAC	1980
	AAAGATTCT	TCTGCATCT	GAGCCCATAG	GTCTCAGAGA	GTTAATAGGA	GTATTTTGG	2040
	GCTATTGCTA	AAGGAGCCAC	TGCTGCCACC	ACTTTTGGAT	TTTATGGGAG	GCTCCTTCAT	2100
	CGAATGCTAA	ACCTTTGAGT	AGAGTCTCCC	TGGATCACAT	ACCAGGTCAG	GGAGGATCTG	2160
15	TTCTTCTCT	ACGTTTATCC	TGGCATGTGC	TAGGGTAAAC	GAAGGCATAA	TAAGCCATGG	2220
	CTGACCTCTG	GAGCACCAGG	TGCCAGGACT	TGTCCTCATG	TGTATCCATG	CATTATATAC	2280
	CCTGGTGCAA	TCACAGCACT	GTCACTTAAA	GTCTCTGGCC	TGGCCCTTAC	TATTAGGAAA	2340
	ATAAACAGAC	AAAAACAAGT	AAATATATAT	GGTCTTATAC	ATATTGTATA	TATATTCTAA	2400
	TACAAACATG	TATGTATACA	TGACCTTAAT	GGATCATAGA	ATTGCAGTCA	TTTGGTGCTC	2460
20	TGCTAACCAT	TTATATAAAA	CTTAAAAACA	AGAGAAAAAG	AAATCAATT	AGATCTAAAC	2520
	AGTTATTCT	GTTTCTCTAT	TAATATAGCT	GAAGTCAAAA	TATGTAAAGAA	CACATTTTAA	2580
	ATACTCTACT	TACAGTTGGC	CCTCTGTGGT	TAGTTCACAA	TCTGTGGATT	CAACCAACCA	2640
	AGGACGGAGC	ATGCTTAAAA	AATAATACAA	CAACACAAA	AAATACATTA	TAACCAACTAT	2700
	TTACTTTTTT	TTTTTCTTTT	TTGAGATGGA	GTCTCGCTCT	GTGCCCCAGG	TTGGAGTGCA	2760
25	GTGGCACGAT	CTCGGCTCAC	TGCAACCTCA	CCTCCCGGGT	TCAAGAGATC	CTCCTGGCTC	2820
	AGCCTCCTGA	GCAGCTGGGA	CTACAGGCGC	ATGCCACCAT	CCCCAGCTAA	TTTTTGTATT	2880
	TTTAGTAGAG	CGCGGGTTTC	ACCATGTTGG	CCAGGATGGT	CTCAATCTCC	TAACCTTAGG	2940
	ATCCACCTCT	CACAGCCTCC	CAAACTGCTG	GGATTACAGG	CGTGAGCCAC	CGCACGTAGC	3000
	ATTTACATTA	GGTATTACAA	GTAATGTAAA	GATGATTTAA	GTATACAGGA	GGATGTGAAT	3060
30	AGGTTATATG	CAAGCACTAT	GCCCTTTTAT	ATAAGTGACT	TGAACATCTG	TGCCCGATTT	3120
	TAGTATGTGC	AGGGGGGCGA	TCTGGGAATC	AGTCCCTGT	GGATACCAAG	GTACAACCTG	3180
	ATTTATTAAC	GCTTACTAGA	TGTGAGGAGA	GTCTGAATAT	TTTCAGTGAT	CTTGGCTGTT	3240
	TCAAAAAAT	CTATTGACTT	TTCAATAAAT	CAGCTGCAAT	CCATTATTTT	CATTACAAA	3300
	AGATTATATG	TAAGCCTCTC	AACTCTGGTT	TTTCAGTTGA	TCTTAAGCAT	GTCAATTCTAT	3360
35	AAAAACAAGT	CATTTTGTGA	TTTTTCATCT	TTAAGAAATG	TTAAAAAAGC	TAATCCCTAA	3420
	AATAGTTAGA	TCTTTGTAAA	TGCATATTAA	ATAATAAAGT	ATGACCCACA	TTACTTTTAA	3480
	TGGGTGAAAA	TAAGACAAAA	ATAATAGTTT	TAGTGAGGAT	GGTGCTGAGT	AAACATAAAA	3540
	ACTGATTTGC	TCTCAGCTGA	TGTGCTCTGT	ACACAGTGGG	AAGATTTTAG	TTCACACTTA	3600
	GTCTAACTCC	CCCATTTTAC	AGATTCTCA	CTATATATAT	TTCTAGAAAG	GGCTATGCAT	3660
40	ATTCAATGTA	TTGAGAACCA	AAGCAACCAC	AAATGCATAA	ATGCATAATT	TATGGTCTTC	3720
	AACCAAGGCC	ACATAATAAC	CCAGTTAACT	TACTCTTTAA	CCAGGAATAT	TAAGTTCTAT	3780
	AACTAGTACT	CAGGTTTAA	CCTTAAAAAT	AAGATTTCCT	TAACCTTAAC	CTTAAAAATG	3840
	ATATTATATT	AAACATACAT	AATACAAATG	AACTCCAATG	TTCTCCTGAA	TATTTTTCG	3900
	TCTAATCTCT	CTGCCGAAAG	TCAAAGTGAT	GGGAGAATTG	GTATCTGGT	ATGACTACGT	3960
45	CTTAAGTCAG	ATTTTATTTT	ATGAGTCTTT	GAGACTAAAT	TCAATCACC	CCAGGTATCA	4020
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	TGCAGTTTTT	AAAAACCTGT	ATCTGACCCA	CTTTGTAAAT	TTTGCTCCAA	TATCCATTCT	4140
	GTAGACTTTT	GAAAAAAAAG	TTTTTAATTT	GATGCCCAAT	ATATTCTGAC	CGTTAAAAAA	4200
	TTCTTGTCTA	TATGGGAGAA	GGGGGAGTAA	TGACTGTGAC	AAACAGTATT	TCTGGTGTAT	4260
50	ATTTTAATGT	TTTTAAAAAG	AGTAATTTCA	TTTAAATATC	TGTTATTCAA	ATTTGATGAT	4320
	GTTAAATGTA	ATATAATGTA	TTTTCTTTTT	ATTTTGCACT	CTGTAATTGC	ACTTTTAAAG	4380
	TTTGAGAGGC	CATTTTGGTA	AACGGTTTTT	ATTAAGATG	CTATGGAACA	TAAAGTTGTA	4440
	TTGCATGCAA	TTTAAAGTAA	CTTATTTGAC	TATGAATATT	ATCGGATTAC	TGAATTTGAT	4500
	CAATTGTGTT	GTGTTCAATA	TCAGCTTTGA	TAATTGTGTA	CCTTAAGATA	TTGAAGGAGA	4560
55	AAATAGATAA	TTTACAAGAT	ATTATTAATT	TTTATTTATT	TTTCTTGGGA	ATTGAAAAAA	4620
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Seq ID NO: C43 DNA Sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

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	CAAGTCCCC	GTGCGTTCTT	CCGTCCTTGA	GTGTCCTTGG	CGCTGCCTTG	TGCCCGCCCA	180
	GCGCCTTGG	ATCCGCTCCT	GGGCACCGAG	GCGCCCTGTA	GGATACTGCT	TGTTACTTAT	240
	TACAGCTAGA	GGCATCATGG	ACCGATCTAA	AGAAAACTGC	ATTTCAGGAC	CTGTTAAGGC	300
70	TACAGCTCCA	GTGGAGGTC	CAAAACGTGT	TCTCGTGACT	CAGCAAAATC	CTTGTGAGAA	360
	TCCATTACCT	GTAATAGTGG	GCCAGGCTCA	GCGGGTCTTG	TGTCTTCAA	ATTCTTCCCA	420
	GCGCGTTCT	TTGCAAGCAC	AAAAGCTTGT	CTCCAGTCAC	AAGCCGTTTC	AGAATCAGAA	480
	GCAGAAGCAA	TTGCAGGCAA	CCAGTGTAAC	TCACTCTGTC	TCCAGGCCAC	TGAATAACAC	540
	CCAAAAGAGC	AAGCAGCCCC	TGCCATCGGC	ACCTGAAAAT	AATCCTGAGG	AGGAACTGGC	600
75	ATCAAAACAG	AAAAATGAAG	AATCAAAAAA	GAGGCAGTGG	GCTTTGGAAG	ACTTTGAAAT	660
	TGGTCGCCCC	CTGGGTAAAG	GAAAGTTTGG	TAATGTTTAT	TTGGCAAGAG	AAAAGCAAAAG	720
	CAAGTTTATT	CTGGCTCTTA	AAGTGTATT	TAAAGCTCAG	CTGGAGAAAG	COGAGTGGGA	780
	GCAATCAGCT	AGAAAGAGAA	TAGAAATACA	GTCCACCTT	CGGCACTCCT	ATATTCTTAG	840
	ACTGTATGAT	TATTTCCATG	ATGCTACCA	AGTCTACCTA	ATTCTGGAAT	ATGACCACT	900
80	TGGAACAGTT	TATAGAGAAC	TTCAAGAACT	TTCAAGTTT	GATGAGCAGA	GAACTGCTAC	960
	TTATATAACA	GAATTGGCAA	ATGCCCTGTC	TTACTGTGAT	TGGAAGAGAG	TTATTCTAG	1020
	AGACATTAA	CCAGAGAACT	TACTTCTTGG	ATCAGCTGGA	GAGCTTAAAA	TTGCAGATTT	1080
	TGGGTGGCTA	GTACATGCTC	CATCTTCCAG	GAGGACCACT	CTCTGTGGCA	CTCTGGACTA	1140
	CCTGCCCCCT	GAAATGATTG	AAGGTGCGAT	GCAATGATGAG	AAGGTGATC	TCTGGAGCCT	1200
	TGGAGTTCTT	TGCTATGAAT	TTTTAGTTGG	GAAGCCTCCT	TTTGAGGCAA	ACACATACCA	1260

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	AGAAATACTT	GAACACCCCT	GGATCAGAGC	AAATTTCATCA	AAACCATCAA	ATTGCCAAAA	1440
5	CAAGAATCA	GCTAGCAAAC	AGTCTTAGGA	ATCGTGCAGG	GGGAGAAATC	CTTGAGCCAG	1500
	GGCTGCCATA	TAACTTGACA	GGAAACATGCT	ACTGAAGTTT	ATTTTACCAT	TGACTGCTGC	1560
	CCTCAATCTA	GAACGCTACA	CAAGAAATAT	TTGTTTTACT	CAGCAGGTGT	GCCTTAACCT	1620
	CCCTATTTCAG	AAAGCTCCAC	ATCAATAAAC	ATGACACTCT	GAAGTGAAAG	TAGCCACGAG	1680
	AATTGTGCTA	CTTATACTGG	TTCAATAATCT	GGAGGCAAGG	TTGACTGCA	GCCGCCCGT	1740
	CAGCCTGTGC	TAGGCATGGT	GTCTTCACAG	GAGGCAATC	CAGAGCCTGG	CTGTGGGGAA	1800
10	AGTGACCACT	CTGCCCTGAC	CCCGATCAGT	TAAGGAGCTG	TGCAATAACC	TTCTAGTAC	1860
	CTGAGTGAGT	GTGTAACTTA	TTGGGTTGGC	GAAGCCTGGT	AAAGCTGTGT	GAATGAGTAT	1920
	GTGATTCTTT	TAAAGTATGA	AAATAAAGAT	ATATGTACAG	ACTTGTATTT	TTTCTCTGGT	1980
	GGCATTCCCT	TAGGAATGCT	GTGTGTCTGT	CCGGCACCCC	GGTAGGCCGT	ATTGGGTTTC	2040
	TAGTCCCTCT	TAACCACTTA	TCTCCCATAT	GAGAGTGTGA	AAAAAGGAA	CACGTGCTCT	2100
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Seq ID NO: C44 DNA Sequence
Nucleic Acid Accession #: NM_013372
Coding sequence: 63..617

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	AGCACAAATGA	CTCAGAGCAG	ACTCAGTGGC	CCGAGCAGCC	TGGCTCCAGG	AACCGGGGCG	240
	GGGGCCAAAG	GCGGGGCAC	GCCATGCCCG	GGGAGGAGGT	GCTGTGAGTCC	AGCCAGAGAG	300
30	CCCTGCATGT	GAGCGAGCGC	AAATACCTGA	AGCGAGACTG	GTGCAAAACC	CAGCCGCTTA	360
	AGCAGACCAAT	CCACGAGGAA	GGCTGCAACA	GTGCAACCAT	CATCAACCGC	TTCTGTTACG	420
	GCCAGTGCAA	CTCTTTCTAC	ATCCCCAGGC	ACATCCGGAA	GGAGGAAGGT	TCCTTTCACT	480
	CCTGCTCCTT	CTGCAAGCCC	AAGAAATTC	CTACCATGAT	GGTCACACTC	AACTGCCCTG	540
	AACTACAGCC	ACCTACCAAG	AAGAAGAGAG	TCACACGTGT	GAAGCAGTGT	OGTTGCATAT	600
35	CCATCGATT	GGATTAAAGC	AAATCCAGGT	GCACCCAGCA	TGTCTTAGGA	ATGCAGCCCC	660
	AGGAAGTCCC	AGACCTAAAA	CAACCAGATT	CTTACTTGGC	TTAAACCTAG	AGGCCAGAG	720
	AACCCCCAGC	TGCCCTCTGG	CAGGAGCCTG	CTGTGCGTA	GTTCTGTGTC	ATGAGTGTGG	780
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40	CCCTATTTTG	TAAACATATC	TGCTTTAATG	GGGATGTACC	AGAAACCCAC	CTCACCCCGG	900
	CTCACATCTA	AAGGGGGGGG	GCOGTGGTCT	GGTCTGACT	TTGTGTTTTT	GTGCCCTCCT	960
	GGGGACCCAG	ATCTCCTTTC	GGAAATGAATG	TTCAATGGAAG	AGGCTCCTCT	GAGGGCAAGA	1020
	GACCTGTTTT	AGTGTGTCAT	TCGACATGGA	AAAGTCCTTT	TAACTGTGTC	TGCACTCCTC	1080
	CTTCTCTCCT	CCTCCTCACA	ATCCATCTCT	TCTTAAGTTG	ATAGTGAATA	TGTCACTCTA	1140
	ATCTCTTGTT	TGCCAAGGTT	CCTAAATTA	TTCACTTAAC	CATGATGCAA	ATGTTTTTCA	1200
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	TGGAGTGAGA	AAGGGAGGGT	GGAGGGTGAG	GCCAAATCAG	GTCCAGCAAA	AGTCAGTAGG	1320
	GACATTGCGA	AGCTTGAA	GGCCAATACC	AGAACACAGG	CTGATGCTTC	TGAGAAAGTC	1380
	TTTTCTTAGT	ATTTAACAGA	ACCCAAAGTA	ACAGAGGAGA	AATGAGATTG	CCAGAAAGTG	1440
	ATTAACCTTG	GCGGTGCAA	CTGTCTCAAA	CCTAACACCA	AACTGAAAC	ATAAATACCT	1500
50	ACCACTCCTA	TGTTTCGGACC	CAAGCAAGTT	AGCTAAACCA	AACCAACTCC	TCTGCTTTGT	1560
	CCCTCAGGTT	GAAAGAGAG	GTAGTTTAGA	ACTCTCTGCA	TAGGGGTGGG	AATTAATCAA	1620
	AAACCKCAGA	GGCTGAAATT	CCTAATACCT	TTCCCTTATC	GTGGTTATAG	TCAGCTCATT	1680
	TCCATTCCAC	TATTTCCCAT	AATGCTTCTG	AGAGCCACTA	ACTTGATTGA	TAAAGATCCT	1740
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55	TTTTAGCAAG	ARATATTKTG	GGGGTCTTTT	TGTTTTAACT	ATTGTACAGA	GATTGGGCTA	1860
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	AGSATCTGAG	GGGACCTGT	TAGGAGAGCA	TAGCATCATG	ATGTATTAGC	TGTTCACTGT	2040
60	CTACTGGTTG	GATGGACATA	ACTATTGTAA	CTATTGAGTA	TTTACTGTTA	GGCACTGTCC	2100
	TCTGATTAAA	CTTGGCCTAC	TGGCAATGGC	TACTTAGGAT	TGATCTAAGG	GCCAAAGTGC	2160
	AGGGTGGGTT	AACTTTATGT	TACTTTGGAT	TTGGTTAACC	TGTTTTCTTC	AAGCCTGAGG	2220
	TTTTATATAC	AACTCCCTG	AATACTCTTT	TTGCCCTGTA	TCTTCTCAGC	CTCCTAGCCA	2280
	AGTCTTATGT	AATATGGA	ACAAACACTG	CAGACTTGAG	ATTGAGTTGC	CGATCAAGGC	2340
65	TCTGGCACTC	AGAGAACCTT	TGCAACTCGA	GAAGCTGTTT	TTATTTGTTT	TTTGTTTTGA	2400
	TCCAGTGCTC	TCCCATCTAA	CAACTAAACA	GGAGCCATTT	CAAGGCGGGA	GATATTTTAA	2460
	ACACCCAAAA	TGTTGGGTCT	GATTTTCAA	CTTTTAAACT	CACACTGAT	GATTTCTCAG	2520
	CTAGGCCAAT	TGTCCAAAC	ACATAGTGTG	TGTGTTTTGT	ATACACTGTA	TGACCCCAAC	2580
	CCAAATCTTT	GTATTTGCCA	CATTCTCCAA	CAATAAAGCA	CAGAGTGGAT	TTAATTAAAG	2640
70	ACACAAATGC	TAAGGCAGAA	TTTTGAGGGT	GGGAGAGAA	AAAAGGGAAA	GAAGCTGAAA	2700
	ATGTAAAAAC	ACACCAAGGA	GGAAAAATGA	CATTGAGAAC	CAGCAACAC	TGAATTTCTC	2760
	TGTGTGTTTT	AACTCTGCCA	CAAGAAATGCA	ATTGTGTTAA	TGGAGATGAC	TTAAGTTGGC	2820
	AGCAGTAATC	TTCTTTTAGG	AGCTTGTACC	ACAGTCTTGC	ACATAAGTGC	AGATTGGGCT	2880
	CAAGTAAAGA	GAAATTTCCCT	AACACTAACT	TCACTGGGAT	AATCAGCAGC	GTAACTACCC	2940
75	TAAAAGCATA	TCACTAGCCA	AAGAGGGAAA	TATCTGTTCT	TCTTACTGTG	CCTATATTTA	3000
	GACTAGTACA	AATGTGGTGT	GTCTTCCAAC	TTTCATTGAA	AATGCCATAT	CTATACCTA	3060
	TTTTATTGGA	GTCACTGATG	ATGTAATGAT	ATATTTTTC	ATTATTATAG	TAGAATATTT	3120
	TTATGGCAAG	ATATTGTGTG	TCTTGATCAT	ACCTATTTAA	ATAATGCCAA	ACACCAATA	3180
80	TGAATTTTAT	GATGTACACT	TTGTGCTTGG	CATTAAAGAA	AAAAAACACA	CATCTGGGAA	3240
	GTCTGTAAAG	TGTTTTTTGT	TACTGTAGGT	CTTCAAGTT	AAGAGTGTAA	TGGAAAAATC	3300
	TGGAGGAGAT	GATAATTTCC	ACTGTGTGGA	ATGTGAATAG	TTAAATGAAA	AGTTATGGTT	3360
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	TTCTCCCTTA	TATGACITTC	TCTGAGTTGG	GCAAGGAAGA	AGCTGACACA	CCGTATGTTG	3480
	TTAGAGTCTT	TTATCTGGTC	AGGGGAAACA	AAATCTTGAC	CCAGCTGAAC	ATGCTTCTCT	3540
	GAGTCAGTGC	CTGAATCTTT	ATTTTTTAAA	TTGAATGTTT	CTTAAAGGTT	AACATTTCTA	3600

5 AAGCAATATT AAGAAAGACT TTAATGTGA TTTTGAAGA CTTACGATGC ATGTATACAA 3660
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10 Seq ID NO: C45 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 200..2932

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 TGGAGATTCC TCCGACAACA TCATGCTAAC TCAGTTTGTCT CAAATGAAT AAGGCAAGGA 2940
 65 ATCATAAAAT CAAGAAAAAA TTTCCAGAAC AACTTGACAT TTAGAGACAA ATGTCAATGA 3000
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 AATGTCTCAG TGGCTTCA 3078

70 Seq ID NO: C46 DNA Sequence
 Nucleic Acid Accession #: NM_000584.1
 Coding sequence: 75..374

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 GCATAAAGAC ATACTCCAAA CCTTCCACC CCAATTTTAT CAAAGAACTG AGAGTGATTG 240
 80 AGAGTGGACC ACACGTGCGC AACACAGAAA TTATTGTAAA GCTTTCGAT GGAAGAGAGC 300
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 5 TTTGCCATAA AGTCAAATTT AGCTGGAAAT CCTGGATTTT TTTCTGTTAA ATCTGGCAAC 840
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 15 AACTATTAAA ACAGCCAAAA CTCACAGTC AATATTAGTA ATTTCTTGCT GGTGAAACT 1440
 TGTTTATTAT GTACAAATAG ATTCTTATAA TATTATTAA ATGACTGCAT TTTTAAATAC 1500
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Seq ID NO: C47 DNA Sequence
 Nucleic Acid Accession #: NM_005603.1
 Coding sequence: 1..3756

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 40 ATGTCACTTG AATACACAGA CAGTACCTC CAAAGAGAGG ATACATTGGC TACATTGTAT 780
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5 GTTGCCATTC GATTCTCTGTC AATGACCATC TGGCCATCAG AAAGTGATAA GATCCAGAAG 3540
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Seq ID NO: C48 DNA Sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

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 GGGGTGCTGG GATGTCATCC AAAGTGGTTG TCTGAGACAG AGTTGGAAC CCTCACCAAC 3180
 TGGCTCTCTC ACCTTCCACA TTATCCCGCT GCCACCGGCT GCCTGTCTC ACTGCAGATT 3240
 CAGGACGAGC TTGGGCTGGG TGCGTCTGCG CTTCGAGTC AGCCGAGGAT GTAGTTGTTG 3300
 CTGCGCTGCT CCCACCACCT CAGGGACCCAG AGGGCTAGGT TGGCACTGCG GCCCTCACCA 3360
 GGTCTTGGGC TCGGACCCAA CTCTGGGACC TTTCAGCCT GTATCAGGCT GTGGCCACAC 3420
 GAGAGGACAG CGCGAGCTCA GGAGAGATT TGTGACAATG TAGCCCTTTC CCTCAGAAAT 3480
 CAGGGAGAGG ACTGTGCGCT GCCTTCTCCG GTTGTGCGT GAGAACCGGT GTGCCCTTTC 3540
 CCACCATATC CACCTCGCT CCATCTTTGA ACTCAACAC GAGGAACATA CTGCACCTG 3600
 GTCCTCTCCC CAGTCCCCAG TTCACCTTCC ATCCCTCAC TTCTCCACT CTAAGGATA 3660
 TCAACACTGC CCAGCACAGG GGCCCTGAAT TTATGTGTTT TTTATACATT TTTTAAATAG 3720
 ATGCACATTA TGTCAATTTT TAATAAAGTC TGAAGAATTA CTGTTT 3766

Seq ID NO: C49 DNA Sequence
 Nucleic Acid Accession #: NM_007019.1
 Coding sequence: 41..580

1 11 21 31 41 51
 GGCACGAGCG AGTTCCTGTC TCTCTGCCAA CGCCGCGCGG ATGGCTTCCC AAAACGCGGA 60

5
10
15
20
25
30
35
40
45
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55
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65
70
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80

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CCGAGCCGCC ACTAGGTCG CCGCCGCCCG TAAAGGAGCT GAGCCGAGCG GGGCGCGCCG 120
CGGGGGTCCG GTGGGCAAAA GGCTACAGCA GGAGCTGATG ACCCTCATGA TGTCTCGCGA 180
TAAAGGGATT TCTGCCTTCC CTGAATCAGA CAACCTTTTC AAATGGGTAG GGACCATCCA 240
TGGAGCAGCT GGAAACAGTAT ATGAAGACCT GAGGTATAAG CTCTCGCTAG AGTTCCCCAG 300
TGGCTACCCCT TACAATGCGC CCACAGTGAA GTTCCTCACG CCTCGTATC ACCCCAACGT 360
GGACACCCAG GGTAAACATAT GCCTGGACAT CCTGAAGGAA AAGTGGTCTG CCCTGTATGA 420
TGTCAAGACC ATTCTGCTCT CCATCCAGAG CCTTCTAGGA GAACCCAACA TTGATAGTCC 480
CTTGAACACA CATGCTGCCG AGCTCTGGAA AAACCCCA CA GCTTTTAAAG AGTACCTGCA 540
AGAAACCTAC TCAGGACAGG TCACCAAGCA GGAGCCCTGA CCCAGGCTGC CCAGCCTGTC 600
CTTGTGTCGT CTTTTTAATT TTTCTTAGA TGGTCTGTCC TTTTGTGAT TTCTGTATAG 660
GACTCTTAT CTGAGCTGT GGTATTTTGT TTTGTTTTT GTCTTTTAAA TTAAGCCTCG 720
GTTAGCCCT TGTATATTAA ATAAATGCAT TTTTGTCTTT TTTTAAAAAA AAAAAAAA 780
AAA 783

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Seq ID NO: C50 DNA Sequence
Nucleic Acid Accession #: NM_014584.1
Coding sequence: 227..1633

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1 11 21 31 41 51
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TGGCGATCGC TGAGAGGCAG GAGGGCCGAG CGGGGCTTGG GAGGCGGCCG GGAGGTGGGG 120
CGCCGCTGGG GCGCGGCCGC ACGGGCTTCA TCTGAGGGCG CACGCGCCCG GACCGAGCGT 180
GCGGACTGGC CTCCCAAGCG TGGGCGGACA AGCTGCCGGA GCTGCAATGG GCGCGGCTG 240
TGGATCTCTG TTTGGCCTCC TGGGCGCGGT GTGGCTGCTC AGCTCGGGCC ACGGAGAGGA 300
GCAGCCCCG GAGACAGCGG CACAGAGGTG CTTCTGCCAG GTTAGTGGTT ACTTGGATGA 360
TTGTACCTGT GATGTTGAAA CCATTGATAG ATTTAATAAC TACAGGCTTT TCCCAAGACT 420
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TCTTTCTTGG AATGACATCA GCCAGTGTGG AAGAAGGGAC TGTGCTGTCA AACCATGTCA 540
ATCTGATGAA GTTCCTGATG GAATTAATC TGCGAGCTAC AAGTATTCTG AAGAAGCCAA 600
TAATCTCATT GAAGAATGTG AACAGCTGA ACGACTTGA GCAGTGGATG AATCTCTGAG 660
TGAGGAAACA CAGAAGGCTG TTCTTCAGTG GACCAAGCAT GATGATTCTT CAGATAACTT 720
CTGTGAAGCT GATGACATTC AGTCCCTGTA AGCTGAATAT GTAGATTGCT TTCTTAATCC 780
TGAGCGCTAC ACTGCTTACA AGGGACCAGA TGCTTGGAAA ATATGGAATG TCATCTACGA 840
AGAAAACGTG TTTAAGCCAC AGACAATTAA AAGACCTTTA AATCCTTTGG CTTCTGGTCA 900
AGGACACAGT GAAGACAACA CTTTTTACAG TTGGCTAGAA GGTCTCTGTG TAGAAAAAAG 960
AGCATTCTAC AGACTTATAT CTGGCCTACA TGCAAGCATT AATGTGCATT TGAGTGCAAG 1020
ATATCTTTTA CAAGAGACCT GGTAGAAAA GAAATGGGGA CACAACATTA CAGAAATTTCA 1080
ACAGCGATTG CATGGAATTT TGACTGAAGG AGAAGGTCCA AGAAGGCTTA AGAACTTGTA 1140
TTTTCTCTAC TTAATAGAAC TAAGGGCTTT ATCCAAAGTG TTACCATTCT TCGAGCGCCC 1200
AGATTTTCAA CTCTTTACTG GAAATAAAA TCAGGATGAG GAAAAAACA TGTTACTTCT 1260
GGAAATACCT CATGAAATCA AGTCATTTC TTTGCATTTT GATGAGAAAT CATTTTTTGC 1320
TGGGGATAAA AAAGAAGCAC ACAAACTAAA GGAGGACTTT CGACTGCATT TTAGAAATAT 1380
TTCAAGAAAT CATGGAATTT TGGTTGTTT TAAATGTCTG CTGTGGGAAA AGCTTCAGAG 1440
TCAGGGTTTG GGCACGTCTC TGAAGATCTT ATTTCTGAG AAATGTAGAT CAAATATGCC 1500
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CGCATTTGGA AGAATTTCTA CAAGTGTGAA AGAATTAGAA AACTTCAGGA ACTTGTGTACA 1620
GAATATTCTT TAAAGAAAAC AAGCTGATAT GTGCCTGTTT CTGGACAATG GAGGCGAAAG 1680
AGTGGAAATT CATTCAAAGG CATAATAGCA ATGACAGTCT TAAGCCAAAC ATTTTATATA 1740
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TTAAGTCTAT GTATAATACT ACTGTGAGTA AAAGTAATAC TTTAATAATG TGGTACAAAT 1860
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GTTCTAAGTC TCTCAACTA CGCTTTTATG TAATAATATG TAATATAAAT AAAACTATGG 1980
TAAATGTGAC AAGCATTTAA TAGGAAAATG CTAAGGAGGC CTCATAAATG ACCCATAAAT 2040
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TTGCCAGTT AGATTGGAAT TTCAGATAAA CAATTAGTTT TTTAATATTT TACATGGAAT 2160
ATTTGGAATA TACTTATACT AAAAAATTAT TTGTTTGAAA TTCACATTTA ACTGGGAGTC 2220
TTGTATTTTA TCTGGCAATC CTAATAATAC TTGGTATGAA ACAATCACT TTTAGAAATG 2280
TATTGCTATT TTGATTGGGT TGTTTTGTG GTAGAAAACG TACAATAACA ACTCAAAGGC 2340
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TTTCACTAAT ACTAAATAAA ATTTGGGAA CACTTTTTAT TTTTATATA TTTCAAATTT 2460
ACAGAAAAGT TTCAAAAATA GTACAAAGAG CTCTCTTACC CAGATTCACT AATTGTTTAT 2520
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ATCATTTGAA AGTCAGTTAT AGGCATCATG CCCCTTAAAC CCTAAACTCT TCAGTGTGTA 2640
ATACTGAATA ATTAATAAAA ATGATTTTCT CAGAAAAAAA AACTCCACCA ATTCTGGAAC 2700
TATAATACGT TAAGCCTTAG AATAAATAAT ACTTTCAGT TCCAATCTAA AGTTCCTTTT 2760
GAGTTTGTGT GCCCGTTTTA TGCTTGATGT GTATAGTAAT AGGGTAGGCT ATTTATTTTA 2820
TTAAAAATTT TTTTAGAGAC AAGGTTTTCG TGTGTGCCCC AAGCTGGAAC TTGAACGACT 2880
GGGCTGAAGT GATCTTCCCA CCTCAGCCTC CCAAGTAGCT GGGAAATACAG GTGTCTGCCA 2940
CCATACCCAG TTTCAATTTT GTTTTTTATA CCGAAGTTC ATTTCCCTTG TCTCCCTAAA 3000
ACTGAACGT AATTTTGGGA GGTTTTCATT AGTGAAGCT CTTCATTTAT AAAGCTATT 3060
GAAGGGTTT AGGAATTTAT ATCACATGGT AATTGTAGAG AAAAAAGAGC TATATACCTC 3120
AAAAATCGTC CCTCTTACA TATGCTTAT CAGGTATAAC ATGTTGAAAT GTCACATTAG 3180
TAGTAAAGTG GGGTTTATT ATATAGTGGT TAAGAAATGT CAGTTTACAC TGCTGTATAC 3240
TTCTTCTCT GTGTCCTTAA GGCCTGGTAC AGTGCCAAGC ACATACTTGG TATCCAATAA 3300
ATATTGTTG GATGAAAAAA AAAAAAAA AAAA 3334

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Seq ID NO: C51 DNA Sequence
Nucleic Acid Accession #: NM_002888.1
Coding sequence: 37..723

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1 11 21 31 41 51
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5 CCAAGTCCGG GGTCCGAGC CAACCTTCCT GCGTCCATGC AGCCCCGCG GCAACGGCTG 60
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 CTGTGTCTCG CCCCGGTGGC GCGCGCGCG GGTCCGCGG GCGCCGACGA CCCTGGGCGAG 180
 CCTCAGGATG CTGGGGTCCC GCGCAGGCTC CTGCAGCAGA AGGCGCGCGC GCGGCTTCAC 240
 TTCTTCAACT TCCGGTCCGG CTGCGCCAGC GCGCTGCGAG TGCTGGCCGA GGTGCAGGAG 300
 GGCCGCGCGC GATTAAATCC AAAAGAGGGA TGTAAAGTTC ACGTGGTCTT CAGCACAGAG 360
 CGCTACACCC CAGAGTCTTT ACTTCAGGAA GGTGAGGAC GTTTGGGAA ATGTTCTGCT 420
 CGAGTGTITT TCAAGAATCA GAAACCCAGA CCAACCATCA ATGTAACCTG TACACGGCTC 480
 10 ATCGAGAAAA AGAAAGACA ACAAGAGGAT TACCTGCTTT ACAAGCAAAT GAAGCAACTG 540
 AAAAAACCCCT TGAATAATG CAGCATACCT GATAATCATG GACATATTGA TCCCTCTCTG 600
 AGACTCATCT GGAATTGGC TTTCCTTGA AGCTCTTACG TGATGTGGGA AATGACAACA 660
 CAGGTGTAC CACTACTACT GGCACAGCTC ACTAGTGTGA GGCAGTGGGT AAGAAAAACC 720
 TGAATAATTA CTGTGCCAC AAGAGTTACA ATCAAAGTGG TCTCTTAGA CTGAATTCA 780
 15 GTGAACCTCT AATTTTCATAT CAAGAGTTGT AATCACATTT ATTTCAATAA ATATGTGAGT 840
 TCTCTC 846

Seq ID NO: C52 DNA Sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

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 25 CAACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GGCTATAGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTGCA TAGGCCCTGG GTTAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCTT GAAAGAAAAT 300
 AAAGGACAAC GATGCCATAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
 30 AAGAGAAAGA ATTTTAAAC ATATCAAAAC ATATGAAGTC CTGGAAGAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAAC TTTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTTCCTGAAT GAATGACAAAT CAGAAATCCA 600
 CTGCCAAAG GAGTCCAGCA ATTAATATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 35 GGTTACCATC GGAGTTTACA AAGTGCTTTC ACGTTCTTAC TTGTGTATT ATACATTCAT 720
 GCATTCTTAG GCTAGAGAAC CTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGTTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCCTCAAAC ATTTTTCAT GCAATATCAC ACTTCTTCC 960
 40 CCAATATCA TGTAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAAATCAT AAAATGTACT ATGAAAAAA TTATACGCTA 1080
 TGGGATACG GCAACAGTGC ACATATTCA TAACCAATT AGCAGCACCG GTCTTAATTT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
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 45 TACAATAATG TTTTGTCTAC CAAAGAAAAA TGTGAAAAA TAAGCAAATG TATACCTAGC 1320
 AATCACTTTT ACTTTTGTG ATTCGTCTC TTGAAAAAT ACATAATCTA ATCAATTTCT 1380
 TTGTTCTATG CTATATACG TAAATTTAG GTATACTCA GACTAGTTTA AAGAAATCAA 1440
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Seq ID NO: C53 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..609

50 1 11 21 31 41 51
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 CTCAGCGCGC TCAACCGCTT CCAGCCGAG GCGGACCTGG AGCGCCTGCT CGCTCCGAGC 180
 60 CACAGCCTGG CCAAGATCGA GCGCAGCCTG GCCAGCAGCC TTTTCCCTCT GGACCACTCC 240
 AAAAGCCAGC TCTATTGCGA CTACACACCC CCTGGGAGGT ATGGCAGGGT GATCCTCTCT 300
 TCCCAACCG GGGCAATAT TTTGCTCCAG GCTGAGGGGA TCCTGCAGAC CCACCGAGCC 360
 GTGCTGGAAT TGAAGGTGAA CCAAGGGGC TATAATTATA CTTTTTCCCA CTCTGTGTGT 420
 TTGAGAAATC AGGATAAGAA ATGCGTGCTG GATGATATTA TTTCACTGCT AGAGGATCTC 480
 AGGCAGGCTG CCGTCTCCAA TAAGACAACA GCCAGGGTGC AAGTGAGGTA TCCCAACACT 540
 65 AAATTAAGG TATGCTCCTT CTGCATGCTT CTGCCAATTA AAGAGGCAGC ACTTCAATTC 600
 TTGCCCTAA 609

Seq ID NO: C54 DNA Sequence
 Nucleic Acid Accession #: NM_002438.1
 Coding sequence: 104..4474

70 1 11 21 31 41 51
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 GGGAACTTGG ATTAGGTGGA GAGGCAGTTG GGGGGCCTCG TTGTTTTCGG TCTTAGTTCC 60
 75 GCGCTCTCTG CCATCAGGAG AAGGAAAGGA TAAACCTCGG GCCATGAGGC TACCCCTGCT 120
 CCTGGTTTTT GCCTCTGTCA TTCCGGGTGC TGTCTCTCTA CTGGACACCA GGCAATTTT 180
 AATCTATAAT GAAGATCACA AGCGCTGCGT GGATGCAGTG AGTCCAGTG CGTCCAAAC 240
 CGCAGCTTGC AACCAGGATG CGAATCACA GAAATTCGGA TGGGTGTCCG AATCTCAGAT 300
 TATGAGTGTG GCATTAAAT TATGCTGCTG AGTGCCATCA AAAACAGACT GGGTGTCTAT 360
 80 CACTCTCTAT GCTGTGACT CAAAAAGTGA ATTTGAGAAA TGGGAGTGCA AAAATGACAC 420
 ACTTTTGGTG ATCAAGGAG AAGATTATT TTTAACTAC GGCAACAGAC AAGAAAAAGAA 480
 TATTATGCTC TACAAGGGAT CGGGTTTATG GAGCAGGTGG AAGATCTATG GAACCAACA 540
 CAATCTGTGC TCCAGAGGTT ATGAAGCCAT GTATACGCTA CTAGGCAATG CCAATGGAGC 600
 AACCTGTGCA TTCCCGTTCA AGTTTGAATA CAAGTGTGAC GCAGATTGCA CGAGTGTCTG 660
 GCGTGTGAT GGTGGCTCT GGTGCGGAAC CACTACTGAC TATGACACAG ACAAGCTATT 720

5	TGGATATTGT	CCATTGAAAT	TTGAGGGCAG	TGAAAGCTTA	TGGAATAAAG	ACCCGCTGAC	780
	CAGCGTTTCC	TACCAGATAA	ACTCCAAATC	CGCTTTAAGC	TGGCACCAG	CGAGGAAAAG	840
	CTGCCAACAA	CAGAACGCTG	AGCTCCTGAG	CATCACAGAG	ATACATGAGC	AAACATACCT	900
	GACAGGATTA	ACCAGTTTCT	TGACCTCAGG	ACTCTGGATT	GGACTTAAAC	GTCTGAGCTT	960
	CAACAGCGGT	TGGCAGTGGG	GTGACCGCAG	TCCTTTCCGA	TATTTGAACT	GGTTACCAGG	1020
	AAGTCCATCA	GCTGAACCTG	GAAAAAGCTG	TGTGTCACTA	AATCCTGGAA	AAAAATGCTAA	1080
	ATGGGAAAAT	CTGGAATGTG	TTCAGAAACT	GGGCTATATT	TGCAAAAAGG	GCAACACCAC	1140
	TTTAAATTCT	TTTGTATTTC	CCTCAGAAAG	TGATGTGCCT	ACTCACTGTC	CTAGTCAGTG	1200
10	GTGGCCGTAT	GCCGGTCACT	GTTCAGAGAT	TCACAGAGAT	GAGAAAAAAA	TCCAGAGGGA	1260
	TGCTCTGAGC	ACCTGCAGGA	AGGAAGGCGG	TGACCTCACA	AGTATCCACA	CCATCGAGGA	1320
	ATTGGACTTT	ATTATCTCCC	AGCTAGGATA	TGAGCCAAAT	GACGAATTGT	GGATCGGCTT	1380
	AAATGACATT	AAGATTCAAA	TGTACTTTGA	GTGGAGTGAT	GGGACCCCTG	TAACGTTTAC	1440
	CAAAATGGCT	CGTGGAGAAC	CAAGCCATGA	AAACAACAGA	CAGGAGGATT	GTGTGGTGAT	1500
15	GAAAGGCAAG	GATGGGTACT	GGGCAGATCG	GGGCTGTGAG	TGGCCTCTTG	GCTACATCTG	1560
	CAAGATGAAA	TCAGGAAGCC	AAGGTCCAGA	AATAGTGGAA	GTGAAAAAAG	GCTGCAGGAA	1620
	AGGCTGGAAA	AAACATCACT	TTTACTGCTA	TATGATTGGA	CATACGCTTT	CAACATTTCG	1680
	AGAAGCAAA	CAAACTGTGA	ATAATGAGAA	TGCTTATTTA	ACAACTATTG	AAGACAGATA	1740
	TGAACAAGCC	TTCTCGACTA	GTTCGTGTGG	CTTAAGGCCT	GAAAAATATT	TCTGGACAGG	1800
20	ACTTTCAGAT	ATACAAACCA	AAGGGACTTT	TCAGTGGACC	ATCGAGGAAG	AGGTTGGGTT	1860
	CACCCACTGG	AAITCAGATA	TGCCAGGGCG	AAAGCCAGGG	TGTGTTGCCA	TGAGAACCGG	1920
	GATTGCAGGG	GGCTTATGGG	ATGTTTTGAA	ATGTGATGAA	AAGGCMAAAT	TTGTGTGCAA	1980
	GCACTGGGCA	GAAGGAGTAA	CCCACCCACC	GAAGCCCAAG	ACGACTCCCG	AACCCAAATG	2040
	TCCGGAGGAT	TGGGGCGCCA	GCAGTAGAAC	AAGCTTGTGT	TTCAAGCTGT	ATGCAAAAAG	2100
25	AAAACATGAG	AAGAAAAAGT	GGTTTGAATC	TCGAGATTTT	TGTCGAGCTC	TGGGTGGAGA	2160
	CTTAGCTAGC	ATCAATAACA	AAGAGGAACA	GCAAAACAATA	TGGCGATTAA	TAAACAGTAG	2220
	TGGAAGCTAC	CACAAACTGT	TTTGGTTGGG	ATTGACATAT	GGAAAGCCCTT	CAGAAGGTTT	2280
	TACTTGGAGT	GATGGTTCTC	CTGTTTTCATA	TGAAAACTGG	GCTTATGGAG	AACCTAATAA	2340
	TTATCAAAAT	GTGAATAACT	GTGGTGAGCT	GAAAGGTGAC	CCTACTATGT	CTTGGAAATGA	2400
30	TATTAATTGT	GAAACCTTTA	ACAACTGGAT	TTGCCAGATA	CAAAAAGGAC	AAACACCAAA	2460
	ACCCTGAGCCA	ACACCAGCTC	CTCAAGACAA	TCCACCAGTT	ACTGAAGATG	GGTGGGTTAT	2520
	TTACAAAGAC	TACCAATATT	ATTTCAAGAA	AGAGAAGGAA	ACCATGGACA	ATGCGCGAGC	2580
	GTTTTGCAAG	AGGAATTTTG	GTGATCTTGT	TTCTATTCAA	AGTGAAAGTG	AAAAGAAGTT	2640
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35	CAGCTTGGAT	AAAAAGTTTG	CTTGGATGGA	TGGAAGCAAA	GTGGATTACG	TGTCTTGGGC	2760
	CACAGGTGAA	CCCAATTTTG	CAAAATGAAGA	TGAAAACGTG	GTGACCATGT	ATTCAAAATTC	2820
	AGGGTTTGG	AATGACATTA	ACTGTGGCTA	TCCAAACGCC	TTCAATTGGC	AGCGACATAA	2880
	CAGTAGTATC	AATGCTACCA	CAGTTATGCC	TACCATGCCC	TGGTCCCAT	CAGGGTGCAA	2940
40	GGAAGGTTGG	AATTTCTACA	GCAACAAGTG	TTTCAAAATC	TTTGGATTTA	TGGAAGAAGA	3000
	AAGAAAAAAT	TGGCAAGAGG	CACGAAAAGC	TTGTATAGGC	TTTGGAGGGA	ATCTGCTCTC	3060
	CATACAAAAT	GAAAAAGAGC	AAGCATTTCT	TACCTATCAC	ATGAAGGACT	CCACTTTCAG	3120
	TGCCTGGACT	GGGCTGAATG	ATGTCATATC	AGAACACACG	TTCTTTTGGG	CGGATGGAGC	3180
	AGGAGTCCAT	TACACAAAAT	GGGGGAAAGG	TTACCTTGGT	GGAAGAAGAA	GCAATCTTTC	3240
	TTATGAGAT	GCTGACTGTG	TTGTTATTAT	TGGAGGTGCA	TCAAAATGAAG	CAGGAAAAATG	3300
45	GATGGATGAT	ACCTGCGACA	GTAAACGAGG	CTACATATGC	CAGACACGAT	CCGACCCCTC	3360
	CTTGACTAAT	CCTCCAGCAA	CGATTCNAAC	AGATGGCTTT	GTAAATATG	GCAAAAAGCAG	3420
	CTATTCACCT	ATGAGACAAA	AATTTCAATG	GCATGAAGCG	GAGACATACT	GCAAGCTTCA	3480
	CAATTCCTCT	ATAGCCAGCA	TTCTGGATCC	CTACAGTAAT	GCAATTGCGT	GGCTGCAGAT	3540
	GGAAACATCT	AATGAACGTG	TGTGGATCGC	CCTGAACAGT	AACCTGAGCT	ATAATCAATA	3600
50	CACCTGGACT	CACTAAGTGA	GGGTGAGGTA	CACCTAAGTG	GCTGCTGATG	AGCCCAAAAT	3660
	GAAATCAGCA	TGTGTTTATC	TGGATCTTGA	TGGCTACTGG	AAGACAGCAC	ATTGCAATGA	3720
	AAGTTTTTAC	TTTCTCTGTA	AAAGATCAGA	TGAAATCCCT	GCTACTGAAC	CCCCCAACT	3780
	GCTGTCAGCA	TGCCCGGAGT	CAGATCACAC	AGCATGGATT	CCTTTCCATG	GTCACTGTTA	3840
	CTATATTGAG	TCCTCATATA	CAAGAAACTG	GGGCCAAGCT	TCTCTGGAAT	GTCTTCGAAT	3900
55	GGGTCTCTCT	CTGGTTTCCA	TTGAAAGTGC	TGCAGAAATCC	AGTTTCTCTG	CATATGGGGT	3960
	TGAGCCACTT	AAAAGTAAAA	CCAATTTTGG	GATAGGATTG	TTCAAAATG	TTGAAGGGAC	4020
	GTGGCTGTGG	ATAAATAACA	GTCCGCTCTC	CTTTGTCAAC	TGGAACACAG	GAGATCCCTC	4080
	TGGTGAACGG	AATGATTGTG	TAGCTTTTACA	TGCGTCTTCT	GGGTTTGGGA	GTAATATTCA	4140
	CTGTTCTTCC	TACAAAGGAT	ATATTGTGAA	AAGACCAAAA	ATTATTGATG	CTAAACCTAC	4200
60	TCATGAATTA	CTTACAACAA	AAGCTGACAC	AAGGAAGATG	GACCTTCTTA	AACCGTCTTC	4260
	CAAGTGGGCC	GGAGTAGTCA	TCATTGTGAT	CCTCCTGATT	TTAACGGGTG	CTGGCCTTGC	4320
	CGCCTATTTC	TTTTATAAGA	AAAGACGTGT	GCACCTACCT	CAAGAGGGCG	CCTTTGAAAA	4380
	CACCTGTGAT	TTTAAACAGTC	AGTCAAGCCC	AGGAACTAGT	GATATGAAAG	ATCTCGTGGG	4440
	CAATATTGAA	CAGAAATGAAC	ACTCGGTCAAT	CTAGTACCTC	AATGCGATTG	TGAGATATTT	4500
65	GAATTTTCATA	AAATTGTAAAC	TGAAATTTAA	AATTTTTAGT	TCAATGTGAT	TGTTTTCTTT	4560
	AAAAAGATTA	CTGAATTGTA	CTGGTCTGTG	CTTTTTCTCT	TTGCCTAATT	GAAGAAATAA	4620
	TTGCTTGTIT	TCTAGCCTGG	CAAGATATTT	TCATAAAAGA	GGGATAACAA	TGCTGATTAC	4680
	TACCTTTTAA	AATATTTTAG	ATAAATGCAC	AGCACCACAG	CACCACATCT	AAGCATTAGT	4740
	GATGGGTAGC	TGATGTCAGC	TTTATGTGGA	TTTTAAGCAC	TCTAGAAACA	ATGAAGCTTC	4800
70	TTGGCATATT	TTAAGGAGCT	CCCAAAATGT	GTTACCTATT	AAATTGTAAAC	TCAGCAAGTA	4860
	GAAGACCATT	TGAAAAGTCA	GGTACAAATT	TCCTCAAGTG	GCAATAAAAT	GTAGTCAGTT	4920
	TTCTCTTTTA	CCAGTTTTTA	TTTCCACTCC	AATTTATTAG	AACCTTTATT	GTACATGTGC	4980
	AGAAGATAAA	GGCAGCTGAG	AATCTTGTIT	CCCCCAAGAG	AGTTTTACAG	GCTGAGTGTG	5040
	GCAAAATGTG	TCTTTGTCCT	GTTATATGTA	TATCAGGAAT	ACAAGGATGT	GAAATAAAAC	5100
75	TGTAATTTG	CATAACTGGA	TGTACTTAGA	TAATGTGAAA	TAAACATTAA	AGACAAGGTC	5160
	TATTTTTTAAT	AAAAAATAAA	AAAAA				5185

Seq ID NO: C55 DNA Sequence
 Nucleic Acid Accession #: NM_024574.2
 Coding sequence: 424..2130

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	AGTGCAGACTA	GCGGCGGCGG	GCGAAGCCCG	CGCCAGCCCC	GCGGGTGCCT	GCGGCATCCT	60
	CCGCGCGGCC	AGCCCCGCA	CGCTCCCTGC	AGTTTAAAG	GACCTCCGCG	CGCTTCTCGG	120

5	CGCTGCCCGG	GGATTCCCCA	GCCCCGCGCG	GCTCCCTACT	CCACTTGGCA	GCAACTTCGG	180
	CGACCGCGCG	CGCGCCGCCC	TCGCCCCGCT	TTGAAGTTTG	CTGTGCCGAC	CGCAAAGTTG	240
	GGACACTTCA	CGCGATTGAA	TTTTTCTCTT	TTATCTGCCT	CCGTCCCGCG	CCTCCAGGCT	300
	TCTCGTTTCT	GGATATTGGT	GCTTAGCATC	TTGGCAGGGT	CCGGGGAAGT	GGACTATTTT	360
	GCACACCACA	CAACGGGGAG	GGATTTTTTT	CTATTTTCCC	TACGAAAAAC	AGATCTTTTT	420
	AAGGATGGTG	CTGCTCCACT	GGTGCTGCT	GTGGCTCTTG	TTTCCACTCA	GCTCAAGGAC	480
	CCAGAAGTTA	CCACCCCGGG	ATGAGGAAGT	TTTTTCAGATG	CAGATCCCGG	ACAAGGCATT	540
	TTTTCATGAT	TCGTGAGTAA	TTCCAGATGG	AGCTGAAATG	AGCAGTTATC	TCITTAGAGA	600
10	TACACCTAAA	AGGATTTTCT	TTGTGGTTGA	AGAAGACAAT	ACTCCATTAT	CAGTCACAGT	660
	GACGCGCTGT	GATGCGCCTT	TGGAGTGGAA	GCTGAGCCTC	CAGGAGCTGC	CAGAGGACAG	720
	GAGCGGGGAA	GGCTCAGGTG	ATCTGGAACC	TCTTGAGCAG	CAGAAGCAGC	AGATCATTAA	780
	TGAGGAAGGC	ACTGAGTTAT	TCTCCTACAA	AGGCAATGAT	GTTGAGTATT	TTATATGCTC	840
	TAGTTCCTCA	TCGGTTTAT	ATCAGTTGGA	TCITCTTTCA	ACAGAGAAAG	ACACACATTT	900
15	CAAAAGTATAT	GCCACCACAA	CTCCAGAATC	TGATCAGCCA	TACCTGAGT	TACCTATGA	960
	CCCAAGATGA	GATGTGACCT	CAGTGGGGCG	CACCAAGGTC	ACTTTGGCCT	GGAAAACCAAG	1020
	CCCACTGCC	TCTTTGCTGA	AACAACCCAT	TCAGTACTGT	GTGGTCATCA	ACAAAGAGCA	1080
	CAATTTCAAA	AGTCTCTGTG	CAGTGGGAAG	AAAAGTGAAGT	GCAGATGATG	CTTTTATGAT	1140
	GGCACCGAAA	CTGTGCTGGG	ACTTCAGCCC	CTTTGACTTT	GGCCACTTTG	GATTTCTCTC	1200
20	TGATAATCTA	GGTAAAGAAC	GCAGTTTCCA	GGCAAAGCCT	TCTCCAAAAC	TGGGGCGTCA	1260
	TGTCTACTCT	AGGCCCAAGG	TTGATATTCA	GAAAATCTGC	ATAGGAAAAC	AGAACATCTT	1320
	CACGCTCTCT	GATCTGAAAC	CCGACACGCA	GTACTACTTT	GACGTATTTG	TGCTCAACAT	1380
	CAACAGCAAC	ATGAGCACCG	CTTATGTAGG	TACCTTTGCC	AGGACCAAGG	AAGAAGCCAA	1440
	ACAGAAGACA	GTGAGGCTCA	AAGATGGGAA	GATAACAGAT	GTATTTGTTA	AAAGGAAGGG	1500
25	AGCAAAGTTT	CTACGGTTTG	CTCCAGTCTC	TTCTCACCAA	AAAGTCACTT	TCTTTATTCA	1560
	CTCTGTCTGT	GATGCTGTCC	AAATCCAAGT	GAGAAGAGAT	GGGAAACTTC	TTCTGTCTCA	1620
	GAATGTGGAA	GGCAITTCAGC	AGTTTCAGCT	TAGAGGAAAA	CCTAAAGCTA	AATACCTCGT	1680
	TCGACTGAAA	GGAAACAAGA	AAGGAGCATC	TATGTTGAAA	ATTCTAGCTA	CCACAAGGCC	1740
	TACTAAGCAG	TCATTTCCCT	CTCTTCTGTA	AGACACAAGA	ATCAAAGCCT	TTGACAAGCT	1800
30	CCGTACTCTG	TCCTCGGCCA	CCGTGGCTTG	GCTAGGCACT	CAGGAAAAGG	ACAAAGTTTG	1860
	CATCTACAAA	AAAGAAATGG	ATGATAACTA	CAATGAAGAC	CAGAAGAAAA	GAGAGCAAAA	1920
	CCAATGTCTA	GGACCAAGTA	TAAGGAAGAA	GTCAGAAAAA	GTCCTCTGTA	AATATTTCCT	1980
	CAGTCAAAAC	CTGCAGAAAG	CAGTGACCAC	AGAAACAATT	AAAGGTCTTC	AGCCTGGCAA	2040
	ATCTTACCTG	CTGGATGTTT	ATGTCATAGG	ACATGGGGGG	CACCTGTGTA	AGTATCAGAG	2100
35	TAAGGTTGTG	AAAACCTAGAA	AGTTCTGTTA	GTACCTTCT	TATAGAGATA	TATTATGTAG	2160
	AACTCCAGGA	GGGACATTAA	ATCACTTTAA	GTATAAACTG	ACTACTCCCA	CAGTTGAGAG	2220
	AAGTTGTGAC	CTGTACTTGT	ACTATGGAAG	GAAGGATATC	AACGTGTGTA	TATTGATGTT	2280
	TATATAAGTA	ACTCTTGAAG	GAGACTTGT	CTAGCGTGCC	CCATGGTACC	TAGTGTGTGT	2340
	CTGATGCGGG	TTGGTGTCAA	AGATAGAGGG	CTTCTGAAG	GAACTTGCCA	TTCTTGCTT	2400
40	TGACCACTGT	ATGAACCTGT	TCTAAATTAT	TTTATTACCT	AAAAATTATA	AATATGCCAT	2460
	TCATTGCACA	CACCCACAAA	TGCAAAATCAT	TCCTCTCTAT	AGATGCTAGG	ATATATATAA	2520
	ATTATTTTAT	AAATTTCTGT	TTTAAATGTC	AGTGTCTCTA	TGATTGTAAA	CTATTAAATT	2580
	CTTTTCTCTAT	TAAAGTACAG	ATCTAATCTA	AGTATTATTA	AGTTGATAGC	CCTCTAGTCA	2640
	GTATATATGC	TATTTGTAAT	TCTTGTTTGT	TGAGTAAAT	GTTTAAATAC	TATATGTATC	2700
45	TCATGTACAA	AGTTGACATA	CATTATATTC	ATGTACATAA	AATTAAGAG	ATTAGATTAT	2760
	ATACTGTTAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA		2808

Seq ID NO: C56 DNA Sequence

Nucleic Acid Accession #: BC034229.1

Coding sequence: 373..1422

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55	CTTCCTCAGC	CTGCTCAATG	TGAAGCCCTT	GATCATGATT	CACCTCCACT	TAATAAATAA	120
	AGTGTTTACA	AATCAGAATA	ACTTTTAGAC	AATATTAAGG	TGGTAATCAT	GAACAGAAAA	180
	GATTTTGTAG	TTCTTCCATG	GGGAAACCTT	GGAAATCTG	TAAAGCTAAA	ATATAGCAAT	240
	GTAAATATTA	AAACAAAGAT	CTAAGATTG	AAGAGATAAT	TTGCTTCAGG	ATTTTGATGG	300
60	AAGGCAATG	CTAAGCTTAA	AAACAGATT	TCGGAGAAGT	ACAAAAGAAA	TAGAAATGCT	360
	CAAGAACTGC	GAATGGAGAA	AGTACAGTTA	GAGTTTGAGA	ACCAAGAGAT	GGAGAAGAAA	420
	CTGCAAGAA	TCCGATCCAC	AAGAAACAAA	GAAAAGGAAG	ATAGAGAGTC	AAGCGAGTAT	480
	TACTGGAAAT	CTGGAAGAGT	GGGCAAAATG	GTCAATCAAT	CATATATGAT	GTCACAAAAT	540
	AAAGGAAATG	TTGTTAAGTT	TTCTGCTGGA	AAAGTGAAAT	TAAATTTGCT	GAAGGAAACG	600
65	ATTCAAGAGC	CAGTGAAACC	AACAGTTAAT	TATAAAATGG	CAAAATCTTC	AGAATGTGAA	660
	AAACCAAGAA	TAAATGGGAA	AGTTTGTGGA	CAGTGTGAGA	ACAAAGCTGC	TCTACTGGTA	720
	TGCCTTGAAT	GTGGAAGA	TTATTGTTCA	GGATGCTTTG	CTAATGTTCA	CCAGAAAGGG	780
	GCACATAAGC	TCCACAGAAC	AACTCTTTTG	CAGGCAAGAT	CTCAAAATAT	ATTCAATGTA	840
70	TTGGATGTTG	CCCATCAGTT	TATAAAGGAT	GTTAATCCAG	ATGAACCCAA	AGAGGAGAA	900
	AATTCTACAA	AGGAAACCCG	TAAAAATCAA	CATAAACCCA	AATCTGTACT	TCTCCAGAGG	960
	AGCAGCTCTG	AGGTAGAAAT	TACAAAGATG	AAAAGAGCAC	AACGTACAAA	ACCAAGAAAG	1020
	AGTCTGTTGT	GTGAAGGCTC	ATTCGATGAA	GAAGCTTCTG	CACAGTCTCT	TCAGGAAGTG	1080
	TTAAGTCAAT	GGAGAACCGG	AAATCATGAT	GACAAACAGA	AACAGAAATT	ACATGCAGCA	1140
	GTAAAGAGCT	CATTGGAAGA	ATGCGAAGTA	CAGACTAATC	TGAAAAATTTG	GAGAGAAACCA	1200
75	CTTAATATTG	AACCTTAAAG	AGACATTCTA	TCCTATATGG	AAAAATATATG	GCTTAAAAAA	1260
	CACAGGAGAA	CTCCACAAGA	GCAACTTTTT	AAATGCTACC	AGATACGTTT	CCACATCCAC	1320
	ATGAAACCCAC	TGGTGATGCA	CAGTGTCTCT	AAAATGAAAA	CGATGAAGAT	AGTGTGTTG	1380
	AGGAGACCAA	AGTACAAACG	ACAGCTCTTT	TATTGCCAGT	AGAAACATTA	AACATAGAGA	1440
	GACCTGAACC	ATCTCTGAAG	ATAGTCAAGC	TGGATGATAC	TTATGAAGAG	GAATTTGAAG	1500
80	AAGCAAGAAA	TATTTGCTCT	TACAAAGTTA	AATTAGCTGA	TGCAGACAGT	CACGGAAGTT	1560
	GTGCTTTTCA	TGATTGTGAG	AAGAATAGCT	TTCCATATGA	AAATGGCATC	CATCAACATC	1620
	ATGTTTTTCA	TAAGGGAAGG	AGAGACTTCT	TAAATCTTTG	TCGTGAGAAC	AGCTCTACTT	1680
	ATTATAAAGA	TAATTCAAAA	GGAGAAACTT	CAAAACACAG	TTTTGACAAAC	ATCGTGGATC	1740
	CTGATGTGTA	TTCTTCTGAC	ATTGAAAAAA	TTGAGGAAAG	CACCTCCTTT	GAAGAGAAAT	1800
	TAAAGGAGAA	AAATATAGGT	TTAGAAAGTA	ATCAAAAGTC	TGATGATTCC	TGTGATATC	1860

5 TTGAAAGCAA GGACACTTTG CTAGGTAGAG ATTTAGAAAA AGCTCCCAT T GAGGAGAAAT 1920
 TATCTCAAGA CATCAAGAA TCCTTGGAA T TGAGCAATCT GTATAAGAGG CCAAGCTTTG 1980
 AAGAATCAAA AACTACAAAG TCATCACTGT TGTTACAAGA AATAGCCTGC AGAAGTAAGC 2040
 CTATAACAAA ACATATATCA GGACTTGAGA GATTCTTTAT TTTTGATACA AATGAAAGAC 2100
 TCAACTTACT TCCTTCTCAT CGTTTGAAT GCAACAATTC CAGTACTAGG ATTACACTTG 2160
 CAGGTGAGAA ATCACAGAGA CCTTCAACAG CAAATTTTCC ACTTTCCAAC TCTGTTAAAG 2220
 AAAGCTCCAG TTGCCTTTCA TCCTCTCATC CTGATCAAG AAGTGCAGCT GCTCAATCAT 2280
 CATCTAGAGC TGCTTCTGAA ATTTGAGAAA TTGAATATAT TGATATTACT GACCAGAATG 2340
 10 AGCTTTCCTT AGATGACACT ACTGATCAAC ATACTTTAGA CAATTTGGAA AAAGAATTAC 2400
 AAGTGCTGAG ATCTCTTGCA GATACTTCAG AAAAGCTTTA CAGCTTAAAC TCAGAAGAGT 2460
 TCCCAGATT T CAGCAGCCAA TCAGTGAATA TAAGTCAGAT TTCCACAGAT TTCCTTAAGA 2520
 CCTCAGATGT GAGGGGTCCC TGTGGAGTTG AGGAATTGAG CTGTCTTGGG AGAGATACCA 2580
 AAATTGAGTC TTTGCTGTCA CTTTCTGAGA GCAGTACAGA TGAGGAGGAG GAAGATTTTC 2640
 15 TCAACAAGCA ACATGTCTC ACATACCGT GGTCAAAGAG TACTTAAAGA TTATTTGTTT 2700
 ATTACTGTTT CCATTTGTA CCCAGAGTAA AGCAAAACAC TGAGAAAAGT AACCAAGTGA 2760
 TTACCTATCC AAGTGTCTGA GATTTTGATT ACTAATGTCT TTGATGTTTC AAGGCTACAA 2820
 ACTAATAAAA GTAAATATAT AAGTCAAAA AAATTTTAA AAAAAAAAT AAAAA 2876

20 Seq ID NO: C57 DNA Sequence
 Nucleic Acid Accession #: NM_024687.1
 Coding sequence: 138..1706

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 AAGACATCTT ATCCTATATG GAAAAATTAT GGCTTAAAAA ACACAGGAGA ACTCCACAAG 180
 30 AGCAACTTTT TAAATGCTA TCAGATACGT TCCCACATCC ACATGAAACC ACTGGTGATG 240
 CACAGTGTTT TCAAAATGAA AACAGTGAAG ATAGTGATGG TGAGGAGACC AAAGTACAAC 300
 ACACAGCTCT TTATTGCCA GTAGAAACAT TAAACATAGA GAGACCTGAA CCATCTCTGA 360
 AGATAGTCGA ACTGGATGAT ACTTATGAAG AGGAATTTGA AGAAGCAGAA AATATTGTGC 420
 CTTACAAAGT TAAATTAGCT GATGCAGACA GTCAACGAAG TTGTGCTTTT CATGATTGTC 480
 35 AGAAGAAATAG CTTTCCATAT GAAAATGGCA TCCATCAACA TCATGTTTTT GATAAGGGAA 540
 AGAGAGACTT CTTAAATCTT TGCTTGAGAA ACAGCTCTAC TTATTATAAA GATAATTCAA 600
 AAGGAGAAAC TTCAAAACACA GATTTTGACA ACATCGTGGG TCCTGATGTG TATTCTTCTG 660
 ACATTGAAAA AATTGAGGAA AGCACCTCCT TTGAAAGAAA TTTAAAGGAG AAAAAATAG 720
 GTTAGAAAG TAAATCAAAAG TCTGATGATT CCTGTGTATC ACTTGAAGAC AAGGACACTT 780
 40 TGCTAGGTAG AGATTTAGAA AAAGCTCCCA TTGAGGAGAA ATTATCTCAA GACATCAAG 840
 AATCCTTGA ATTGAGCAAT CTGTATAAGA GGCCAAGCTT TGAAGAAATCA AAAACTACAA 900
 AGTCATCTT GTTGTACAA GAAATAGCCT GCAGAAATGAA GCCTATAACA AAACAATATC 960
 AAGGACTTGA GAGATTCTTT ATTTTGTATA CAAATGAAAG ACTCAACTTA CTCTCTCTC 1020
 ATCGTTTGA ATGCAACAA TCCAGTACTA GGTATTACAT TGCAAGAGAC AGAAGATGGA 1080
 45 TTCCAGACCA TAGCTTAAGT GAATATGCTG ATAATGCAAT TGTCTTGGGT GTTCTGCAGG 1140
 GTGCTCAGAG TCCATCATCA AGTAGAAAAC AGCAAAAGAT GGGTCAGAAA TCACAGAGAC 1200
 CTTCAACAGC AAATTTTCCA CTTTCCAAC TGTGTTAAAGA AAGCTCCAGT TGCCTTTCTAT 1260
 CCTCTCATCC TCGATCAAGA AGTGCAGCTG CTCAATCATC ATCTAGAGCT GCTTCTGAAA 1320
 TTTCAAAAAT TGAATATATT GATATTACTG ACCAGAATGA GCTTTCTCTA GATGACACTA 1380
 50 CTGATCAACA TACTTTAGAC AATTTGGAAG AAGAATTACA AGTGTGAGAG TCTCTGCAAG 1440
 ATACTTCAGA AAAGCTTTAC AGCTTAAOCT CAGAAGAGT CCCAGATTTT AGCAGCCAAAT 1500
 CACTGAATAT AAGTCAAGAT TTCCACAGAT TCCTTAAGAC CTCACATGTG AGGGGTCCCT 1560
 GTGAGTTTGA GGAATTGAGC TGTCTGGAAG GAGATACCAA AATTCAGTCT TTGCTGTAC 1620
 TTTCTGAGAG CAGTACAGAT GAGGAGGAG AGAATTTTCT CAACAAGCAA CATGTCATCA 1680
 55 CACTACCGTG GTCAAAGAGT ACTTAAAGAT TATTTGTTCA TTAAGTTTTC CATTTGTATC 1740
 CCAGAGTAAA GCAAAACACT GAGAAAAGTA ACCAAGTGAT TACCTATCCA AGTGTGAGAG 1800
 ATTTTGATTA CTAATGTCTT TGATGTTTCA AGGCTACAAA CTAAATAAAG TAAATATATA 1860
 AGTTCAAAAA AAAAAA AAAA 1884

60 Seq ID NO: C58 DNA Sequence
 Nucleic Acid Accession #: NM_005408.1
 Coding sequence: 76..372

65 1 11 21 31 41 51
 AAAAGGCCGG CGAACACAGC AGAGGAGCAG AGAGGCAAAG AAACATGTGT AAATCTCCAA 60
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 GCTTTCAACC CCCAGGAGCT TGCTCAGCCA GATGCACTCA ACGTCCCATC TACTTGCTGC 180
 70 TTCACATTTA CAGTAAGAA GATCTCCTTG CAGAGGCTGA AGAGCTATGT GATCACCACC 240
 AGCAGGTGTC CCCAGAAGGC TGTCTCTTTC AGAACCACAA TGGGCAAGGA GATCTGTGCT 300
 GACCCAAAGG AGAAGTGGGT CCAGAATTAT ATGAAACACC TGGGCCGGAA AGCTCACACC 360
 CTGAAGACTT GAACTCTGCT ACCCTACTG AAATCAAGCT GGAGTACGTG AAATGACTTT 420
 TOCATTTCTC TCTGGCTCTC TCTTCTATGC TTTGGAATAC TTCTACCATA ATTTTCAAAT 480
 AGGATGCATT CGTCTTTTGT ATTCAAAATG TACTATGTGT TAAGTAATAT TGGCTATTAT 540
 75 TTGACTTGTT GCTGTTTGG AGTTTATTG AGTATTGCTG ATCTTTTCTA AAGCAAGGCC 600
 TTGAGCAAGT AGGTTGCTGT CTCTAAGCCC CCTTCCCTTC CACTATGAGC TGCTGGCAGT 660
 GGGTTTGTAT TCGTTTCCCA GGGGTTGAGA GCATGCCTGT GGGAGTCATG GACATGAAGG 720
 GATGCTGCAA TGTAGGAAGG AGAGCTCTTT GTGAATGTGA GGTGTGCTGA AATATGTTAT 780
 TGTGGAAGA TGAATGCAAT AGTAGGACTG CTGACATTTT GCAGAAAATA CATTTTATTT 840
 80 AAAATCTCCA AAAAAA AAAA 860

Seq ID NO: C59 DNA Sequence
 Nucleic Acid Accession #: AK097746.1
 Coding sequence: 185..2224

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CTTCACATAC AACTTATATT GTAATATATG CCGATCACTA TTGAGAGAGG ACAAGCTGTT 120
ATTTTCCCTT TTATTATGTG CCAATCTTCT TCTGGCAAGG AAAGAGATTG AATACCAGGA 180
ACTGATGTTT CTTTAACTG GAGGAGTAAG TCTTAAAGT GCTGAGAAAA ATCCTGATCC 240
AACTTGGCTA CAGGACAAAA GCTGGGAGGA AATCTGTGCG GCAAGTGAAT TTCTGCCTT 300
CAGAGGACTC AGGCAACATT TTGTGAAACA TATATATGAA TGGCGAGAAA TCTATGACAG 360
10     TAAAGAGCCA CATAATGCTA AATTTCCAGC ACCAATGGAT AAGAACTTAA ATGAACATA 420
GAAAATAATA ATTCTTCGGT GTTAAAGACC TGATAAGATA ACCCCAGCTA TAACAACTA 480
TGTAACAGAC AAAGTAGGGA AAAAGTTTGT AGAGCCTCCA CCATTTGATT TGACAAAGAG 540
TTACTTGGAT TCAAAATGCA CCATTCCTT AATTTTGTG CTATCTCCAG GAGCAGATCC 600
TATGGCCAGC CTGCTGAAAT TTGCAAAATGA TAAATCTATG TCTGGAATA AGTTTCAAGC 660
15     TATTTCACTG GGACAGGGAC AAGGACCGAT TGCAGCAAAA ATGATTAAAG CAGCAATTGA 720
AGAAGGAAGT TGGGTGTGCC TACAGAATTG CCATCTTGCA GTGTCTGGA TGCCCATGTT 780
GGAAAAAATA TTGAAGATT TTACCTCTGA AACCTGTAAC TCATCTTTA GGCTTTGGCT 840
GACAAAGCTAT CCATCTTCAA AATTCCTCAGT AACCAATTCTA CAGAAATGGAG TAAAAATGAC 900
TAATGAACTT CCAACGGGCTC TTGGGCTGAA TCTCTTCAA TCATATCTCA CTGATCCAGT 960
20     TTCTGATCCT GAGTTTTTCA AGGGATGCGC TGGAAAGGAA CTGTTATTTA TCAATGAATA 1020
TGATACAATT CCATTTGAAG CTATATCTTA CCTGACTGGG GAGTGTAAIT ATGGAGGAAG 1080
AGTGACACAG GATGGGACAG GACGTCTTCT ATTAACCATG CTGGCTGACT TTTATAATCT 1140
GTACATAGTT GAAAACCCCT ATTATAAGTT TTCTCCCACT GGAAGCAAT TCGCACTCTC 1200
TAAAGGCACT TATGAGGACT ACATTGAATT CATTAAGAAA CTTCATTTA CTCACACCTC 1260
25     TGAGATATTT GGATTACATG AAAACGTTGA CATCTCCAAG GATCTTCAAC AAACAAAAAC 1320
CCTCTTTGAG TCCTTGCTCC TCAACCCAGG AGGCTCCAAA CAGACAGGAG CCTCAGGAAG 1380
TACTGATCAG ATTCTGTTAG AAATTACCAA AGATATCTTC AACAACTGCT CTAGTGATT 1440
CGACATTTGA ATGGCACTAC GGAAGTATCC TGTGAGATAT GAAGAAAGCA TGAATACTGT 1500
GTTAGTACAA GAAATGGAAA GATTTAACAA TTTAATTATA ACTATACGTA ACACCTTACG 1560
30     GGACCTTGAA AAAGCTATTA AGGGTGTGGT TGTGATGGAT TCTGCTTGG AGGCACTCTC 1620
CAGTAGCTTA CTGTGTGAAA AGGTTCCAGA AATATGGGCC AAACGTTTCA ACCCAAGCTT 1680
TAAGCCCCCT GGAAGTTACA TCACAGATT CTAGCCCGG TTGAACTTT TACAGGACT 1740
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TTTAACCTGA GCTATGCAGA ATTATGCCAG AAAATATACC ACCCCTATTG ATTTGCTAGG 1860
35     ATATGAATTT GAGGTTATCC CATCTGATAC ATCTGACACA TCACAGAAAG ATGGTGTTTA 1920
TATCCACGGA CTGTATCTCG ATGGCGCAGC CTGGGACCGA GAAAGTGGAT TGCTTGCTGA 1980
ACAAATATCC AAATCTCTGT TTGACCTGAT GCCCATCATA TGGATAAAAC CAACCTCAAA 2040
ATCTCGAATT ATAAAGTCGG ATGCCTATGT CTGTCCCCTC TACAGACAA GTGAACGTAA 2100
AGGAACCTCT TCACTACCGG GACATTCTAC TAACTTTGTC ATTGCAATGT TGTAAAAAC 2160
40     AGACCAACCT ACTCGGCACT GGATCAAGCG CGGGGTGCTC TTGCTTTGTC AGTTGGATGA 2220
CTAAATTGGA CAAATTTATA AAACATCCAA AAGTTT 2256

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Seq ID NO: C60 DNA Sequence
Nucleic Acid Accession #: J02761.1
Coding sequence: 14..1159

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GCTCTGTGGC CCAGGCACTG CTGCCTGGAC CACCTCATCC TTGGCTGTG CCCAGGGCCC 120
TGAGTCTCGG TGCCAAGGCC TGGAGCAAGC ATTGCAGTGC AGAGCCCTAG GGCATTGCTC 180
ACAGGAAGTC TGGGGACATG TGGGAGCCGA TGACCTATGC CAAGAGTGTG AGGACATCGT 240
CCACATCCTT AACAGATG GCAAGGAGGC CATTTTCAG GACACGATGA GGAAGTTCTC 300
GGAGCAGGAG TGCAACGTCC TCCCCTTGAA GCTGCTCATG CCCCAGTGCA ACCAAGTGT 360
55     TGACGACTAC TTCCCTCTG TCATCGACTA CTTCCAGAAC CAGACTGACT CAAACGGCAT 420
CTGTATGCACT CTGGGCTGTG GCAAAATCCC GCAGCCAGAG CCAGAGCAGG AGCCAGGGAT 480
GTACAGCCCC CTGCCCAAAC CTCTGCGGGA CCCTCTGCCA GACCCTCTGC TGGACAAGCT 540
CGTCTCCCTC GTGCTGCCCG GGGCCCTCCA GGGCAGGCT GGGCTTACA CACAGGATCT 600
CTCCGAGCAG CAATTCCTCC TTCTCTCTCC CTATTGCTGG CTCTGCAGGG CTCTGATCAA 660
GCGGATCCAA GCCATGATT CCAAGGGTGC GCTAGCTGTG GCAGTGGCCC AGGTGTGCG 720
CGTGTACCT CTGTGTGCG GCGGCATCTG CCAGTGCCCT GCTGAGCGCT ACTCCGTCT 780
CCTGCTCGAC ACGCTGCTGG GCGCATGCT GCGCCAGCTG GTCTGCCGCC TCGTCTCTCG 840
GTGTCTCATG GATGACAGCG CTGGCCCAAG GTGCGGACA GGAGAAATGGC TGCGGAGAGA 900
CTCTGAGTGC CACCTCTGCA TGTCCGTGAC CACCCAGGCC GGAACAGCA GCGAGCAGGC 960
65     CATACACAG CCAATGCTCC AGGCTCTGTG TGGCTCTGG CTGGACAGGG AAAAGTGCAA 1020
GCAATTTGTG GAGCAGCACA CGCCCCAGCT GCTGACCTG GTGCCACGG GCTGGGATGC 1080
CCACACCACT TGCCAGGCC TGGGGTGTG TGGGACCATG TCCAGCCCTC TCCAGTGTAT 1140
CCACAGCCCC GACCTTGAT GAGAACTCAG CTGTCCAGCT GCAAAGGAAA AGCCAAGTGA 1200
GAOCCGCTCT GGGACCATG TGACCAAGCT CTTCCTCTGC TCCCTGGCCC TCGCCAGCTG 1260
CCAGGCTGAA AAGAAGCTC AGCTCCACA CGGCCCTCT CACCTCCCTT CCTGGCAGT 1320
CACTTCCACT GGTGGACAC GGGCCCCAG CCCTGTGTG GCCTTGTCTG TCTCAGCTCA 1380
ACCAAGTCT GACACAGAG CCACTTCCA TCCTCTCTGG TGTGAGGCAC AGCGAGGGCA 1440
GCATCTGGAG GAGCTCTGCA GCCTCCACAC CTACCAAGAC CTCCCAGGC TGGGCTCAGG 1500
70     AAAAAACG CACTGCTTTA CAGGACAGGG GGTGAAGCT GAGCCCCGCC TCACACCCAC 1560
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AAAAATGGAA CATACAGAAC TCTAAAGAT AGACATCAGA AATTTGTAA TTAAGCTTTT 1680
TCAAAATATC AGCAATTCCC CAGCGTAGTC AAGGGTGGAC ACTGCAOGCT TGGCATGAT 1740
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80     TTGTTAAGAT AAAAAAGGG GTTCTTTTT GTCTTCTGT AAGGTGAGT TCCAGATTTT 1860
GATTGAAAGT GATTGGGTGA TTCTATTTCT GCTGTGATT ATCTGCTGAA AGCTCAGCTG 1920
GGGTGTGCA AGCTAGGAC CCATTCCTGT GTAATACAA GTCTGACCA ATGCTAATAA 1980
AGTCCTATTC TCTTTTAAAA AAAAAAAGG AAAAAAAG GAATTC 2026

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Seq ID NO: C61 DNA Sequence

Nucleic Acid Accession #: NM_139172.1
Coding sequence: 19..552

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      CTGCAGGCGCT CGGACAGCGG AAATGGAATC CAGGGATTCT TCTACCCATG GAGCTGTGAG 120
      GGTGACATAT GGGACCGGGA GAGCTGTGGG GGCCAGGCGG CCATCGATAG CCCCAACCTC 180
      TGCCGTGCGTC TCCGTGCTGT CTACCGCAAT GGGGTCTGCT ACCACCAAGG TCCAGACGAA 240
      AACGTGCGGA GGAAGCACAT GTGGGCGCTG GTCTGGACGT GCAGCGGCGT CCTCCTCCTG 300
      AGCTGCAGCA TCTGCTTGT TGGTGGGCC AAGCGCGGG ACCTGCTGCA TATGCCCGGT 360
      TTCTGGCGG GTCCGTGTGA CATGTCCAAG TCCGTCTCGC TGCTCTCCAA GCACCGAGGG 420
      ACCAAGAGGA CGCCGTCCAC GGGCAGCGTG CCAGTCGCCC TTGCCAAGA GTCCAGGGAT 480
      GTGGAGGGAG GCACCGAGGG GGAAGGGACG GAGGAGGGTG AGGAGACAGA GGGCGAGGAA 540
15     GAGGAGGATT AGGGGAGTCC CGGGGGACT GCTCAATACA GATACGCTGG ACG 593

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Seq ID NO: C62 DNA Sequence
Nucleic Acid Accession #: NM_054023.2
Coding sequence: 98..379

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      GCTATCACAC TTGGTGTGAC ATCAAGATAA AGAGCGGAGG TGGATGGGGA TGGAAGATGA 420
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Seq ID NO: C63 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2874

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Seq ID NO: C64 DNA Sequence
 Nucleic Acid Accession #: XM_168571.1
 Coding sequence: 155..988

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 Coding sequence: 122..1198

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Seq ID NO: C66 DNA Sequence
Nucleic Acid Accession #: NM_014459.2
Coding sequence: 738..3407

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Nucleic Acid Accession #: NM_005601.2
Coding sequence: 101..598
  
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GGCCATGGCG GTGTACACCA GCGAGCGGTG GGACCCAGCT CCACACCCCC AGATCCAGAC 480
CTTCTTCTCT TGGTCTTCT ACCTGGGCTG GGTCTCAGCT ATCCTCTTGC TGTGTACAGG 540
TGCCCTGAGC CTGGGTGCTC ACTGTGGCGG TCCCGTCTCT GGCTATGAAA CTTGTGAGC 600
AGAAAGGCAAG AGCGGCAAGA TGAGTTTGA GCGTTGTATT CCAAGGCCCT CATCTGAGC 660
CTCGGGAAG TCTGGTCTTA CATTTGCCCG CCCTTCCAGC CCTTCCCCAG CCCTCTCTCT 720
TGTCTCTTCA TTCATTCAAC AAAATTGGC TGGAAAAAAA AAAAAAATAA AAAAAAATAA 780
AAA
  
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40

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Seq ID NO: C68 DNA Sequence
Nucleic Acid Accession #: NM_006433.2
Coding sequence: 129..566
  
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45
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 55

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1      11      21      31      41      51
|      |      |      |      |      |
GTATCTGTGG TAAACCCAGT GACACGGGGG AGATGACATA CAAAAGGGC AGGACCTGAG 60
AAAGATTAAAG CTGCAGGCTC CCTGCCATA AAACAGGGTG TGAAGGCAT CTCAGCGGCT 120
GCCCAACCAT GGTCTACCTG GCCCTCCTCG TCCTTGACGC CATGCTCTCG GGCAACCCAG 180
GTCTGGTCTT CTCTGCTCTG AGCCCTGAGT ACTACGACCT GGCAGAGCC CACCTGCGTG 240
ATGAGGAGAA ATCTTGCCCG TGCTTGGCCC AGGAGGGGCC CCAGGGTGAC CTGTTGACCA 300
AAACACAGGA GCTTGGCCGT GACTACAGGA CCTGTCTGAC GATAGTCCA AACTGAAGA 360
AGATGGTGA TAAGCCCAAC CAGAGAAAGT TTTCCAATGC TGGACCCCG GTGTGTAGGA 420
CGGGGAGGTC ACGATGGGCG GAGCTCTGCA GAAATTTTCA GAGGAGTAT CAGTCTAGAG 480
TTACCCAGGG CCTCTGGGCG GGAGAACTG CCCAGCAGAT CTGTGAGGAC CTCAGGTTGT 540
GTATACCTTC TACAGGTCCC CTCTGAGCCC TCTCACCTTG TCCTGTGAAA GAAGCACAGG 600
CTCTGTCTCT CAGATCCCGG GAACCTCAGC AACCTCTGCC GGTCTCTCGC TTCTCGATC 660
CAGAAATCCAC TCTCCAGTCT CCCTCCCTCG ACTCCCTCTG CTGTCTCTCC CTCTCAGAG 720
AATAAAGTGT CAAGCAAG
  
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60

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Seq ID NO: C69 DNA Sequence
Nucleic Acid Accession #: NM_002985.2
Coding sequence: 69..344
  
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65
 70
 75
 80

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1      11      21      31      41      51
|      |      |      |      |      |
GCTGCAAGG ATTCTGCGAG AGGATCAAGA CAGCAAGTGG ACCTCGCACA GCCTCTCCCA 60
CAGGTACCAT GAAGGTCTCC GCGGCAGCCC TCCTGTCTAT CCTATTGCT ACTGCCCTCT 120
GCGCTCCTCG ATCTGCTCTC CCATATTCCT CCGACACCAC ACCCTGCTGC TTTGCCCTACA 180
TTGCCCGCCC ACTGCCCGGT GCCACATCA AGGAGTATTT CTACACCAAT GGCAGTGTCT 240
CCAACCCAGC AGTGTCTTT GTCAACCGAA AGAACCGCCA AGTGTGTGCC AACCCAGAGA 300
AGAAATGGGT TCGGGAGTAC ATCAACTCTT TGGAGATGAG CTAGGATGGA GAGTCTTTGA 360
ACCTGAACCT ACACAAATTT GCCTGTTTCT GCTTGTCTTT GTCTAGCTTT GGGAGGCTTC 420
CCCTCACTAT CCTACCCAC CCGCTCCTTG AAGGGCCAG ATTCTACCAC ACAGCAGCAG 480
TTACAAAAAC CTTCCCCAGG CTGGAAGTGG TGGCTCAGGC CTGTAATCCC AGCACTTTGG 540
GAGGCCAAGG TGGGTGATC ACTTGAGGTC AGGAGTTTGA GACCAGCCTG GCCAACATGA 600
TGAAACCCCA TCTCTACTAA AAATACAAAA AATTAGCCGG GCGTGGTAGC GGGGCGCTGT 660
AGTCCAGCT ACTCGGGAGG CTGAGGAGG AGAATGGGTT GAACCCGGGA GGGGAGCTTT 720
GCAGTGAGGC GAGATCGGCG CACTGCACTC CAGCCTGGGC GACAGAGCGA GACTCCGTCT 780
CAAAAAAATA AAAAAAATA AAAATACAAA AATTAGCCGG GCGTGGTAGC CCAGCGCTGT 840
AATCCAGCT ACTCGGGAGG CTAAGGAGG AAAATTGTTT GAACCCAGGA GGTGGAGGCT 900
CAGGTGAGCT GAGATTGTGC CACTTCACTC CAGCCTGGGT GACAAAGTGA GACTCCGTCA 960
CAACAAACAA AAAAAAAGC TTCCCAACT AAAGCCTAGA AGAGCTTCTG AGGCGCTGCT 1020
TTGTCAAAG GAAGTCTCTA GGTCTGAGC TCTGGCTTTG CCTTGGCTTT GCCAGGGCTC 1080
  
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TGTGACCAGG AAGGAAGTCA GCATGCCCTCT AGAGGCAAGG AGGGGAGGAA CACTGCACTC 1140
 TTAAGCTTCC GCGCTCTCAA CCCCTCACAG GAGCTTACTG GCAAAACATGA AAAATCGGCT 1200
 TACCATTAAT GTTCTCAATG CAACCATATA AAAAAA 1237

5

Seq ID NO: C70 DNA Sequence
 Nucleic Acid Accession #: NM_022154.2
 Coding sequence: 1381..1722

10

1	11	21	31	41	51		
AGTGTGGTTT	TAGTTTTTC	TAAGAAGTGG	CGTGGTTTGG	GGCTTTATAT	COGGGAGGAG	60	
CATATGTACG	CAAATCCTGG	GGCGTTTGCA	AACCCGGATC	CGGGGCGTCT	GGCCCCATGC	120	
COGGCCGGGC	GTITGAGGGC	TACTGCCACG	CAGCGTTTCT	GGAGCCTGCC	GGCTGGTGCC	180	
15	CTGGTGGCCT	TATCTCTGT	CCCCCTTGT	CCTCTTTATC	TCAGGCTCTC	240	
GGGGGCCAC	TCGCCTATC	GCTCCCTCG	GCTACGCTGC	CATCCCAATG	CCCCGAGGT	300	
CGCAGCTGC	TGTCTTTTC	AAGGCGCGG	AGAACCAGGG	GCGTCCGCG	CCACCTCTGA	360	
CTCGAGCAG	CGCCGAGCAC	TGACGCTCCC	GCCCTTGGG	AAGGACGCCA	GTGCGCCCG	420	
CGCGTCCCT	CTGGCGGCA	GCCGTCGCG	GGCCCTCAAG	GGGAAGCCCA	GGCCAGGATG	480	
20	GCCCCGGGTC	GCGCGGTGGC	CGGGCTCCTG	TTGCTGGCGG	CCGCCGCGCT	CGGAGGAGTG	540
CGGAGGGGGC	CAGGCTAGC	CTTCAGCGAG	GATGTGCTGA	GCGTGTTCGG	CGCGAATCTG	600	
AGCCTGTGCG	CGCGCGAGCT	CCAGCACTTG	CTGGAGCAGA	TGGGAGCCGC	CTCCCGCTG	660	
GGCGTCCCG	AGCCTGGCCA	GCTGCACTTC	AACCACTGTT	TAACTGCTGA	AGAGATCTTT	720	
TCCTTCTATG	GCTTTTCAAA	TGCTACCCAA	ATAACCAAGT	CCAAATTTCT	TGTCATCTGT	780	
25	CCAGCAGTCT	TACAGCAATT	GAACCTTCAC	CCATGTGAGG	ATCGGCCCAA	GCACAAAACA	840
AGACCAAGTC	ATTGAGAAAT	TTGGGGATAT	GGATTCTCTG	CAGTGACGAT	TATTAAATCTG	900	
GCATCTCTCC	TCGGATTGAT	TTTGACTCCA	CTGATAAAGA	AATCTTATTT	CCCAAGGATT	960	
TTGACCTTTT	TTGTGGGGCT	GGCTATTGGG	ACTCTTTTTC	CAAAATGCAAT	TTTCCAACTT	1020	
ATTCCAGAGG	CATTGGGATT	TGATCCCAAA	GTGACAGATT	ATGTTGAGAA	GGCAGTTGCT	1080	
30	GTGTTTGGTG	GATTTTACCT	ACTTTTCTTT	TTTGAAAGAA	TGCTAAAGAT	GTTATTAAAG	1140
ACATATGGTC	AGAATGGTCA	TACCCACTTT	GGAAATGATA	ACTTTGGTCC	TCAAGAAAAA	1200	
ACTCATCAAC	CTAAAGCATT	ACCTGCCATC	AATGGTGTGA	CATGCTATGC	AAATCCTGCT	1260	
GTACAGAAAG	CTAATGGACA	TATCCATTTT	GATAATGTCA	GTGTGGTATC	TCTACAGGAT	1320	
GGAAAAAAG	AGCCCAAGTT	ATGTACCTGT	TTGAAGGGGC	CCAAACTGTC	AGAAATAGGG	1380	
35	ACGATTGCCT	GGATGATAAC	GCTCTGGGAT	GCCCTCCACA	ATTTTCATGA	TGGCCTGGCG	1440
ATTGGGGGCT	CCTGCACCTT	GTCTCTCCTT	CAGGGACTCA	GTACTTCCAT	AGCAATCCTA	1500	
TGTGAGGAGT	TTCCCAACGA	GTTAGGAGAC	TTTGTGATCC	TACTCAATGC	AGGGATGAGC	1560	
ACTCGACAA	CCTGTCTATT	CAACTTCCCT	TCTGCATGTT	CCTGCTATGT	TGGGCTAGCT	1620	
40	TTTGGCATTG	GTGTGGGCAA	CAATTTCCGT	CCAAATATTA	TATTTGCACT	TGCTGGAGGC	1680
ATGTTCTCTT	ATATTCTCTT	GGCAGATATG	TTTCCAGAGA	TGAATGATAT	GCTGAGAGAA	1740	
AAGGTAACTG	GAAGAAAAAC	CGATTTCACC	TTCTTCATGA	TTCAAGATGC	TGGAATGTTA	1800	
ACTGATTTCA	CAGCCATCTT	ACTCATTACC	TTGTATGCAG	GAGAAATCGA	ATTGGAGTAA	1860	
TAGAAAAATG	AAGATGGTGT	TGTTAATAAA	GGCATTAAAT	AGATAAAAC	ATCTCCAAAA	1920	
45	AGGATTTTGA	AGCTGATCCT	ATTTAGTTAA	AAAGATAAAT	TTGCTTTCAA	CTGTAGGTCC	1980
AGAAAAATGA	TTATTGGCAT	CAGTCTGTGA	AATAGTCCAT	TATTTGTGTG	TAAAAATGCT	2040	
TCAAAAGGTT	TTCAAGTCTA	GTCTGAGATG	CCTGGTATAT	AGGAGCCTTT	GGGAAATACT	2100	
TATTTTTCAG	TATTTTCATG	ATATTAGATA	TCACCATGAA	GCAAGAGACA	TGCATTCTAT	2160	
AATCATGTAG	ACACTCAGAC	TCAGGGGAAA	ATACAAGTTA	TATCCTGAAA	GCCTTTAAAA	2220	
50	CTCTATGGTA	GGATCAAGAA	TTCAAAATGGT	TTCAAGAGAG	TTTTATTTC	ATTAATTTGT	2280
TCTAGTGGTT	TCAGAGAGCA	GTACATCAAA	ATGTAGAAGG	TAAATGTAT	GCAACACTAA	2340	
TATAAATTTT	TCCAAGTCTT	TAAGAGAGCA	AAGAAAAAAA	AGATTCTCA	CAGCTTTTGT	2400	
TTCTGTTTGG	TATTTCAATT	AGGAACTTGC	AGTATTATTT	TGAAAAACAT	TCTAAAAATA	2460	
TAGGAGTTAG	GAAATAAATA	AAGTTTGTCT	AGCCCTGCTA	AGTTCAGGCT	TAGAGGCTTA	2520	
55	TGCTAAGTN	TAAACTTCAC	CAGATTCCAC	GAAAAAGCTG	ATAGCTTTT	TTCTGACTTA	2580
TGTTTGTGTT	TCAAGGCTCA	CAAAATGGCAG	AACAGTATGT	AAAGCTGGTA	ACACCTCGGT	2640	
TTCAAGTGAC	CATGTGTTTG	CTTTGTGAAG	GTGAAGAATA	TGTTGGTTTA	GAGAAAGAAA	2700	
TTGGATGTTA	TTTTATGCAA	TTTACTTTTA	AAGACAAACA	TAACTATTTA	GCAGAGATA	2760	
TTTAAATAAA	TGCAAAACAA	CAGCTGGACT	GCTGTACATC	AAGGACAGAT	TAACTGGAAA	2820	
60	ACATATGTTT	CTTATGTGTG	ATTGAGAGCC	ATTGAGAAAA	GACTTCTCTT	GTGTTTCAGCC	2880
TATACCTTTT	CATATGGTAT	ACCTTGAAAA	AAATTAGCAC	ACCATGGTTA	TTTTTCTACC	2940	
TTTATAAAAA	GACAGAGCCT	GTTTACTCAT	TTAGAAGATA	GAGAAAAATG	GTCTAAAAAT	3000	
GAACATCCTA	GATTCACACT	CCCAAGTCAC	TTAAGGTGAT	TTGATGGTGA	GGAAAAATGAT	3060	
TGACAAAGCC	CAACAATGAT	CTCAGGAATT	ACATTTTCCA	ACAGACCAAA	AAATGTTTTC	3120	
65	ATGTAGCAGC	AATGCAGATT	TGTTGAATAT	TTAATATATA	TTTTAGTATG	TATTTCACTT	3180
TATGACTGAC	AATTAAAAAA	TATTGTTTGG	CCAAATAGTA	AACACCTTT	TGAAACCATG	3240	
AAAAAA						3246	

70

Seq ID NO: C71 DNA Sequence
 Nucleic Acid Accession #: NM_004184.2
 Coding sequence: 188..1603

75

1	11	21	31	41	51		
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CTCAACTGCC	CAGCGTGACC	AGTGCCACCC	TCTGCAGTGT	CTTCCACAAC	CTGGTCTTGA	120	
CTGCTCTGCT	GAAACAAATCC	TCTGACCTCA	GGCCGGCTGT	GAACTGATTT	CCTGAGAGAT	180	
AGCAACCATG	CCCAACAGTG	AGCCCGCATC	TCTGCTGGAG	CTGTTCAACA	GCAATGCCAC	240	
80	ACAAGGGGAG	CTCGTAAGGT	CCCTCAAAGC	GGGAAATGCG	TCAAAGGATG	AAATTGATTC	300
TGCAGTAAAG	ATGTTGGTGT	CATTAAAAAT	GAGCTACAAA	GCTGCCGCGG	GGGAGGATTA	360	
CAAGGCTGAC	TGTCTCCAG	GGAACCCAGC	ACCTACCACT	AATCATGGCC	CAGATGCCAC	420	
AGAAGCTGAA	GAGGATTTTG	TGGACCCATG	GACAGTACAG	ACAAGCAGTG	CAAAAGGCAT	480	
AGACTACGAT	AAGCTCATTG	TTGGTTTGG	AAGTAGTAAA	ATTGACAAAG	AGCTAATAAA	540	
CCGAATAGAG	AGAGCCACCG	GCCAAAGACC	ACACCACTTC	CTGCGCAGAT	GCATCTTCTT	600	

5	CTCACACAGA	GATATGAATC	AGGTTCTTGA	TGCCTATGAA	AATAAGAAGC	CATTTTATCT	660
	GTACACGGGC	CGGGGCCCTT	CTTCTGAAGC	AATGCATGTA	GGTCACCTCA	TTCCATTTAT	720
	TTTCACAAAG	TGGCTCCAGG	ATGTATTAA	CGTGCCCTTG	GTCACTCCAGA	TGACGGATGA	780
	CGAGAAGTAT	CTGTGGAAAG	ACCTGACCTT	GGACCAGGCC	TATGGCGATG	CTGTTGAGAA	840
	TGCCAAGGAC	ATCATCGCCT	GTGGCTTTGA	CATCAACAAG	ACTTTCATAT	TCTCTGACCT	900
	GGACTACATG	GGGATGAGCT	CAGGTTTCTA	CAAAATGTG	GTGAAGATTG	AAAAGCATGT	960
	TACCTTCAAC	CAAGTGAAAG	GCATTTTCGG	CTTCACTGAC	AGCGACTGCA	TTGGAAGAT	1020
	CAGTTTTCTT	GCCATCCAGG	CTGCTCCCTC	CTTCAGCAAC	TCATTTCCAC	AGATCTTCCG	1080
10	AGACAGGACG	GATATCCAGT	GCCTTATCCC	ATGTGCCATT	GACCAGGATC	CTTACTTTAG	1140
	AATGACAAAG	GACGTGCGCC	CCAGGATCGG	CTATCTCTAA	CCAGCCCTGT	TGCACTCCAC	1200
	CTTCTTCCCA	GCCCTGCAGG	GCGCCAGAC	CAAAATGAGT	GCCAGCGACC	CAAACTCCTC	1260
	CATCTTCTCT	ACCGACACGG	CCAAGCAGAT	CAAAACCAAG	GTCAATAAGC	ATGCGTTTTT	1320
	TGGAGGGAGA	GACACCATCG	AGGAGCACAG	GCAGTTTGGG	GGCAACTGTG	ATGTGGACGT	1380
15	GTCTTTTATG	TACCTGACCT	TCCTTCTCGA	GGACGACGAC	AAGCTCGAGC	AGATCAGGAA	1440
	GGATTACACC	AGCGGAGCCA	TGCTCACCGG	TGAGCTCAAG	AAGGCACCTA	TAGAGGTTCT	1500
	GCAGCCCTTG	ATCGCAGAGC	ACCAGGCCCG	GCGCAAGGAG	GTCAOGGATG	AGATAGTGAA	1560
	AGAGTTTATG	ACTCCCCGGA	AGCTGTCCCT	CGACTTTCAG	TAGCACTCGT	TTTACATATG	1620
	CTTATAAAAG	AAGTGATGTA	TCAGTAATGT	ATCAATAATC	CCAGCCCATG	CAAAGCACCG	1680
20	CCACCTGTAG	GCTCTCTGCT	CATGGTAATT	ACTGGGCTTG	GCCTCTGTAA	GCCTGTGTAT	1740
	GTATATCAATA	CTGTTTCTTC	CTGTGAGTTC	CATTATTCTT	ATCTCTTATG	GGCAAGCAT	1800
	TGTGGTAAT	TGGTGTGCG	TAACATTGCA	TGGTGGGATA	GAGAAGTCCA	CGTGTGAGTC	1860
	TCTCCCCAAA	GCAGCCCCAC	AGTGGAGCCT	TGGCTGGGAA	GTCCATGGGC	CACCTGTGTC	1920
	TTGTCCATGG	AGGACTTCCG	AGGGTTCCAA	GTATACTCTT	AAGACCCACT	CTGTTTAAAA	1980
25	ATATATATTC	TATGTATGCG	TATATGGAAT	TGAAATGTCA	TTATTGTAA	CTAGAAAGTG	2040
	CTTTGAAATA	TTGATGTGGG	GAGGTTTATT	GAGCACAGA	TGTATTTCAG	CCCATGCCCC	2100
	CTCCCAAAA	GAAATTGATA	AGTAAAGCT	TCGTTATACA	TTTGACTAAG	AAATCACC	2160
	GCTTTAAAGC	TGCTTTTAA	AATGAAGATT	GAACAGAGTT	CAGCAATTTT	GATTAAATTA	2220
	AGACTTGGGG	GTGAACACTT	CCAGTTTACT	GAACCTCAGA	CCATGCATGT	AGTCCACTCC	2280
30	AGAAATCATG	CTCGCTTCCC	TTGGCACACC	AGTGTCTCC	TGCCAAATGA	CCCTAGACCC	2340
	TCTGTCTGCG	AGAGTCAGGG	TGGCTTTTCC	CCTGACTGTG	TCCGATGCCA	AGGAGTCTGT	2400
	GCCTCCGACG	ATGCTTCATT	TTGACCCCTG	GCTGCAGTGG	AAGTCAGCAC	AGAGCAGTGC	2460
	CCTGTGCTGT	TCCTGGACGG	GTGGACTTAG	CTAGGGAGAA	AGTCGAGGCA	GCAGCCCTCG	2520
	AGGCCCTCAC	AGATGTCTAG	GCAGGCCCTA	TTTCATCAGC	CAGCATGTGC	AGGCCCTGGA	2580
35	GAGCAAAAGC	AAATCTCAGG	GAAGTCCTTG	GTTGATGTAT	CTGGGTCTCC	CTTGGAGCAC	2640
	TCTGCCCTCC	TGTACCCAG	TAGAGTAAT	AAACTTCCTT	GGCTCTTAAA	AAA	2693

Seq ID NO: C72 DNA Sequence
Nucleic Acid Accession #: NM_004938.1
Coding sequence: 337..4632

40	1	11	21	31	41	51	
	CGGAGGACAG	CGGAGCCGAG	CCAACGCCGG	GGACTTTGTT	CCCTCCACGG	AGGGGACTCG	60
45	GCAACTCGCA	GCGGCGAGGT	CTGGGGCCGG	CGCCTGGGAG	GGATCTGCGC	CCCCACTCA	120
	CTCCCTAGCT	GTGTTCCCGC	CGCGGCCCGG	GCTAGTCTCC	GGCGCTGGCG	CCTATGGTGG	180
	GCCCTCGACA	GCGCTCCGGA	GGGACCGGGG	GAGCTCCAG	GCGCCCGGGA	CTGGAGACTG	240
	ATGCATGAGG	GGCTTACGGA	GGCGCAGGAG	CGGTGGTGAT	GGTCTGGGAA	GCGGAGCTGA	300
	AGTCCCTTGG	CTTTTGGTGA	GGCGTGACAG	TTTATCATGA	CGGTGTTTCA	GCAGGAAAAC	360
50	GTGGATGATT	ACTACGACAC	CGGCGAGGAA	CTTGGCAGTG	GACAGTTTGC	GGTTGTGAAG	420
	AAATGCCGTG	AGAAAAGTAC	CGGCCCTCAG	TATGCCGCCA	AATTCTATCA	GAAAAGGAGG	480
	ACTAAGTCCA	GCCGCGCGGG	TGTGAGCCCG	GAGGACATCG	AGCGGGAGGT	CAGCATCCTG	540
	AAGGAGATCC	AGCACCCTCA	TGTCATCACC	CTGCACGAGG	TCTATGAGAA	CAAGACGGAC	600
	GTCACTCCGA	TCTTGGAACT	CGTTGCAGGT	GGCGAGCTGT	TTGACTTCTT	AGCTGAAAAG	660
55	GAATCTTTAA	TTGAAGAGGA	AGCAACTGAA	TTTCTCAAAC	AAATTCTTAA	TGGTGTTTAC	720
	TACCTGCACT	CCCTTCAAAT	CGCCCACTTT	GATCTTAAGC	CTGAGAACAT	AATGCTTTTG	780
	GATAGAAATG	TCCCAAAACC	TCGGATCAAG	ATCATTGACT	TTGGGTTGGC	CCATAAAATT	840
	GACTTTGGAA	ATGAATTTAA	AAACATATTT	GGGACTCCAG	AGTTTGTTCG	TCCTGAGATA	900
	GTCAACTATG	AACTCTCTGG	TCTTGAGGCA	GATATGTGGA	GTATCGGGGT	AATAACCTAT	960
60	ATCCTCTTAA	GTGGGGCCTC	CCCATTTCTT	GGAGACACTA	AGCAAGAAAC	GTTAGCAAAT	1020
	GTATCCGCTG	TCAACTACGA	ATTGAGGAT	GAATACTTCA	GTAATACCA	TGCCCTAGCC	1080
	AAAGATTTC	TAAGAAGACT	TCTGGTCAAG	GATCCAAAGA	AGAGAATGAC	AATTCAAGAT	1140
	AGTTTGCAGC	ATCCCTGGAT	CAAGCCTAAA	GATACACAAC	AGGCACCTAG	TAGAAAAGCA	1200
	TCAGCAGTAA	ACATGGAGAA	ATTCAAGAAG	TTTGACGCC	GGAAAAATG	GAAACAATCC	1260
65	GTTCGCTTGA	TATCACTGTG	CCAAAGATTA	TCCAGGTCT	TCCTGTCCAG	AAGTAACATG	1320
	AGTGTTCGCA	GAAGCGATGA	TACTCTGGAT	GAGGAAGACT	CCTTTGTGAT	GAAAGCCATC	1380
	ATCCATGCCA	TCAAAGATGA	CAATGTCCCA	GGCCTGCAGC	ACCTTCTGGG	CTCATATTAC	1440
	AACTATGATG	TTAACCAACC	CAACAAGCAC	GGGACACCTC	CATTACTCAT	TGCTGCTGGC	1500
	TGTGGGAATA	TTCAAATACT	ACAGTTGCTC	ATTAAAGAG	GCTCGAGAAT	CGATGTCCAG	1560
70	GATAAGGGCG	GGTCCAATGC	CGTCTACTGG	GCTGCTCGGC	ATGGCCACGT	CGATACTTGT	1620
	AAATTTCTCA	GTGAGAACAA	ATGCCCTTTG	GATGTGAAAG	ACAAGTCTGG	AGAGATGGCC	1680
	CTCCACGTGG	CAGCTCGCTA	TGGCCATGCT	GACGTGGCTC	AAGTTACTTG	TGCAGCTTGG	1740
	GCTCAAAATC	CAATATCCAG	GACAAAGGAA	GAAGAAACCC	CCCTGCACTG	TGCTGCTTGG	1800
	CACGGCTATT	ACTCTGTGGC	CAAGGCCCTT	TGTGAAGCCG	GCTGTAAAGT	GAACATCAAG	1860
75	AAACGAGAAG	GAGAGACGCC	CCTCCTGACA	GCTCTGCGCA	GGGGCTACCA	CGACATCGTG	1920
	GAGTGTCTGG	CCGAACATGG	AGCCGACCTT	AATGCTTTCG	ACAAGGACCG	ACACATTGCC	1980
	CTTCATCTGG	CTGTAAAGAG	GTGTCAGATG	GAGGTAATCA	AGACTCTCCT	CAGCCAAAGG	2040
	TGTTTCGTGG	ATTATCAAGA	CAGGCACGGC	AATACTCCCC	TCCATGTGGC	ATGTAAGAT	2100
	GGCAACATGC	CTATCGTGTG	GGCCCTCTGT	GAAGCAAACT	GCAATTTGGA	CATCTCCAAC	2160
80	AAGTATGGGC	GAAACGCCCT	GCACCTTGGG	GCCAAACAAG	GAATCTTAGA	CGTGGTCCGG	2220
	TATCTCTGTC	TGATGGGAGC	CAGCGTTGAG	GCGCTGACCA	CGGACGGAAA	GACGGCAGAA	2280
	GATCTTGCTA	GATCTGGAACA	GCACGAGCAC	GTAGCAGGTC	TCCTTGTCAAG	ACTTCGAAAG	2340
	GATACGCACC	GAGGACTCTT	CATCCAGCAG	CTCCGACCCA	CACAGAACCT	GCAGCCCAAG	2400
	ATTAAGCTCA	AGCTGTTTGG	CCACTCGGGA	TCCGGGAAAA	CCACCTTGTG	AGAACTCTCT	2460
	AACTGTGGGC	TGCTGAGGAG	CTTTTTCAGA	AGGCGTCGGC	CCAGACTGTC	TTCACCAAC	2520

5	TCCAGCAGGT	TCCACCTTC	ACCCCTGGCT	TCTAAGCCCA	CAGTCTCAGT	GAGCATCAAC	2580
	AACTCTTACC	CAGGCTGCGA	GAACGTGAGT	GTGAGGAGCC	GCACGATGAT	GTTCGAGCCG	2640
	GGTCTTACCA	AAGGGATGCT	GGAGGTGTTT	GTGGCCCGGA	CCCACCAACC	GCACCTGCTG	2700
	GCCGATGACC	AGTCCACCAA	GGCCATCGAC	ATCCAGAACG	CTTATTTGAA	TGGAGTTGGC	2760
	GATTTCAGCG	TGTGGGAGTT	CTCTGGAAAT	CCTGTGTATT	TCTGCTGTTA	TGACTATTTT	2820
	GCTGCAAAATG	ATCCCACGTC	AATCCATGTT	GTTGTCTTTA	GTCTAGAAGA	GCCCTATGAG	2880
	ATCCAGCTGA	ACCCAGTGAT	TTTCTGGCTC	AGTTTCTCTG	AGTCCCTTGT	CCCAGTTGAA	2940
	GAACCCATAG	CCTTCGGTGG	CAAGCTGAAG	AACCCACTCC	AAGTTGTCTT	GGTGGCCACC	3000
10	CACGCTGACA	TCATGAATGT	TCCTCGACCG	GCTGGAGGCG	AGTTTGGATA	TGACAAAGAC	3060
	ACATCGTTCG	TGAAAGAGAT	TAGGAACAGG	TTTGGAAATG	ATCTTCACAT	TTCAAATAAG	3120
	CTGTTTGTTC	TGATGCTGGG	GGCTTCTGGG	TCAAAGGACA	TGAAGGTACT	TCGAAATCAT	3180
	CTGCAAGAAA	TACGAAGCCA	GATTGTTTCG	GTCTGTCTCT	CCATGACTCA	CCTGTGTGAG	3240
	AAAAATCATCT	CCAGCTGCCC	TTCTTGGAGG	AAGCTCAATG	GACCCAAACC	GCTGATGTCT	3300
	CTGCAGCAGT	TTGTGTACGA	CGTGCAGGAC	CAGCTGAACC	CCCTGGCCAG	CGAGGAGGAC	3360
15	CTCAGGCGCA	TGTCTCAGCA	GCTCCACAGC	ACAGGCGAGA	TCAACATCAT	GCAAAGTGAA	3420
	ACAGTTCAGG	ACGTGCTGCT	CCTGGACCCC	CGCTGGCTCT	GCACAAACGT	CCTGGGGAAG	3480
	TTGCTGTCCG	TGGAGACCCC	ACGCGCGCTG	CACCACTACC	GGGGCCGCTA	CACCGTGGAG	3540
	GACATCCAGC	GCCTGGTGCC	CGACAGCGAC	GTGGAGGAGC	TGCTGCAGAT	CCTCGATGCC	3600
20	ATGGACATCT	GCGCCCGGGA	CCTGAGCAGC	GGGACCATGG	TGGAGCTCCC	AGCCCTGATC	3660
	AAGACAGACA	ACCTGCACCG	CTCTGGGCTT	GATGAGGAGG	ACGAGGTGAT	GGTGTATGGT	3720
	GGCTGTGCGA	TGCTGCCCGT	GGAAACACCT	ACCCCTTCCC	CATGTGGCAT	CTTTCACAAG	3780
	GTCCAGGTGA	ACCTGTGCCG	GTGGATCCAC	CAGCAAAGCA	CAGAGGGCGA	CGCGGACATC	3840
	CGCTGTGGGG	TGAATGGCTG	CAAGCTGGCC	AACCGTGGGG	CCGAGCTGCT	GGTGTCTGCT	3900
25	GTCAACGAGC	GCCAGGGCAT	TGAGGTCCAG	GTCCGTGGCC	TGGAGACGGA	GAAGATCAAG	3960
	TGCTGTCTGC	TGCTGGAATC	GGTGTGCAGC	ACCATTTAGA	ACGTTCATGC	CACCACTGAG	4020
	CCAGGGCTCC	TGACGTGAAA	GCAATTAACG	AGCCCGCAGC	AGCTGCGGGA	GCACCATGAG	4080
	CCCGTCTATGA	TCTACCAAGC	ACGCGGACTT	TTCCGGGCAC	AGACTCTGAA	GGAAACCTCA	4140
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Nucleic Acid Accession #: NM_002081.1
Coding sequence: 222..1898

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Seq ID NO: C74 DNA Sequence
Nucleic Acid Accession #: BC030205.1
Coding sequence: 45..878

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AATAACAGCT CACCTACGCA GAAGCTAAGG CGTGTGTGA ATTGGAAGGC GGCCATCTCG 240
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Seq ID NO: C75 DNA Sequence
Nucleic Acid Accession #: NM_001982.1
Coding sequence: 199..4227

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Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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      G A G G A T C T A C   C T G A G A G G A   G G A T C T A C C T   G A A G T T A A G C   C T A A A T C A G A   A G A A G A G G G C   360
      T C C C T G A A G T   T A G A G G A T C T   A C C T A C T G T T   G A G G C T C C T G   G A G A T C C T C A   A G A A C C C C A G   420
      A A T A A T G C C C   T A C A G G A C A A   A G A A G G G G A T   G A C C A G A G T C   A T T G G C G C T A   T G G A G G C G A C   480
      C C G C C C T G G A   C C C G G T G T C   C C C A G C C T G C   G C G G G C C G C T   T C C A G T C C C C   G G T G G A T A T C   540
      C G C C C C C C G C   T C G C C G C C T T   C T G C C C G G C C   C T G C G C C C C C   T G G A A C T C C T   G G G C T T C C A G   600
      C T C C G C C C G C   T C C C A G A A C T   G C G C T G C G C   A A C A A T G G C C   A C A G T G T G C A   A C T G A C C C T G   660
      C C T C C T G G G C   T A G A G A T G G C   T C T G G T C C C   G G G C G G A G T   A C C G G C T C T   G C A G C T G C A T   720
      C T G C A C T G G G   G G G C T G C A G G   T C G T C C G G C   T C G G A G C A C A   C T G T G G A A G G   C C A C C G T T T C   780
      C C T G C C G A G A   C C C G G T G G T   T C A C C T C A G C   A C C G C C T T T G   C A G A G T T G A   C G A G G C C T T G   840
      G G G C C C C C G G   G A G G C C T G G C   C G T G T T G C C   G C C T T T C T G G   A G G A G G G C C C   G G A A G A A A A C   900
      A G T G C C T A T G   A G C A G T G C T   G T C T C G C T T G   G A A G A A A T C G   C T G A G G A A G G   C T C A G A G A C T   960
      C A G G T C C C A G   G A C T G G A C A T   A T C T G C A C T C   C T G C C C T C T G   A C T T C A G C C G   C T A C T T C C A A   1020
      T A T G A G G G G T   C T C T G A C T A C   A C C G C C C T G T   G C C A G G G T G   T C A T C T G A C   T G T G T T T A A C   1080
      C A G A C A G T G A   T C T G A G T G C   T A A G C A G C T C   C A C A C C C T C T   C T G A C A C C C T   G T G G G A C C T   1140
      G G T G A C T C T C   G G C T A C A G C T   G A A C T T C C G A   G C A G C A G C   C T T T G A A T G G   G C G A G T G A T T   1200
      G A G G C C T C C T   T C C C T G C T G G   A G T G G A C A G C   A G T C C T C G G G   C T G C T A G A C C   A G T C C A G C T G   1260
      A A T T C C T G C C   T G G C T G C T G G   T G A C A T C C T A   G C C C T G G T T T   T T G G C C T C C T   T T T T G C T G T C   1320
      A C C A G G T C G   C G T T C C T T G T   G C A G A T G A G A   A G G C A G C A C A   G A A G G G G A A C   C A A A G G G G G T   1380
      G T G A G C T A C C   G C C C A G C A G A   G G T A G C C G A G   A C T G A G C C T   A G A G G C T G G A   T C T T G G A G A A   1440
      T G T G A G A A G C   C A G C C A G A G G   C A T C T G A G G G   G G A G C C G G T A   A C T G T C C T G T   C C T G C T C A T T   1500
      A T G C C A C T T C   C T T T T A A C T G   C C A G A A A A T T   T T T T A A A A T A   A A T A T T T A T A   A T   1552
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Seq ID NO: C77 DNA Sequence

Nucleic Acid Accession #: NM_004207.1
Coding sequence: 63..1460

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      C C A T G G G A G G   G G C C T G G T G T   G A C G A G G G C C   C C A C A G G C G T   C A A G G C C C C T   G A C G G C G G C T   120
      G G G G C T G G G C   C G T G C T C T T C   G G C T G T T T C G   T C A T C A C T G G   C T T C T C C T A C   G C C T T C C C C A   180
      A G G C C G T C A G   T G T C T T C T T C   A A G G A G C T C A   T A C A G G A G T T   T G G A T C G G C   T A C A G C G A C A   240
      C A G C C T G G A T   C T C C T C C A T C   C T G C T G G C C A   T G C T C T A C G G   G A C A G G T C C G   C T C T G C A G T G   300
      T G T G G T G A A   C G C T T T G G C   T G C C G G C C C G   T C A T G C T T G T   G G G G G T C T C   T T T G C G T C G C   360
      T G G G A T G G T   G G C T G C G T G C   T T T T G C C G G A   G C A T C A T C C A   G G T C A C C T C   A C C A C T G G G G   420
      T C A T C A C G G G   G T T G G G T T T G   G C A C T C A A C T   T C C A G C C C T C   G C T C A T C A T G   C T G A A C G C T   480
      A C T T C A G C A A   G C G G C G C C C C   A T G G C C A A C G   G G C T G G C G G C   A G C A G G T A G C   C C T G T C T T C C   540
      T G T G T G C C C T   G A G C C C G C T G   G G G C A G C T G C   T G C A G G A C C G   C T A C G G C T G G   C G G G C G G C T   600
      T C C T C A T C C T   G G G C G G C C T G   C T G C T C A A C T   G C T G C G T G T G   T G C C G C A C T C   A T G A G G C C C C   660
      T G T G G T C A C   G C C C A G C C G   G G C T C G G G G C   G C C C G C G A C C   C T C C G G C G C   C T G C T A G A C C   720
      T G A G G T C C T   C G G G A C C G C   G G C T T T G T G C   T T T A C G C O G T   G G C C G C C T C G   G T C A T G G T G C   780
      T G G G G C T C T T   C G T C C C G C C C   G T G T T G T G G   T G A G C T A C G C   C A A G G A C C T G   G G C G T G C C C G   840
      A C A C C A A G G C   C G C C T T C C T G   C T C A C C A T C C   T G G G C T T C A T   T G A C A T C T T C   G C G C G G C C G G   900
      C C G C G G C T T   C G T G G C G G G G   C T T G G G A A G G   T G C G G C C C T A   C T C C G T C A C   C T C T T C A G C T   960
      T C T C C A T G T T   C T T C A A C G G C   C T C G C G G A C C   T G G C G G G C T C   T A C G G C G G G C   G A C T A C G G G C   1020
      G C C T G T G G T   C T T C T G C A T C   T T C T T T G G C A   T C T C C T A C G G   C A T G T G G G G   G C C C T G C A G T   1080
      T C G A G G T G C T   C A T G G C C A T C   G T G G G C A C C C   A C A A G T T C T C   C A G T G C A T T   G G C C T G G T G C   1140
      T G C T G A T G G A   G G C G G T G G C C   G T G C T C G T C G   G C C C C C T T C   G G G A G G C A A A   C T C C T G G A T G   1200
      C G A C C A C A G T   C T A C A T G T A C   G T G T T C A T C C   T G G C G G G G G C   C A G G T G C T C   A C C T C C T C C C   1260
      T G A T T T T G C T   G C T G G G C A A C   T T C T T C T G C A   T T A G G A A G A A   G C C C A A A G A G   C C A C A G C C T G   1320
      A G G T G G C G G C   C G C G A G G A G   G A G A A G C T C C   A C A A G C C T C C   T G C A G A C T C G   G G G G T G G A C T   1380
      T G C G G G A G G T   G G A G C A T T T C   C T G A A G G C T G   A G C C T G A G A A   A A A C G G G G A G   G T G G T T C A C A   1440
      C C C C G A A A C   A A G T G T C T G A   G T G G C T G G G C   G G G C C G G C A   G G C A C A G G A   G G A G T A C A G   1500
      A A G C C G G C A A   C G C T T G C T A T   T T A T T T T A C A   A A C T G G A C T G   G C T C A G G C A G   G G C C A C G G C T   1560
      G G G C T C C A G C   T G C C G G C C C A   G C G G A T C G T C   G C C C G A T C A G   T G T T T T G A G G   G G G A A G G T G G   1620
      C G G G T G G G A   A C C G T G T C A T   T C C A G A G T G G   A T C T G C G G T G   A A G C C A A G C C   G C A A G G T T A C   1680
      A A G G C A T C C T   C A C C A G G G G C   C C C G C C T G C T   G C T C C C A G G T   G G C C T G C G G C   C A C T G C T A T G   1740
      C T C A A G A C C   T G G A A A C C C A   T G C T T C G A G A   C A A C G T G A C T   T T A A T G G G A G   G G T G G G T G G G   1800
      C C G C A G A C A G   G C T G G C A G G G   C A G G T G C T G C   G T G G G G C C C T   C T C C A G C C C G   T C C T A C C C T G   1860
      G G C T C A C A T G   G G G C C T G T G C   C C A C C C C T C T   T G A G T G T C T T   G G G A C A G C T   C T T T C C A C C C   1920
      C T G G A A G A T G   G A A A T A A A C C   T G C G T G T G G G   T G G A G T G T T C   T C G T G C C G A A   T T C A A A A A G C   1980
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Seq ID NO: C78 DNA Sequence

Nucleic Acid Accession #: NM_000358.1
Coding sequence: 48..2099

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      T G C G G C T G C T   G G C T C T C G C C   C T G G C T C T G G   C C C T G G G C C C   C G C G C G A C C   C T G G C G G G T C   120
      C C G C A A G T C   G C C C T A C C A G   C T G G T G C T G C   A G C A C A G C A G   G C T C G G G G G C   C G C C A G A C A G   180
      G C C C C A A C G T   G T G T G C T G T G   C A G A A G G T T A   T T G G C A C T A A   T A G G A A G T A C   T T C A C C A A C T   240
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5	GCAAGCAGTG	GTACCAAAGG	AAAATCTGTG	GCAAATCAAC	AGTCATCAGC	TACGAGTGCT	300
	GTCTGTGATA	TGAAAAGGTC	CCTGGGGAGA	AGGGCTGTCC	AGCAGCCCTA	CCACTCTCAA	360
	ACCTTTACGA	GACCCCTGGGA	GTGGTTGGAT	CCACCACCAC	TCAGCTGTAC	ACGGACCGCA	420
	CGGAGAAGCT	GAGGCTCTGAG	ATGGAGGGGC	CCGGCAGCTT	CACCATCTTC	GCCCTTAGCA	480
	ACGAGGCGTG	GGCCTCCTTG	CCAGCTGAAG	TGCTGGACTC	CCTGGTCAGC	AATGTCAACA	540
	TTGAGCTGCT	CAATGCCCTC	CGCTACCATA	TGGTGGSCAG	GCGAGTCTTG	ACTGATGAGC	600
	TGAAACACGG	CATGACCCCTC	ACCTCTATGT	ACCAGAATTC	CAACATCCAG	ATCCACCACT	660
	ATCCTAATGG	GATTGTAACT	GTGAACTGTG	CCCGGCTCCT	GAAAGCCGAC	CACCATGCAA	720
10	CCAAOOGGGT	GGTGCACTTC	ATCGATAAGG	TCATCTCCAC	CATCACCAC	AACATCCAGC	780
	AGATCATTGA	GATCGAGGAC	ACCTTTGAGA	CCCTTCGGGC	TGCTGTGGCT	GCATCAGGGC	840
	TCAACACGAT	GCTTGAAGGT	AACGGCCAGT	ACAGCTTTT	GGCCCCGACC	AATGAGGCTT	900
	TGAGAGAAGT	CCCTAGTGAG	ACTTTGAACC	GTATCCTGGG	CGACCCAGAA	GCCCTGAGAG	960
	ACCTGCTGAT	CAACCAATC	TTGAAGTCAG	CTATGTGTGC	TGAAGCCATC	GTTCGGGGGC	1020
15	TGCTGTGATA	GACCCCTGGAG	GGCAGCACAC	TGGAGGTGGG	CTGCAGCGGG	GACATGCTCA	1080
	CTATCAACGG	GAAGGCGATC	ATCTCCAATA	AAGACATCCT	AGCCACCAAC	GGGGTGATCC	1140
	ACTACATTGA	GCTGTACTCT	ATCCAGACT	CAGCCAAGAC	ACTATTTGAA	TTGGCTGCAG	1200
	AGTCTGATGT	GTCCACAGCC	ATTGACCTTT	TCAGACAAGC	CGGCTCGGCT	AATCATCTCT	1260
	CTGGAAGTGA	CGGGTTGACC	CTCCTGGCTC	CCCTGAATTC	TGTATTCAAA	GATGGAACTC	1320
20	CTCCAATTGA	TGCCCATACA	AGGAATTTGC	TTCCGAACCA	CATAATTAAA	GACCAGCTGG	1380
	CTCTTAAGTA	TCGTGTACAT	GGACAGACCC	TGGAACTCT	GGGGGGCAAA	AAACTGAGAG	1440
	TTTTTGTTTA	TCGTAATAGC	CTCTGCATTG	AGAACAGCTG	CATCGCGGCC	CACGACAAGA	1500
	GGGGGAGGTA	CGGGACCCCTG	TTCAAGATGG	ACCGGGTGCT	GACCCCCCA	GTGGGGACTG	1560
	TCATGGATGT	CCTGAAGGGA	GACAATCGCT	TTAGCATGCT	GGTAGCTGCT	ATCCAGTCTG	1620
25	CAGGACTGAC	GGAGACCCCTC	AACCGGGAAG	GAGTCTACAC	AGTCTTTGCT	CCCACAAATG	1680
	AAGCCTTCCG	AGCCCTTGCCA	CCAGAGAGAC	GGAGCAGACT	CTTGGGAGAT	GCCAGGAAC	1740
	TTGCCAATCAT	TCGATAAATAC	CACATTGGTG	ATGAAATCCT	GGTTAGCGGA	GGCATCGGGG	1800
	CCCTGGTCCG	GCTAAAGTCT	CTCCAAGGTG	ACAAGCTGGA	AGTCAGCTTG	AAAAACAATG	1860
	TGGTGAGTGT	CAACAAGGAG	CCTGTTGCCG	AGCCTGACAT	CATGGCCACA	AATGGCGTGG	1920
30	TCCATGTCTAT	CACCAATGTT	CTGCAGCCTC	CAGCCAACAG	ACCTCAGGAA	AGAGGGGATG	1980
	AACTTGCAGA	CTCTGCGCTT	GAGATCTTCA	AACAAGCATC	AGGCTTTTCC	AGGGCTTCCC	2040
	AGAGGTCTGT	CGCACTAGCC	CCTGTCTATC	AAAAGTTATT	AGAGAGGATG	AAGCAATTAGC	2100
	TGGAAGCACT	ACAGGAGGAA	TGCACCAAGG	CAGCTCTCCG	CCAATTTCTC	TCAGATTTC	2160
	ACAGAGACTG	TTTGAATGTT	TTCAAAACCA	AGTATCACAC	TTTAATGTAC	ATGGGCGCGA	2220
35	CCATAATGAG	ATGTGAGCCT	TGTGCATGTG	GGGGAGGAGG	GAGAGAGATG	TACTTTTAA	2280
	ATCATGTCTC	CCCTAAACAT	GGCTGTTAAC	CCACTGCATG	CAGAAACTTG	GATGTCACTG	2340
	CTTGACATTC	ACTTCCAGAG	AGGACCTATC	CCAAATGTGG	AATTGACTGC	CTATGCCAAG	2400
	TCCTCGGAAA	AGGAGCTTCA	GTAATTGTGG	GCTCATAAAA	CATGAATCAA	GCAATCCAGC	2460
	TCATGGGAAA	GTCTTGCCAC	AGTTTTGTGA	AAGCCCTTGC	ACAGCTGGAG	AAATGGCATG	2520
40	ATTATAAGCT	ATGAGTTGAA	ATGTTCTGTC	AAATGTGTCT	CACATCTACA	CGTGGCTTGG	2580
	AGGCTTTTAT	GGGGCCCTGT	CCAGGTAGAA	AAGAAATGGT	ATGTAGAGCT	TAGATTTCCT	2640
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Seq ID NO: C79 DNA Sequence

Nucleic Acid Accession #: NM_006536.2

Coding sequence: 109..2940

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	AGCATTGACG	GTCTTATTTC	CAACCTGAAG	TTTGTGACTC	TCCTGGTTGC	CTTAAGTTCA	180
	GAACTCCCAT	TCCTGGGAGC	TGGAGTACAG	CTTCAAGACA	ATGGGTATAA	TGGATTGCTC	240
55	ATTGCAATTA	ATCCTCAGGT	ACCTGAGAAT	CAGAACCTCA	TCTCAAAACAT	TAAAGGAAATG	300
	ATAAAGTGAAG	CTTCAATTTA	CCTATTATAT	GCTACCAAGA	GAAAGAGTAT	TTTCAGAAAT	360
	ATAAAGATTT	TAATAACCTGC	CACATGGAAA	GCTAATAATA	ACAGCAAAAT	AAAAACAAGAA	420
	TCATATGAAA	AGGCAATGT	CATAGTGACT	GACTGGTATG	GGGCAATGG	AGATGATCCA	480
	TACACCCCTAC	AATACAGAGG	GTGTGAAAA	GAGGAAAAAT	ACATTCAATT	CACACCTAAT	540
60	TTCTACTGA	ATGATAACTT	AACAGCTGGC	TACGGATCAC	GAGGCGAGT	GTTTGTCCAT	600
	GAATGGGCCC	ACCTCCGTTG	GGGTGTGTTT	GATGAGTATA	ACAATGACAA	ACCTTTCTAC	660
	ATAAATGGGC	AAAATCAAAAT	TAAAGTGACA	AGGTGTTTAT	CTGACATCAC	AGGCATTTTT	720
	GTGTGTGAAA	AAGGTCCCTG	CCCCCAAGAA	AACGTATTTA	TTAGTAAGCT	TTTTAAAGAA	780
	GGATGCACCT	TTATCTACAA	TAGCACCCAA	AATGCAACTG	CATCAATAAT	GTTTCATGCA	840
65	AGTTTATCTT	CTGTGGTTGA	ATTTTGTAAAT	GCAAGTACCC	ACAACCAAGA	AGCACCAAAC	900
	CTACAGAAC	AGATGTGCAG	CCTCAGAAAT	GCAATGGGATG	TAATCAACAG	CTCTGCTGAC	960
	TTTCAACCA	GCTTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCAC	ATTCTCGCTT	1020
	GTACAGGCTG	GTGACAAAGT	GGTCTGTTTA	GTGCTGGATG	TGTCACAGAA	GATGGCAGAG	1080
	GCTGACAGAC	TCCTTCAACT	ACAACAAGCC	GCAGAAATTT	ATTTGATGCA	GATTGTGAA	1140
70	ATTTCATCCT	TCGTGGGCAT	TGCCAGTTTC	GACAGCAAG	GAGAGATCAG	AGCCCCAGCTA	1200
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	TCAGCTAAAA	CAGACATCAG	CATTGTGTTA	GGGCTTAAGA	AAGGATTGGA	GGTGGTTGAA	1320
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	CTTCTTGCCA	ATTGCTTACC	CACGTGTGCTC	AGCAGTGGTT	CAACAATTCA	CTCCATTGCC	1440
75	CTGGGTTTCAT	CATGACCCCC	AAATCTGGAG	GAATTATCAC	GTCTTACAGG	AGGTTTAAAG	1500
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	TCTGGAAATG	GAGACATTTT	CCAGCAACAT	ATTGAGCTTG	AAAGTACAGG	TGAAAATGTC	1620
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80	GGACGAAAA	ACTACACAAA	TAATTTTATC	ACCAATCTAA	CTTTTCGGAC	AGCTAGTCTT	1800
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	TCTCTGCAAG	CCCTGAAAGT	GACAGTGACC	TCTCGCGCCT	CCAACCTCAGC	TGTGCCCCCA	1920
	GCCACTGTGG	AAGCCTTTGT	GAAAAGAGAC	AGCCTCCATT	TTCTCTATCC	TGTGATGATT	1980
	TATGCCAATG	TGAAACAGGG	ATTTTATCCC	ATTCCTTAATG	CCACTGTGAC	TGCCACAGTT	2040
	GAGCCAGAGA	CTGGAGATCC	TGTTACGCTG	AGACTCCTTG	ATGATGGAGC	AGGTGCTGAT	2100

5	GTATATAAAA	ATGATGGAAT	TTACTCGAGG	TATTTTTTCT	CCTTGCTGTC	AAATGGTAGA	2160
	TATAGCTTGA	AAGTGCATGT	CAATCACTCT	CCCAGCATAA	GCACCCGAGC	CCACTCTATT	2220
	CCAGGGAGTC	ATGCTATGTA	TGTACCAAGT	TACACAGCAA	ACGGTAATAT	TCAGATGAAT	2280
	GCTCCAAGGA	AATCAGTAGG	CAGAAATGAG	GAGGAGOGAA	AGTGGGGCTT	TAGCOGAGTC	2340
	AGCTCAGGAG	GCTCCTTTTC	AGTGTCTGGA	GTTCACAGCTG	GCCCCCAGCC	TGATGTGTTT	2400
	CCACCATGCA	AAATTATTTA	CCTGGAAGCT	GTAAGAGTAG	AAGAGGAATT	GACCCATCTT	2460
	TGGACAGCAC	CTGGAGAAGA	CTTTGATCAG	GGCCAGGCTA	CAAGCTATGA	AATAAGAAATG	2520
	AGTAAAAGTC	TACAGAATAT	CCAAGATGAC	TTTAACAATG	CTATTTTAGT	AAATACATCA	2580
10	AAGCGAAATC	CTCAGCAAGC	TGGCATCAGG	GAGATATTTA	CGTTCTCACC	CCAGATTTC	2640
	ACGAATGGAC	CTGAACATCA	GCCAAATGGA	GAAACACATG	AAAGCCACAG	AATTTATGTT	2700
	GCAATTACGAG	CAATGGATAG	GAACCTCTTA	CAGTCTGCTG	TATCTAACAT	TGCCCCAGGOG	2760
	CCTCTGTTTA	TTCCCCCAA	TTCTGATCCT	GTAOCTGCCA	GAGATTATCT	TATATTGAAA	2820
	GGAGTTTAA	CAGCAATGGG	TTTGATAGGA	ATCATTTGCC	TTATTATAGT	TGTGACACAT	2880
15	CATACCTTAA	GCAGSAAAAA	GAGAGCAGAC	AAGAAAGAGA	ATGGAACAAA	ATTATTATAA	2940
	ATAAATATCC	AAAGTGTCTT	CCTTCTTAGA	TATAAGACCC	ATGGCCTTCG	ACTACAAAAA	3000
	CATACATAAC	AAATTAATTT	AACATCAAAA	CTGTATTAAA	ATGCATTGAG	TTTTTGTA	3060
	ATACAGATAA	GATTTTATCA	TGGTAGATCA	ACAATTCTTT	TTGGGGGTAG	ATTAGAAAAA	3120
	CCTTACACTT	TGGCTATGAA	CAAATAATAA	AAATTATCTT	TTAAAGTAAT	GTCTTTAAAG	3180
20	GCAAAGGGAA	GGGTAAAGTC	GGACCAAGT	CAAGGAAAGT	TTGTTTATTT	GAGGTGGAAA	3240
	AATAGCCCCA	AGCAGAGAAA	AGGAGGTAG	GTCTGCATTA	TAACCTGTCTG	TGTGAAGCAA	3300
	TCATTTAGTT	ACTTTGATTA	ATTTTCTTTT	TCTCCTTATC	TGTGCAGTAC	AGGTTGCTGT	3360
	TTTACATGAA	GATCATGCTA	TATTTATAT	ATGTAGCCCC	TAATGCAAAG	CTCTTTACCT	3420
	CTTGCTATTT	TGTTATATAT	ATTTACAGATG	ACATCTCCCT	GCTAATGCTC	AGAGATCTTT	3480
25	TTTCACTGTA	AGAGGTAAACC	TTTAAACAATA	TGGGTATTAC	CTTTGTCTCT	TCATACCGGT	3540
	TTTATGACAA	AGGTCTATTG	AAATTATTTG	TNTGTAAGTT	TCTACTCCCA	TCAAAGCAGC	3600
	TTTCTAAGTT	TATTGCCTTG	GGTTATTATG	GAATGATAGT	TATAGCCCN	TATAATGCCT	3660
	TACCTAGGAA	A					3671

Seq ID NO: C80 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1413

35	1	11	21	31	41	51	
	ATGAAGTTTC	TTCTAATACT	GCTCCTGCAG	GCCACTGCTT	CTGGAGCTCT	TCCCTGAAC	60
	AGCTCTACAA	GCCCTGAAAA	AAATAATGTG	CTATTTGGTG	AAAGATACTT	AGAAAAATTT	120
	TATGGCCTTG	AGATAAACAA	ACTTCCAGTG	ACAAAAATGA	AATATAGTGG	AAACTTAATG	180
	AAGGAAAAAA	TCCAAGAAAT	GCAGCACTTC	TTGGGTCTGA	AAGTGACCGG	GCAACTGGAC	240
40	ACATCTAACC	TGGAGATGAT	GCAAGCACCT	CGATGTGGAG	TCCCCGATGT	CCATCATTTT	300
	AGGGAAATGC	CAGGGGGGCC	CGTATGGAGG	AAACATTATA	TCACCTACAG	AATCAATAAT	360
	TACACACCTG	ACATGAACCG	TGAGGATGTT	GACTAGCCAA	TCCGAAAGC	TTTCCAAGTA	420
	TGGAGTAATG	TTACCCCTTT	GAAATTCAGC	AAGATTAAAC	CAGGCATGGC	TGACATTTTG	480
	GTGGTTTTTG	CCCGTGGAGC	TCATGGAGAC	TTCCATGCTT	TTGATGGCAA	AGGTGGAATC	540
45	CTAGCCCATG	CTTTTGGACC	TGGATCTGGC	ATTGGAGGGG	ATGCACATTT	CGATGAGGAC	600
	GAAATCTGGA	CTACACATTC	AGGAGGCACA	AACTTGTTC	TCACCTGCTGT	TCACGAGATT	660
	GGCCATTCTT	TAGGTCTTGG	CCATTCTAGT	GATCCAAAGG	CCGTAATGTT	CCCCACCTAC	720
	AAATATGTTG	ACATCAACAC	ATTTGCGCTC	TCTGCTGATG	ACATACGTGG	CATTTCAGTCC	780
	CTGTATGGAG	ACCCAAAGAA	GAACCAACGC	TTGCCAAATC	CTGACAATTC	AGAACCAAGT	840
50	CTCTGTGACC	CCAAATTTGAG	TTTTGATGCT	GTCACTACCG	TGGGAAATAA	GATCTTTTTT	900
	TTCAAAGACA	GTTTCTTCTG	GCTGAAGGTT	TCTGAGAGAC	CAAGACCAG	TGTTAATTTA	960
	ATTTCTTCTT	TATGGCCAAAC	CTTGCCATCT	GGCATTGAAG	CTGCTTATGA	AATTGAAGCC	1020
	AGAAATCAAG	TTTTTCTTTT	TAAAGATGAC	AAATACGTGT	TAATTAGCAA	TTTAAAGCCA	1080
	GAGCCAAATT	ATCCCAAGAG	CATACATTCT	TTTGGTTTTT	CTAACTTTGT	GAAAAAAATT	1140
55	GATGCAGCTG	TTTTTAAACC	ACGTTTTTAT	AGGACCTACT	TCTTTGTAGA	TAACCGATAT	1200
	TGGAGGTATG	ATGAAAGGAG	ACAGATGATG	GACCCGTGTT	ATCCCAAACT	GATTACCAAG	1260
	AACTTCCAA	GAAATCGGCC	TAAATTTGAT	GCAGTCTTCT	ACTCTAAAAA	CAAATACTAC	1320
	TATTTCTTCC	AAGGATCTAA	CCAATTGAA	TATGACTTCC	TACTCCAAG	TATCACCAAA	1380
	ACACTGAAAA	GCAATAGCTG	GTTTGGTTGT	TGA			1413

Seq ID NO: C81 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 1..1413

65	1	11	21	31	41	51	
	ATGAAGTTTC	TTCTAATACT	GCTCCTGCAG	GCCACTGCTT	CTGGAGCTCT	TCCCTGAAC	60
	AGCTCTACAA	GCCCTGAAAA	AAATAATGTG	CTATTTGGTG	AAAGATACTT	AGAAAAATTT	120
	TATGGCCTTG	AGATAAACAA	ACTTCCAGTG	ACAAAAATGA	AATATAGTGG	AAACTTAATG	180
70	AAGGAAAAAA	TCCAAGAAAT	GCAGCACTTC	TTGGGTCTGA	AAGTGACCGG	GCAACTGGAC	240
	ACATCTAACC	TGGAGATGAT	GCAAGCACCT	CGATGTGGAG	TCCCCGATGT	CCATCATTTT	300
	AGGGAAATGC	CAGGGGGGCC	CGTATGGAGG	AAACATTATA	TCACCTACAG	AATCAATAAT	360
	TACACACCTG	ACATGAACCG	TGAGGATGTT	GACTAGCCAA	TCCGAAAGC	TTTCCAAGTA	420
	TGGAGTAATG	TTACCCCTTT	GAAATTCAGC	AAGATTAAAC	CAGGCATGGC	TGACATTTTG	480
75	GTGGTTTTTG	CCCGTGGAGC	TCATGGAGAC	TTCCATGCTT	TTGATGGCAA	AGGTGGAATC	540
	CTAGCCCATG	CTTTTGGACC	TGGATCTGGC	ATTGGAGGGG	ATGCACATTT	CGATGAGGAC	600
	GAAATCTGGA	CTACACATTC	AGGAGGCACA	AACTTGTTC	TCACCTGCTGT	TCACGCCATT	660
	GGCCATTCTT	TAGGTCTTGG	CCATTCTAGT	GATCCAAAGG	CCGTAATGTT	CCCCACCTAC	720
	AAATATGTTG	ACATCAACAC	ATTTGCGCTC	TCTGCTGATG	ACATACGTGG	CATTTCAGTCC	780
80	CTGTATGGAG	ACCCAAAGAA	GAACCAACGC	TTGCCAAATC	CTGACAATTC	AGAACCAAGT	840
	CTCTGTGACC	CCAAATTTGAG	TTTTGATGCT	GTCACTACCG	TGGGAAATAA	GATCTTTTTT	900
	TTCAAAGACA	GGTCTTCTG	GCTGAAGGTT	TCTGAGAGAC	CAAGACCAG	TGTTAATTTA	960
	ATTTCTTCTT	TATGGCCAAAC	CTTGCCATCT	GGCATTGAAG	CTGCTTATGA	AATTGAAGCC	1020
	AGAAATCAAG	TTTTTCTTTT	TAAAGATGAC	AAATACGTGT	TAATTAGCAA	TTTAAAGCCA	1080
	GAGCCAAATT	ATCCCAAGAG	CATACATTCT	TTTGGTTTTT	CTAACTTTGT	GAAAAAAATT	1140

5
 10
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 20
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GATGCAGCTG TTTTAAACCC ACGTTTTTAT AGGACCTACT TCTTTGTAGA TAACCAGTAT 1200
TGGAGGTATG ATGAAAGGAG ACAGATGATG GACCCCTGGT ATCCCAAAC TATTACCAAG 1260
AACTTCCAAG GAATCGGGCC TAAAATTGAT GCAGTCTTCT ACTCTAAAAA CAAATACTAC 1320
TATTTCTTCC AAGGATCTAA CCAATTTGAA TATGACTTCC TACTCCAACG TATCACCAAA 1380
ACACTGAAAA GCAATAGCTG GTTGTGTTGT TGA 1413
  
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Seq ID NO: C82 DNA Sequence
 Nucleic Acid Accession #: NM_006952.1
 Coding sequence: 11..793

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TGGAATGTG ATATTGTGTT GTTGCGGCAT TGCCCTGACT GGGAGTGTGA TCTTCTTTGT 120
ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
GGCTGCCTGG ATCGGCATAT TTGTGGGCAT CTGCTCTTTC TGCTGTCTG TTCTAGGCAT 240
TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTCAITC TGATGTTTAT 300
AGTATATGCC TTTGAAGTGG CATCTTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
ACCCAACCTC TTCTGGAAGC AGATGCTAGA GAGGTACCAA AACCAACAGCC CTCCAAACAA 420
TGATGACCAG TGGAAAAACA ATGGAGTCA CAAAACCTGG GACAGGCTCA TGCTCCAGGA 480
CAATTGCTGT GCGGTAAATG GTCCATCAGA TTGGCAAAAA TACACATCTG CCTTCCSGAC 540
TGAGAATAAT GATGCTGACT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
AGAACCTCTC AACCTGGAGG CTGTGAAACT AGGCGTGCCT GGTTTTATC ACAATCAGGG 660
CTGCTATGAA CTCGCTCTCG GTCCAATGAA CCGACACGCC TGGGGGTTG CCTGGTTTGG 720
ATTTGCCATT CTCTGCTGGA CTTTITGGGT TCTCCTGGGT ACCATGTTCT ACTGGAGCAG 780
AATTGAATAT TAAGAA 796
  
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Seq ID NO: C83 DNA Sequence
 Nucleic Acid Accession #: NM_001793.2
 Coding sequence: 71..2560

30
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 55
 60
 65
 70
 75
 80

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1      11      21      31      41      51
|      |      |      |      |      |
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CCGCGTCCG GGCAGCTGCT TCACCCCTCT 60
CTCTGCAGCC ATGGGGCTCC CTCTGTGACC TCTCGCTCT CTCTCCCTTC TCCAGGTTTG 120
TGCGCTGCAG TGCGCGGCTC CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
CTTGAGGGCG GAGGGCGCGG AGCAGGAGCC CCGCCAGGCG CTGGGGAAGG TATTCATGGG 240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
TGAAATGGC AAGGTTCCCT TCCCCAGAG ACTGAATCAG CTCAGTCTA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGCCA GACAGCCCCC CTGAGGGTGT 540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG GTCATGCTCT TTGGCCACGC TGTGTCAAGG AATGGTGCCT CAGTGGAGGA 660
CCCATGAAAC ATCTCCATCA TCGTGAACGA CCAAGATGAC CACAAGCCCA AGTTTACCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTTCTG TGATGCAGGT 780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
CCATAGCCAA GAACCAAGAG ACCCACACGA CCTCATGTTT ACCATTCAAC GGAGCACAGG 900
CACCATCAAC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGAACCC CAGAAGTACG AGGCCCATGT 1080
GCCTGAGAA TGCAGTGGGC ATGAGGTGCA GAGGCTGACG GTCAGTGATC TGGACGCCCC 1140
CAACTCACC ACGTGGGCTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
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ACCTGTGTTT GTCCCAACCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCCG 1500
CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGAACCA GACAGTGGGC AGGTCAACAG 1560
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GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGTAAAC 1680
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CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCTCT AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
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CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GTTGGTTTCT CGCAATGACG TGGCACCAAC 2280
CATCATCCCG ACACCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCACCA GCCCGCCCTC ACGACACCTC 2400
CTTGGTGTTC GTTGTGCTTC TTAGCCTTTC AGGATGAGG AATGTGGGCA GTTTGACTTC 2460
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ACGTTAGAGT GGTGTGCTTC TTAGCCTTTC AGGATGAGG AATGTGGGCA GTTTGACTTC 2760
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GCTGGGCCCA CTGGCCGCTC TGCAATTCTG GTTTCAGAC CCAATGCTC CCACTTCGGA 3060
  
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TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT 3120
 GTTGGCTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTAT 3180
 TAAAGAACT TTTCCAGAA AAAAA 3205

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Seq ID NO: C84 DNA Sequence
 Nucleic Acid Accession #: NM_005629.1
 Coding sequence: 639..2546

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 CCGCCGCGCC CACCGCCACC GGAGTCGCGG GCCAGCGCGG CAGCCTCCGC GGGCCCCCGC 180
 CGGGGCGGGG GCGCGCGGCC ACAGGCCCTT GCTCGGCGCG TCGTTTGCAG ACCGCGGGCG 240
 15 CCGATGTCCG CCGCGCCCCG TTAGGATGAG TCTCGGGTGG GCGGAGGAGC CCGCGCAGCC 300
 GCGCGCGCGC GAGCGCGGCC CAGGAGCCTC GCGAGCGCGC CCGCGCGCGC CCGCGCGCGC 360
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 20 CCTCGGGCGC CTCGCCGGTG CCGCGCGTGC CCGCGCGCGT ACCGCGCGCC CCGGTGAGGC 600
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 ACGGGGCGCC GGGCAAGGGC GACGGCGCGC TGGGCGTGGG GACACCGCGC GCGCGCGTGG 780
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 25 TCGCGCGTGG CTGGGCAAC GTGTGGCGCT TCCCTACCTT GTGTACAAG AACGCGGAG 900
 GTGTGTCTCT TATTCTCTAC GTCTGATCG CCTGTGTTGG AGGAATCCCT ATTTCTTCT 960
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 35 CCTAAGTGTG CCTGGTGTGG CTGCTGTGTC GTGGAGTGTG GCTGCTCTAG GCCCTGGATG 1500
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 40 ACAGTGGGAC CAGCTTCTTT GCTGGCTTGC TGGTCTTCTC CATCTGGGCG TTGATGGTGT 1740
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 TCATGTCTGT GCTGCTTGGT CTGACAGGCC AGTTTGTAGG TGTGGAGGGC TTCTACACCG 1920
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 45 CCCTCTGTGG TTTGTCTGCG TTTGTCTGCG ATCTCTCATG GTGACTGAT GCGGGGATGT 2040
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 50 ACAACACCTA CGTGTACCGG TGGTGGGGTG AGGCCATGGG CTGGGCGCTC GTTCTGCTGA 2340
 CCATGTCTGT CGTGCCGCTG CACCTCTCTG GCTGCTCTCT CAGGGCCCAAG GGCACCATGG 2400
 CTGAGCGCTG GCAGCACCTG ACCCAGCCCA TCTGGGGCCT CCACCATTTG GAGTACCGAG 2460
 CTCAGGACGC AGATGTCAGG GGCCTGACCA CCTGACCCC AGTGTCCGAG AGCAGCAAGG 2520
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 55 GCCATAGCAG CCGCTGCTTC AGCCCCACCG CACCCCTCCA GGGGGCGTGC CTTTCCCTGA 2640
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 60 CTCTGCAGCA CACCCGTGGG TGACCCCTCA CCGCAGAAAG AGCAGTGGCA GCTTGGGAAA 2940
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 GAGGGGAGAG AGAACCAAGG CAAATATTTC AGCTGGGCTA TACCCCTCTC CCCATCCCTG 3060
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 75 CTTCTGTGTA GCAGCTTTAA CCGAGTTTGG TCTGTCAAGT CCAAGTCCGA GACGGCTGAG 3780
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 AAAACATGTC ATTTTCC 3917

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Seq ID NO: C85 DNA Sequence
 Nucleic Acid Accession #: NM_006516.1
 Coding sequence: 180..1658

1 11 21 31 41 51
 TAGTCGCGGG TCCCGAGATG AGCAAGCCAG GGAGCAGGAG ACCAAACGAC GGGGGTCGGA 60

Seq ID NO: C87 DNA Sequence
Nucleic Acid Accession #: NM 005268.1

Coding sequence: 168..989

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	TCTGGATATG	AAATTCAAGC	TGCTTGCTGA	GTCTATTGCG	CGGCTGCTGG	GAGCCAGGAG
	AGCCCTGAGG	AGTAGTCACT	CAGTAGCAGC	TGACGCGTGG	GTCCACCATG	AACCTGGAGTA
	TCCTTGAGGG	ACTCCTGAGT	GGGGTCAACA	AGTACTCCAC	AGCCTTTGGG	CGCATCTGGC
10	TGTCCTGCTG	CTTCATCTTC	CGCGTGCTGG	TGTACTGCTG	GACGGCCGAG	CGTGTGTGGA
	GTGATGACCA	CAAGGACTTC	GACTGCAATA	CTGCCAGGCC	CGGCTGCTCC	AACGTCTGCT
	TTGATGAGTT	CTTCCCTGTG	TCCCATGTGC	GCCTCTGGGC	CCTGCAGCTT	ATCCTGTGTA
	CATGCCCCCTC	ACTGCTCGTG	GTCTGTCAGC	TGGCCTACCG	GGAGGTTTCA	GAGAAGAGGC
	ACCGAGAAAG	CCATGGGGAG	AACAGTGGGC	GCCTCTACCT	GAACCCCGGC	AAGAAGCGGG
15	GTGGGCTCTG	GTGGACATAT	GTCTGCAGCC	TAGTGTTCAA	GGCGAGCGTG	GACATCGCCT
	TTCTCTATGT	GTTCACCTCA	TTCTACCCCA	AATATATCCT	CCCTCCTGTG	GTCAAGTGCC
	ACGCAGATGT	ATGTCCCAAT	ATAGTGGAAT	GCTTCATCTC	CAAGCCCTCA	GAGAAGAACT
	TTTTTACCCCT	CTTCATGGTG	GCCACAGCTG	CCATCTGCAT	CCTGCTCAAC	CTCGTGGAGC
	TCATCTACCT	GGTGAGCAAG	AGATGCCAAG	AGTGCTGGC	AGCAAGGAAA	GCTCAAGCCA
20	TGTGCACAGG	TCATCAACCC	CACGGTACCA	CCTCTTCCCT	CAAAACAGAG	GACCTCCTTT
	CGGGTACCT	CATCTTCTG	GGCTCAGACA	GTCTCTCTCC	TCTCTTACCA	GACCGCCCCC
	GAGACCATGT	GAAGAAAACC	ATCTTGTGAG	GGGCTGCTCT	GACTGGTCTG	GCAGGTGGGG
	CCTGGATGGG	GAGGCTCTAG	CATCTCTCAT	AGGTGCAACC	TGAGAGTGGG	GGAGCTAAGC
	CATGAGGTAG	GGGCAGGCAA	GAGAGAGGAT	TCAGACGCTC	TGGGAGCCAG	TTCTAGTCC
25	TCAACTCCAG	CCACTGGCCC	CAGCTGGAGC	GCATCGGGCC	AGTTCCCCCT	CTGCTCTGCA
	GCTCGGTTTC	CTTTTCTAGA	ATGGAAATAG	TGAGGGCCAA	TGC	1243

Seq ID NO: C88 DNA Sequence
Nucleic Acid Accession #: NM_005130
Coding sequence: 98..802

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	CGTGTGCTCA	GAACAAGGTG	AACGCCAGGC	TGCAGCCATG	AAGATCTGTA	GCCTCACCTT
35	GCTCTCCTTC	CTCCTACTGG	CTGCTCAGGT	GCTCCTGGTG	GAGGGGAAAA	AAAAAGTGAA
	GAATGGAATT	CACAGCAAG	TGGTCTCAGA	ACAAAAGGAC	ACTCTGGGCA	ACACCCAGAT
	TAAGCAGAAA	AGCAGGCCCC	GGAAACAAAG	CAAGTTTGTG	ACCAAAGACC	AAGCCCACTG
	CAGATGGGCT	GCTACTGAGC	AGGAGGAGGG	CATCTCTCTC	AAGGTTGAGT	GCACTCAATT
40	GGACCATGAA	TTTTCTCTGT	TCTTTGCTGG	CAATCCAACT	TCATGCCTAA	AGCTCAAGGA
	TGAGAGAGTC	TATTGGAAAC	AAGTTGCCCG	GAATCTGGCG	TCACAGAAAG	ACATCTGTAG
	ATATTCCAAG	ACAGCTGTGA	AAACCCAGAT	GTGCAGAAAG	GATTTTCCAG	AATCCAGTCT
	TAAGCTAGTC	AGCTCCATCT	TATTTGGGAA	CACAAAGCCC	AGGAAGGAGA	AAACAGAGAT
	GTCCCCCAGG	GAGCACATCA	AGGGCAAAGA	GACCAACCCC	TCTAGCCTAG	CAGTGACCCA
45	GACCATGGCC	ACCAAAGCTC	CCGAGTGTGT	GGAGGACCCA	GATATGGCAA	ACCAGAGGAA
	GACTGCCCTG	GAGTTCTGTG	GAGAGACTTG	GAGCTCTCTC	TGCACATTCT	TCTCAGCAT
	AGTGCAGGAC	AGCTCATGCT	AATGAGGTCA	AAAGAGAACG	GGTTCCTTTA	AGAGATGTCA
	TGTGTAAGT	CCCTCTGTAT	ACTTTAAAGC	TCTCTACAGT	CCCCCAAAA	TATGAACCTT
	TGTGCTTAGT	GAGTGCAACG	AAATATTAA	ACAAGTTTGT	TATTTTGTGC	TTTGTGTTTT
50	TGGAATTGTC	CTTAATTTTC	TTGGATGCGA	TGTTCAAGAG	CTGTTTCTGT	CAGCATGTAT
	TTCCATGGCC	CACACAGCTA	TGTGTTTGAG	CAGCGAAGAG	TCTTTGAGCT	GAATGAGCCA
	GAGTGATAAT	TTCAAGTGCAA	CGAATTTCT	GCTGAATTAA	TGGTAATAAA	ACTCTGGGTG
	TTTTTCAAAA	AAAAAAAAAA	AAA			1163

Seq ID NO: C89 DNA Sequence
Nucleic Acid Accession #: BC022542
Coding sequence: 274..927

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	CCTTCTCTGG	TCCGCACCTG	GCCCCGCGCG	CCCCCTCTGG	GCCTCCGCGT	TCCGCGGTCC
	TGGCGGCTCG	GCTGGCGGGG	GTTCGGGGCG	CGGCTGGGCT	GCTCTCTGGG	CGCGGAGCGG
	GGCTCAGCGG	CGGGCCCGCC	ACGGCCTTCA	CGCGCGCGGG	CTCTGACGCC	GGCATAAGGG
65	CCATGTGTTG	TGAAATTATT	TTGAGGCAAG	AAGTTTGTGA	AGATGGTTTC	CACAGAGACC
	TTTTAATCAA	AGTGAAGTTT	GGGGAAGCA	TTGAGGACTT	GCACAGCTGC	CGTCTCTTAA
	TTAAACAGGA	CATTCCTGCA	GGACTTTATG	TGGATCCGTA	TGAGTTGGCT	TCATTACGAG
	AGAGAAACAT	AACAGAGGCA	GTGATGGTTT	CAGAAAATTT	TGATATAGAG	GCCCCTAATC
	ATTTGTCCAA	GGAGTCTGAA	GTCTCTCAAT	ATGCCAGACG	AGATTACAG	TGCATTGACT
70	GTTTTCAGC	CTTTTGGCT	GTGCACTGCC	GCTATCATCG	GCGGCACAGT	GAAGATGGAG
	AAGCCTCGAT	TGTGGTCAAT	AACCCAGATT	TGTTGATGTT	TTGTGACCAA	GAGTTCGCCA
	TTTTGAAATG	CTGGGCTCAC	TCAGAAAGTG	CAGCCCCCTG	TGCTTTGGAT	AATGAGGATA
	TATGCCAATG	GAACAAAGAT	AAGTATAAAT	CAGTATATAA	GAATGTGATT	CTACAGATTG
	CAGTGGGACT	GACTGTACAT	ACCTCTCTAG	TATGTTCTGT	GACTCTGCTC	ATTCAATGCC
75	TGTGCTCTAC	ATTGATCCCT	GTAGCAGTTT	TCAAATATGG	CCATTTTTC	CTATAAGTTT
	TATGTAGTTA	AATGCTTCTC	AGAAACCTAA	ATAAGATCTA	TTAATTTCTG	ACGAGAGGTG
	TTCTTCTAGA	ATTAAATTACT	TTTATCTTTT	GTCTTCAATT	GTGGCCAAAA	TTATGTTTAC
	TAGAGGAAAT	TTGGGATCAT	TCTCAGCTAA	TTCCAAAATG	TAGTGCTCTA	TTGCATGGAT
80	CCTTGGTAAT	CCTCAAGCAT	CAGATGCCAT	AAGGGGAAAC	TTAATTTCTG	TAAATTAATG
	TTTATTTTGT	GAGAAAGTGAC	TTTATCTTCA	TTTGGGGTAG	AAAAATTATT	TCTTTATGTA
	GTAGAGACAA	ATTATTTCTCA	TTTTGCAAGT	ACTTTCAATT	TAAAGCTACA	ATTGAGAAAA
	CGTTTATAAA	TAAGAAATAA	ATAGGCCAGG	CACAGTGCTC	CACACTGTGA	ATCCACGAC
	TTTGGGAGGC	CGAGGTGGGC	GGATCACCAG	AGGTCAAGAG	TTTGAGACCA	GCTTGGTGAA
	ACCTGTGCTC	TACTAAAAAT	ACAAAAGTTA	GCTGGGGCTG	GTGGTGGA	TCTGTAGTCC
	CAGCTAATGT	GAAGGGTGAG	GCGGGAGGAT	CGCTTGAACC	TGGGAGGCGG	AGGTTCCAGA

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AGACCAAGAT	OGCAACACTG	CACTACAGCC	TGGGGGACAG	AACGAGACCC	TGTCTCCAAA	1560
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ATGTCTAGAG	ACTATTAAAG	ATGTGCCAGA	GTTTCAATGA	AAATCATTAA	AGTAGGACAG	1680
CTAAGAAATT	AATATTAAATA	TAAAAATTAT	TGATAATCTT	AAATTATTGA	TTATTCTTTA	1740
ACGCACTCCA	TTCTCTTTT	ACATTTTATC	ATGTTTCTTT	TGAATATATG	AATTGGCAAA	1800
GGACTTGATG	AAACTGAGTA	CTAAGATTTG	GTACAGAGTA	TGTCAGGAAG	ACAACCTAGA	1860
TTGCCATTTT	AAATAAAGTT	GTACATGAAC	AAAAAAAAAA	AAAAAA		1906

Seq ID NO: C90 DNA Sequence
Nucleic Acid Accession #: NM_004994
Coding sequence: 20..2143

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CCTGAGAACC	AATCTCACCG	ACAGGCAGCT	GGCAGAGGAA	TACCTGTACC	GCTATGGTTA	180
CACCTGGGTG	GCAGAGATGC	GTGGAGAGTC	GAAATCTCTG	GGCCCTGCGC	TGCTGCTTCT	240
CCAGAAGCAA	CTGTGCTCTG	CCGAGACCCG	TGAGCTGGAT	AGGCCACAGC	TGAAGGCCAT	300
CGGAACCCCA	CGGTGCGGGG	TCCAGACCTT	GGGCAAGTTC	CAAACTTTTG	AGGGGACCTT	360
CAAGTGGCAC	CACCACAACA	TCACCTATTG	GATCCAAAAC	TACTCGGAAG	ACTTGCCCGG	420
GGCGGTGATT	GACGAGCCCT	TTGCCCGCGC	CTTGCACATG	TGGAGCGCGG	TGACGCGGCT	480
CACCTTCACCT	CGCGTGTACA	GCCGGGACCG	AGACATCGTC	ATCCAGTTTG	GTGTGCGGGA	540
GCACGGAGAG	GGGTATCCCT	TGACCGGGAA	GGACGGGCTC	CTGGCACACG	CCTTTCCCTC	600
TGGCCCCCGG	ATTGAGGAG	ACGCCCATTT	CGACGATGAC	GAGTTGTGGT	CCCTGGGCAA	660
GGGCTCTCTG	GTCCAACTC	GSTTTGGAAG	CGCAGATGGC	GCGGCTGCGC	ACTTCCCTCT	720
CATCTTCGAG	GGCGCTCTCT	ACTCTGCTCT	CACCACCGAC	GGTCTGCTCG	ACGGCTTGCC	780
CTGTGTGCACT	ACCCGCGCCA	ACTACGACAC	CGACGACCGG	TTTGGCTTCT	GCCCCAGCGA	840
GAGACTCTAC	ACCCGGGAGC	GCAATGCTGA	TGGGAAACCC	TGCCAGTTTC	CATTCACTCT	900
CCAAGGCCAA	TCCTACTCCG	CCTGCACACC	GGACGGTGGC	TCCGACGGCT	ACCGCTGGTG	960
CGCCACCACC	GCCAACTACG	ACCGGGACAA	GCTCTTCCGC	TTCTGCCCGA	CCCGAGCTGA	1020
CTGACGCTG	ATGGGGGGCA	ACTCGGCGGG	GGAGCTGTGC	GTCTTCCCTT	TCACTTTCTT	1080
GGGTAAAGAG	TACTGACCTT	GTACACGCGA	GGGCGCGCGA	GATGGGCGCC	TCTGTGCGC	1140
TACCACCTCG	AACCTTGACA	CGACAAAGAA	GTGGGGCTTC	TGCCCGGACC	AAGGATACAG	1200
TTTGTCTCTC	GTGGCGCGCG	ATGAGTTCCG	CCAACGCGCTG	GGCTTAGATC	ATTCTCACTG	1260
CCCGGAGCGG	CTCATGTACC	CTATGTACCG	CTTCACTGAG	GGGCCCCCTT	TGCATAAGGA	1320
CGACGTGAAT	GGCATCCGGC	ACCTCTATGG	TCTTCCCTCT	GAACTGTAGC	CACGGCTTCC	1380
AACCAACACC	ACACCGCAGC	CCACGGCTCC	CCCGACGCTC	TGCCCCACCG	GACCCCCAC	1440
TGTCCACCCC	TCAGAGCGCC	CCACAGCTGG	CCCCACAGGT	CCCCCTCAG	CTGGCCCCAC	1500
AGGTCCCCCC	ACTGCTGGCC	CTTCTACGGC	CACTACTGTG	CCTTTGAGTC	CGGTGGACGA	1560
TGCGTGCAG	GTGAACATCT	TGACGCCAT	CGCGGAGATT	GGGAACAGC	TGTATTGTGT	1620
CAGGATGGG	AAGTACTGGC	GATTCTCTGA	GGGCAGGGGG	AGCCCGCGCG	AGGGCCCTTT	1680
CCTTATCGCC	GACAGTGGG	CCGCGCTGCC	CCGCAAGCTG	GACTCGGTCT	TTGAGGAGCC	1740
GCTCTCCAAG	AAGCTTTTCT	TCTTCTCTGG	GCGCCAGGTG	TGGGTGTACA	CAGGCGCGTC	1800
GGTGTCTGGG	CCGAGGCGTC	TGGACAAGCT	GGGCTGGGA	GCGACGCTGG	CCCAAGGTGAC	1860
CGGGGCCCTC	CGGAGTGGCA	GGGGGAAGAT	GCTGTGTGTC	AGCGGCGCGC	GCCTCTGGAG	1920
GTTCGAGTGG	AAGGCGCAGA	TGGTGGATCC	CCGAGCGGCC	AGCGAGGTGG	ACCGGATGTT	1980
CCCCGGGGTG	CCTTTGGACA	CGCACGAGCT	CTTCCAGTAC	CGAGAGAAAG	CCTATTCTCT	2040
CCAGGACCGC	TCTACTGGG	CGGTGAGTTC	CCGAGTGGAG	TTGAACCAAG	TGGAACCAAGT	2100
GGGTACGCTG	ACCTATGACA	TCCTGCAGTG	CCCTGAGGAC	TAGGGCTCCC	GTCTGCTCTT	2160
GCAGTGGCAT	GTAAATCCCC	ACTGGGACCA	ACCCTGGGGA	AGGAGCCAGT	TTGCCCGATA	2220
CAAACTGGTA	TTCTGTTCTG	GAGGAAAGGG	AGGAGTGGAG	GTGGGCTGGG	CCCTCTCTTC	2280
TCACCTTTGT	TTTTTGTG	AGTGTCTCTA	ATAAACTTGG	ATTCTCTAAC	CTTT	2334

Seq ID NO: C91 Sequence
Nucleic Acid Accession #: NM_000213
Coding sequence: 188..5656

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TGCCCCCGCG	GCTGCGAGCC	CATCTCCTAG	CGGCAGCCCA	GGCGCGGAGG	GAGCGAGTCC	120
GCCCCGAGGT	AGGTCCAGGA	CGGGCGCACA	GCAGCAGCCG	AGGCTGGCCG	GGAGAGGGAG	180
GAAGAGGATG	GCAGGGCCAC	GCCCAGCCCT	ATGGGCCAGG	CTGCTCCTGG	CAGCCTTGAT	240
CAGCGTCAGC	CTCTCTGGGA	CCTTGGCAAA	CCGCTGCAAG	AAGGCCCCAG	TGAAGAGCTG	300
CACGAGTGTG	GTCCGTGTGG	ATAAGGACTG	CGCCTACTGC	ACAGACGAGA	TGTTCAAGGA	360
CCGCGCTCTG	AACACCCAGG	CGGAGCTGCT	GGCCCGCGGC	TGCCAGCGGG	AGAGCATCGT	420
GGTCATGGAG	AGCAGCTTCC	AAATCACAGA	GGAGACCCAG	ATTGACACCA	CCCTGCGGCG	480
CAGCCAGATG	TCCCCCAAG	GCCTGCGGGT	CCGTCTGCGG	CCCGGTGAGG	AGCGGCATTT	540
TGAGCTGGAG	GTGTTTGAGC	CACCTGGAGG	CCCCGTGGAC	CTGTACATCC	TCATGAGCTT	600
CTCCAACTCC	ATGTCGGATG	ATCTGGACAA	CCTCAAGAAG	ATGGGGCAGA	ACCTGGCTCG	660
GGTCTGAGC	CAGCTCACCA	GCGACTACAC	TATTGGATTT	GGCAAGTTTG	TGGAACAAGT	720
CAGCGTCCCG	CAGACGGACA	TGAGGCGCTG	GAAGCTGAAG	GAGCCCTGGC	CCAAACAGTGA	780
CCCCCCTTTC	TCTTCAAGA	ACGTATCAG	CCTGCACAGAA	GATGTGGATG	AGTTCCGGAA	840
TAAACTGCGC	GGAGAGCGGA	TCTCAGGCAA	CCTGGATGCT	CCTGAGGGCG	GCTTCGATGC	900
CATCTCTGAG	ACAGCTGTGT	GCACGAGGGA	CATTGGCTGG	CGCCCGGACA	GCACCCACCT	960
GCTGCTCTTC	TCCACCGAGT	CAGCCTTCCA	CTATGAGGCT	GATGGCGCCA	ACGTGCTGGC	1020
TGGCATCATG	AGCCGCAACG	ATGAACGGTG	CCACCTGGAC	ACCAACGGGCA	CCTACACCCA	1080
GTACAGGACA	CAGGACTACC	CGTGGGTGCC	CACCTGGGTG	CGCTGCTCG	CCAAGCACAA	1140
CATCATCCCC	ATCTTTGCTG	TCACCAACTA	CTCCTATAGC	TACTACGAGA	AGCTTCAAC	1200
CTATTTCCTT	GCTCTCTCAC	TGGGGGTGCT	GCAGGAGGAC	TGTTCCAACA	TGTTGGAGCT	1260
GCTGAGGAGG	GCCTTCAATC	GGATCCGCTC	CAACCTGGAC	ATCCGGGGCC	TAGACAGCCC	1320
CCGAGGCTCT	CGGACAGAGG	TCACCTCCAA	GATGTTCCAG	AAGACGAGGA	CTGGGTCTCT	1380
TCACATCCGG	CGGGGGGAAG	TGGGTATATA	CCAGGTGCAG	CTGCGGGCCC	TTGAGCAGCT	1440

	GGATGGGACG	CACGTGTGCC	AGCTGCCGGA	GGACCAGAAG	GGCAACATCC	ATCTGAAACC	1500
	TTCTCTCTCC	GACGGCTCTCA	AGATGGAGCG	GGGCATCATC	TGTGATGTGT	GCACTTGCGA	1560
	GCTGCAAAAG	GAGGTGGGGT	CAGCTCGCTG	CAGCTTCAAC	GGAGACTTCG	TGTGCGGACA	1620
5	GTGTGTGTGC	AGCGAGGGCT	GGAGTGGCCA	GACCTGCAAC	TGCTCCACCG	GCTCTCTGAG	1680
	TGACATTTCAG	CCCTGCTGTC	GGGAGGGCGA	GGACAAGCCG	TGCTCCGGCC	GTGGGGAGTG	1740
	CCAGTGGGGG	CAGTGTGTGT	GCTACGGCGA	AGGCGCTAC	GAGGGTCAGT	TCTGCGAGTA	1800
	TGACAACTTC	CAGTGTCCCC	GCACTTCCGG	GTCTCTGTGC	AATGACCGAG	GACGCTGCTC	1860
	CATGGGCCAC	TGTGTGTGTG	AGCCTGGTTG	GACAGGCCCA	AGCTGTGACT	GTCCCTCTAG	1920
10	CAATGGCACC	TGACTCGACA	GCAATGGGGG	CATCTGTAA	GGACGTGGCC	ACTGTGAGTG	1980
	TGGCCGCTGC	CAGTGCACCC	AGCAGTCTCT	CTACACGGAC	ACCATCTGCG	AGATCAACTA	2040
	CTCGGCGATC	CACCGGGGCC	TCTGCGAGGA	CCTACGCTCC	TGCGTGCAGT	GCCAGGCGTG	2100
	GGGCAACGGC	GAGAGAAAGG	GGCGCACGTG	TGAGGAATGC	AACCTCAAGG	TCAAGATGGT	2160
	GGACGAGCTT	AAGAGAGCCG	AGGAGGTGGT	GGTGGCTGTC	TCCTTCCGGG	ACGAGGATGA	2220
	GCACTGCACC	TACAGCTACA	CCATGGAAAG	TGACGGCGCC	CCTGGGCCCA	ACAGCACTGT	2280
15	CCTGGTGCAC	AAGAAGAAAG	ACTGCCCTCC	GGGCTCCTTC	TGGTGGCTCA	TCCCTCTGCT	2340
	CCTCCTCTCT	CTCGCGCTCC	TGGCCCTGCT	ACTGCTGCTA	TGCTGGAAAT	ACTGTGCGTG	2400
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20	GCTGCGCAGC	GGCAACCTCA	AGGGCCGTGA	CGTGGTCCGC	TGGAAGGTCA	CCAACAACAT	2580
	GCAGCGCCCT	GGCTTTGGCA	CTCATGCCGC	CAGCATCAAC	CCCAACAGAG	TGGTGCCTTA	2640
	CGGGCTGTTC	TGCGCCCTGG	CCCGCCTTTG	CACCGAGAAC	CTGCTGAAGC	CTGACACTCG	2700
	GGAGTGGCCC	CAGCTGCCCC	AGGAGGTGGA	GGAGAACCTG	AACGAGGTCT	ACAGGCAGAT	2760
	CTCCGGTGTA	CACAAGCTCC	AGCAGACCAA	GTTCGGGCAG	CAGCCCAATG	CCGGGAAAAA	2820
25	GCAAGACACC	AGCACTTGGG	ACACAGTGGT	GATGGCGCCC	CGCTCGGCCA	AGCCGCGCCT	2880
	GCTGAAGCTT	ACAGAGAAAG	AGGTGGAAAC	GAGGGCCTTC	CACGACCTCA	AGGTGGCCCC	2940
	CGGCTACTAC	ACCCCTACTG	CAGAACAGGA	CGCCCGGGGC	ATGGTGGAGT	TCCAGGAGGG	3000
	CGTGAGCTGT	GTGGACGTAC	GGGTGCCCTT	CTTATTCGGG	CCTGAGGATG	ACGACGAGAA	3060
	GCAGCTGCTG	GTGGAGGCCA	TGACGTGCC	CGCAGGCACT	GCCACCTCG	CGCGCGCCTT	3120
30	GGTAAACATC	AGCATCATCA	AGGAGCAAGC	CAGAGACGTG	GTGTCTTTTG	AGCAGCCTGA	3180
	GTCTCTGGTC	AGCCCGGGGG	ACCAGGTGGC	CCGCATCCCT	GTCTCTGGGC	GTGTCTCTGA	3240
	CGCGGGGAAG	TCCCAAGTCT	CCTACCGCAC	ACAGGATGGC	ACCGCGCAGG	GCAACCGGGA	3300
	CTACATCCCC	GTGGAGGGTG	AGCTGCTGTT	CCAGCCTGGG	GAGGCTTGGA	AAGAGCTGCA	3360
	GGTGAAGCTC	CTGGAGCTGC	AAGAAGTTGA	CTCCCTCCTG	CGGGGCCGCG	AGGTCCGCGG	3420
35	TTTCCAAGTC	CAGCTCAGCA	ACCCTAAGTT	TGGGGCCAC	CTGGGCCAGC	CCCACTCCAC	3480
	CAACCATCATC	ATCAGGGACC	CAGATGAACT	GGACCGGAGC	TTACAGAGTC	AGATGTTGTC	3540
	ATCAGACCA	CCCCCTCACG	GCGACCTGGG	CGCCCGCAG	AACCCCAATG	CTAAGGCCCG	3600
	TGGGTCCAGG	AAGATCCATT	TCAACTGGCT	GCCCCCTTCT	GGCAAGCCAA	TGGGTACAG	3660
	GGTAAAGTAC	TGGATTTCAGG	GCGACTCCGA	ATCGAAGCC	CACCTGCTCG	ACAGCAAGGT	3720
40	GCCCTCAGTG	GAGCTCACCA	ACCTGTACCC	GTATTGCGAC	TATGAGATGA	AGGTGTGCGC	3780
	CTACGGGGCT	CAGGGCGAGG	GACCTACAG	CTCCCTGGTG	TCCTGCGCGA	CCCAACAGGA	3840
	AGTGGCGAGC	GAGCGAGGGC	GTCTGGCCTT	CAATGTGCTC	TCCTCCACGG	TGACCCAGCT	3900
	GAGCTGGGCT	GAGCCGGCTG	AGACCAACCG	TGAGATCACA	GCCTACGAGG	TCTGCTATGG	3960
	CCTGGTCAAC	GATGACAAAC	GACCTATTGG	GCCCATGAAG	AAAGTGTCTG	TTGACAAACC	4020
45	TAAAGAACGC	ATGCTGCTTA	TTGAGAACTT	TCGGGAGTCC	CAGCCCTACC	GCTACACGGT	4080
	GAGGGCGGCG	AACGGGGGCG	GCTGGGGGCC	TGAGCGGGAG	GCCATCATCA	ACCTGGCCAC	4140
	CCAGCCCAAG	AGCCCTCATG	CCATCCCCAT	CATCCCTGAC	ATCCCTATCG	TGGAAGCCCA	4200
	GAGCGGGGAG	GACTACGACA	GCTTCCTTAT	GTACAGCGAT	GACGTTCTAC	GCTCTCCATC	4260
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50	GCTGGGGGAG	GAGCTCGAAC	TGCGGCGCGT	CACGTGGCGG	CTGCCCCCGG	AGCTCATCCC	4380
	GCGCTGTGCG	GCCAGCAGCG	GGGCTCTCTC	CGACGCGGAG	GCCCCCAACG	CCCCCGGAGC	4440
	GACGGCGGCG	CGGGCGGGAA	GGGCGGCAGC	CGTGGCCCGC	AGTGGCGAC	CGGGGCCCGC	4500
	CGGAGAGCAC	CTGGTGAATG	GCCGATGGA	CTTTGCCCTT	CGGGGCAGCA	CCAACTCCCT	4560
	GCACAGGATG	ACCAAGACCA	GTGCTGTGTC	CTATGGCACC	CACCTGAGCC	CACAGCTGCC	4620
55	CCACCGCGTG	CTAAGCACAT	CCTCCACCTT	CACACGGGAC	TACAACTCAC	TGACCCGCTC	4680
	AGAACACTCA	CACCTGACCA	CACCTGCCAG	GGACTACTCC	ACCTTCACTT	CGTCTCTCTC	4740
	CCAAGACTCT	CGCTGACTGT	CTGGTGTGCC	CGACACGCCC	ACCCGCTCTG	TGTTCTCTGC	4800
	CCTGGGGCCC	ACATCTCTCA	GAGTGAGCTG	GCAGGAGCCG	CGGTGCGAGC	GGCGCGTGCA	4860
	GGGCTACAGT	GTGGAGTACC	AGCTGTCTGA	CGGCGGTGAG	CTGCATCGGC	TCAACATCCC	4920
60	CAACCTCTGC	CAGACTCCGG	TGGTGGTGGG	AGACCTCCTG	CCCAACCACT	CCTACGTGTT	4980
	CGCGCTGCGG	GCCAGAGGCC	AGGAAGGCTG	GGGCGGAGAG	CGTGAGGGTG	TCATCACCAT	5040
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	GAGCACTCCC	AGTGCCCCAG	GCCCGCTGGT	GTTCAGTGCC	CTGAGCCCA	ACTGCTGCTA	5160
	GCTGAGCTGG	GAGCGGCCAC	GGAGGCCCAA	TGGGATATC	GTCCGCTACC	TGCTGACCTG	5220
65	TGAGATGTGC	CAAGGAGGAG	GGCCAGCCAC	CGCATTCGGG	GTGGATGGAG	ACAGCCCGGA	5280
	GAGCGCGCTG	ACCGTGCCGG	GCCTCAGCGA	GAACTGCCCC	TACAACTTCA	AGGTGCAGGC	5340
	CAGGACCACT	GAGGGCTTGG	GGCCAGAGCG	CGAGGCGATC	ATCAACATAG	AGTCCCAAGG	5400
	TGGAGGACCC	TTCCCGCAGC	TGGGCGAGCG	TGCGGGGCTC	TTCCAGCACC	CGCTGCAAGG	5460
	CGAGTACAGC	AGCATCACCA	CCACCCACAC	CAGCGCCACC	GAGCCCTTCC	TAGTGGATGG	5520
70	GCTGACCCCT	GGGGCCAGC	ACCTGGAGGC	AGGGCGCTCC	CTCACCCGCG	ATGTGAACCA	5580
	GGAGTTTGTG	AGCGGACAC	TGACCAACAG	CGGAACCTTT	AGCACCCACA	TGGAACCAAC	5640
	GTCTCTTCCA	ACTTGACCGC	ACCTTGCCCC	ACCCCGCCCA	TGTCCTACTA	GGGTCTCTCC	5700
	GCACTCTCTT	CCCGAGGCTT	CCTCAGCTAC	TCCATCCTTG	CACCCCTGGG	GGCCAGGCCC	5760
	ACCGCATGCG	ACAGAGCAGG	GGCTAGGTGT	CTCCTGGGAG	GCACTGAAGG	GGCAAGGTCC	5820
75	GTCTCTGTGT	GGCCCAAAAC	TATTTGTAAC	CAAGAGCTGT	GGAGCAGCAC	AAGGACCCAG	5880
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Seq ID NO: C92 DNA Sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 250..1326

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25 Seq ID NO: C93 DNA Sequence
 Nucleic Acid Accession #: NM_020789.1
 Coding sequence: 208..3699

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 35 CTGGTCAATC GCCAGGGGGC TGAAGCTCGA GGAAGCCTG AGTGGTATC GGTGGTGGGC 300
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 Nucleic Acid Accession #: NM_006875
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Seq ID NO: C95 DNA Sequence
 Nucleic Acid Accession #: NM_002510.1
 Coding sequence: 92..1774

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Seq ID NO: C96 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..4247

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	TGCACTAATG	GCTTATATGG	AAAATACAGC	GACCAACTGA	TTGTGACAT	GCCTACTGAT	1380
	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAATC	AAGAAATAAT	CAAGGAGGAG	1440
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55	ACGAAATACA	TGAAGGCCAA	GACTAACCGA	TCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
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	ACAGAAAAAG	ATATTTCTTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
	GAAGGTACTT	CAGCCTCTTT	AAATGATGGC	TCTAAAACCT	TTCTTAGATC	TCCACATATG	1800
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	GAAGATTCAA	CTTCAGAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
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	CATTATCTTA	CCTTTGCTTA	CTTCCCAACT	GAGGTAACAC	CTCATGCTTT	TACCCCATCC	2340
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70	ACCCCTTTGT	TGCTTGACAA	TCAGATCCTC	AACACTACCC	CTGCTGCTTC	AAGTAGTGAT	2520
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	TTTGGCATTC	TGCAATACAG	TTCTCAAATC	CTTCCACAG	TTACTTCAGC	TACGAGAGGT	2700
	GATAAGGTGC	CCTTGCAATG	TTCTCTGCCA	GTGGCTGGGG	GTGATTTGCT	ATTAGAGCCC	2760
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	GATTCTGTGG	GTGTAACTTA	TCAAGGTTCC	TTATTAGGCG	GCCTAGCCA	TATACCAATA	3060
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	GAGTCTTTAG	TTTAAACAG	AAAGGGGTGG	GGGACTCAC	ATCTGAGCAT	TGTTTCTCTC	7140
	TTCTAAATAT	TAGGCAGGAA	AATCAGTCTA	GTCTGTATT	CTGTGATTT	CCCATCACTT	7200
65	GACAGTAACT	TTCTATGACAT	AGGAITCTGC	CGCCAAATTT	ATATCATTAA	CAATGTGTGC	7260
	CTTTTGTCAA	GACTTGTAA	TTACTTATTA	TGTTTGAAT	AAAATGATTG	AATTTTACAG	7320
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Seq ID NO: C98 DNA Sequence
Nucleic Acid Accession #: NM_002851
Coding sequence: 77..4518

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	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
	CTTGTGAAG	AGATTGGCTG	GTCCCTATACA	GGAGCACTGA	ATCAAAAAAA	TTGGGGAAAG	300
5	AAATATCCAA	CATGTAATAG	CCCAAAACAA	TCTCCTATCA	ATATTGATGA	AGATCTTACA	360
	CAAGTAATG	TGAATCTTAA	GAAACTTAAA	TTTCAGGGTT	GGGATAAAAC	ATCATTGGAA	420
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	AATGGCTCAT	TSACATCTCC	TCCCTGCACA	GACACAGTTG	ACTGGATTGT	TTTTAAAGAT	900
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Seq ID NO: C99 DNA Sequence
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	AGGGGCGCAG	GAATTTCTGAT	GTGAAACTAA	CAGTCTGTGA	GGCTTGGAAAC	CTCCGCTCAG	120
	AGAAGATGAA	GGATATCGAC	ATAGGAAAAG	AGTATATCAT	CCCCAGTCTT	GGGTATAGAA	180
10	GTGTGAGGGA	GAGAACACAG	ACTTCTGGGA	CGCAGAGAGA	CCGTGAAGAT	TCCAAAGTTCA	240
	GGAGAACTCG	ACCGTTGGAA	TGCCAAGATG	CCTTGGAAAC	AGCAGCCCGA	GCCGAGGGCC	300
	TCTCTCTTGA	TGCCCTCATG	CATTCTCAGC	TCAGAACTCT	GGATGAGGAG	CATCCCAAGG	360
	GAAAGTACCA	TGATGGCTTG	AGTGTCTTGA	AGCCCATCCG	GACTACTTCC	AAACACCCAG	420
	ACCCAGTGGG	CAATGTCTGG	CTTTTTTCTT	GTATGACTTT	TTCGTGGCTT	TCTTCTCTGG	480
15	CCCGTGTGGC	CCACAAGAAG	GGGGAGCTCT	CAATGGAAGA	CGTGTGGTCT	CTGTCCAAGC	540
	ACGAGTCTTC	TGACGTGAAC	TGCAGAAAGC	TAGAGAGACT	GTGGCAAGAA	GAGCTGAATG	600
	AAGTTGGGCC	AGACGCTGCT	TCCCTGCGAA	GGTTGTGTG	GATCTTCTGC	CGCACCCAGG	660
	TCATCTGTGC	CATCGTGTGC	CTGATGATCA	CGCAGCTGGC	TGGCTTCAGT	GGACCAAGCT	720
	TCATGGTGAA	GCACCTCTTG	GAGTATACCC	AGGCAACAGA	GTCTAACCTG	CAGTACAGCT	780
20	TTTGTGTAGT	GCTGGGCTCT	CTCTGACCG	AAATCGTGGC	GTCTTGTGCG	CTTGCACTGA	840
	CTTGGGCAAT	GAATTAACGA	ACCGTGTGCC	GCTTGGGGGG	GGCCATCTTA	ACCATGGCAT	900
	TTAAGAAGAT	CCTTAAGTTA	AAGAACATTA	AAGAGAAATC	CCTGGGTGAG	CTCATCAACA	960
	TTTGTCTCAA	CGATGGGCAG	AGAATGTTTG	AGGCAGCAGC	CGTTGGCAGC	CTGCTGGCTG	1020
	GAGGACCCGT	TGTTGCCATC	TTAGGCATGA	TTTATAATGT	AATTATTCTG	GGACCAACAG	1080
25	GCTTCTCTGG	ATCAGCTGTT	TTTATCCTCT	TTTACCACAG	AATGATGTTT	GCATCACGGC	1140
	TCACAGCATA	TTTCAAGGAA	AAATGCGTGG	CCGCCACGGA	TGAACGTGTC	CAGAAAGATG	1200
	ATGAAGTTCT	TACTTACATT	AAATTTATCA	AAATGTATGC	CTGGGTCAAA	GCATTTTCTC	1260
	AGAGTGTTC	AAAAATCCGC	GAGGAGGAGC	GTCCGATATT	GGAAAAAGCC	GGGTACTTCC	1320
	AGGGTATCAC	TGTGGGTGTG	GCTCCCATTG	TGGTGGTGAT	TGCCAGCGTG	GTGACCTTCT	1380
30	CTGTTCATAT	GACCCCTGGC	TTGATCTGTA	CAGCAGCACA	GGCTTTCACA	GTGGTGACAG	1440
	TCTTCAATTC	CATGACTTTT	GCCTTGAAAG	TAAACCGGTT	TTCAGTAAAG	TCCCTCTCAG	1500
	AAGCCTCAGT	GGCTGTTGAC	AGATTTAAGA	GTTTGTCTCT	AATGGAAGAG	GTTCACATGA	1560
	TAAAGAACAA	ACCAGCCAGT	CCTCACAATC	AGATAGAGAT	GAAAAATGCC	ACCTTGGCAT	1620
	GGGACTCTCT	CCACTCCAGT	ATCCAGAATC	CGCCCAAGCT	GACCCCAAAA	ATGAAAAAAG	1680
35	ACAAGAGGGC	TTCCAGGGGC	AAGAAAGAGA	AGGTGAGGCA	GCTGCAGCGC	ACTGAGCATC	1740
	AGCGGTGCT	GGCAGGACAG	AAAGGCCACC	TCCTCTTGGA	CAGTGAAGAG	CGGCCCATGC	1800
	CCGAAGAGGA	AGAAAGCAAG	CACATCCACC	TGGGCCACCT	GGCCTTACAG	AGGACACTGC	1860
	ACAGCATCGA	CTCTGAGATC	CAAGAGGGTA	AATCTGGTGG	AATCTGCGGC	AGTGTGGGAA	1920
	GTGGAAAAAC	TCTCTCTATT	TCAGCCATTT	TAGGCCAGAT	GACGCTTCTA	GAGGGCAGCA	1980
40	TTGCAATCAG	TGGAACCTTC	GCTTATGTGG	CCCAGCAGGC	CTGGATCCTC	AATGCTACTC	2040
	TCAGAGACAA	CATCCTGTTT	GGGAAGGAAT	ATGATGAAGA	AAGATACAAC	TCTGTGCTGA	2100
	ACAGCTGCTG	CCTGAGGCCT	GACCTGGCCA	TTCTTCCGAG	CAGCGACCTG	ACGAGATATG	2160
	GAGAGCGAGG	AGGCAACCTG	AGCGGTGGGC	AGCGCCAGAG	GATCAGCCTT	GCCCGGGCCT	2220
	TGTATAGTGA	CAGGAGCATC	TACATCCTGG	ACGACCCCTC	CAGTGCCTTA	GATGCCCATG	2280
45	TGGGCAACCA	CATCTCAAT	AGTGCTATCC	GGAAACATCT	CAAGTCCAAG	ACAGTTCTGT	2340
	TTGTTACCCA	CCAGTTACAG	TACCTGTTTG	ACTGTGATGA	AGTGTCTTTC	ATGAAAGAGG	2400
	CGTGTATTAC	GGAAAGAGGC	ACCCATGAGG	AATGTATGAA	TTTAAATGGT	GACTATGCTA	2460
	CCATTTTTAA	TAACTGTTTG	CTGGAGAGAG	CACCGCCAGT	TGAGATCAAT	TCAAAAAGAG	2520
	AAACCAAGAG	TTCAAGAAAG	AAGTCAAAAG	ACAAGGGTCC	TAAACAGGTA	TCAGTAAAGA	2580
50	AGGAAAAAGC	AGTAAAGCCA	GAGGAAGGGC	AGCTTGTGCA	GCTGGAAGAG	AAAGGGCAGG	2640
	GTTCAGTGCC	CTGGTCACTA	TATGGTGTCT	ACATCCAGGC	TGCTGGGGGC	CCCTTGGCAT	2700
	TCTTGTATT	TATGGCCCTT	TTTATGCTGA	ATGTAGGCAG	CACCGCCTTC	AGCACCTGGT	2760
	GGTTGAGTTA	CTGGATCAAG	CAAGGAAGGG	GGAAACCCAC	TGTGACTCGA	GGGAACGAGA	2820
	CCTCGGTGAG	TGACAGCATG	AAGGACCAAT	CTCATATGCA	GTAATATGCG	AGCATCTACG	2880
55	CCCTCTCCAT	GGCAGTCATG	CTGATCTGTA	AAGCCATTGG	AGGAGTGTGC	TTTGTCAAGG	2940
	GCAAGCTGCG	AGCTTCTCTC	CGGCTGCTAG	ACGAGCTTTT	CCGAAGGATC	CTTCAAGGCC	3000
	CTATGAAGTT	TTTGAACAG	ACCCCAACAG	GGAGGATTCT	CAACAGGTTT	TCCAAAGACA	3060
	TGGATGAAGT	TGACGTGGGG	CTGCGGTTC	AGGCGAGAT	GTTCATCCAG	AACGTTATCC	3120
	TGGTGTCTTT	CTGTGTGGGA	ATGATCGCAG	GAGTCTTCCC	GTGGTTCCTT	GTGGCAGTGG	3180
60	GGCCCTCTGT	CATCTCTTT	TGATCTCTGC	ACATTGTCTC	CAGGGTCTCG	ATTGGGAGGC	3240
	TGAAGCGTCT	GGACAATATC	ACGCACTCAC	CTTCTCTCTC	CCACATCAAG	TCCAGCATAC	3300
	AGGGCCTTGC	CACCATCCAC	GCCTACATA	AAGGGCAGGA	GTTTCTGCAC	AGATACCAGG	3360
	AGCTGTCTGA	TGACAAACAA	GCTCTCTTTT	TTTTGTTTAC	GTGTGCGATG	CGGTGGCTGG	3420
	CTGTGCGGCT	GCACTCTATC	AGCATCGCCC	TCATCACCAC	CACGGGGCTG	ATGATCGTTC	3480
65	TTATGCAAGG	GCAGATTCCC	CCAGCCTATG	CGGGTCTCGC	CATCTCTTAT	GCTGTCCAGT	3540
	TAAAGGGGCT	GTTCCAGTTT	ACGGTCAGAC	TGGCATCTGA	GACAGAAGCT	CGATTCACTT	3600
	CGGTGGAGAG	GATCAATCAC	TACATTAAAG	CTCTGTCTCT	GGAGACACCT	GCCAGAATTA	3660
	AGAACAAGGC	TCCCTCCCTT	GACTGGCCCC	AGGAGGAGAG	GGTGACCTTT	GAGAACGAGC	3720
	AGATGAGGTA	CCGAGAAAAC	CTCCCTCTTG	TCCTAAAGAA	AGTATCCTTC	ACGATCAAAAC	3780
70	CTAAAGAGAA	GATTGGCATT	GTGGGGCGGA	CAGGATCAGG	GAAGTCTCTG	CTGGGGATGG	3840
	CCCTCTTCCG	TCTGGTGGAG	TTATCTGGAG	GCTGCATCAA	GATTGATGGA	GTGAGAATCA	3900
	GTGATATTGG	CCTTGGCGAC	CTCGAAGCA	AATCTCTTAT	CATTCTCTAA	GAGCCGGTGC	3960
	TGTTCACTGG	CAGTGTGAGA	TCAAAATTTG	ACCCCTTCAA	CCAGTACACT	GAGACCCAGA	4020
	TTTGGGATGC	CCTGAGAGAG	ACACACATGA	AAGAATGTAT	TGCTCAGCTA	CCTCTGAAAC	4080
75	TTGAATCTGA	AGTGTATGAG	AATGGGGATA	ACTTCTCAGT	GGGGGAACGG	CAGCTCTTGT	4140
	GCATAGCTAG	AGCCCTGCTC	CGCCACTGTA	AGATTCTGAT	TTTATGATGA	GCCACAGCTG	4200
	CCATGGACAC	AGAGACAGAC	TTATTGATTC	AAGAGACCAT	CCGAGAAGCA	TTTGCAGACT	4260
	GTACCATGCT	GACCAATGCC	CATCGCTCGC	ACAAGGTTCT	AGGCTCOGAT	AGGATTATGG	4320
	TGCTGGCCCA	GGGACAGGTG	GTGGAGTTTG	ACACCCCATC	GGTCTCTCTG	TCCAAAGACA	4380
80	GTTCCTGATT	CTATGCCATG	TTTGTGCTCG	CAGAGAACAA	GGTCTGCTGC	AAGGGCTGAC	4440
	TCCTCCCTGT	TGACGAAGTC	TCTTTTCTTT	AGAGCAATTG	CATTCTCTGC	CTGGGGCGGG	4500
	CCCTCTATCG	CGTCTCTCTA	CCGAAACCTT	GCCTTTCTCG	ATTTTATCTT	TCGCACAGCA	4560
	GTTCGCGATT	GGCTTGTGTG	TTTCACTTTT	AGGGAGAGTC	ATATTTTGAT	TATTGTATT	4620
	ATTCCATATT	CATGTAAACA	AAATTTAGTT	TTTGTCTCTA	ATTGCACTCT	AAAAGGTTCA	4680

5	GGGAACCGTT ATTATAATTG TATCAGAGGC CTATAATGAA GCTTTATACG TGTAGCTATA 4740
	TCTATATATA ATTCTGTACA TAGCCTATAT TTACAGTGAA AATGTAAGCT GTTTATTTTA 4800
	TATTAAATA AGCACTGTGC TAATAACAGT GCATATTCTT TTCTATCATT TTTGTACAGT 4860
	TTGCTGTACT AGAGATCTGG TTTTGCTATT AGACTGTAGG AAGAGTAGCA TTTTATTCTT 4920
	CTCTAGCTGG TGGTTTCACG GTGCCAGGTT TTCTGGGTGT CCAAAGGAAG ACSTGTGGCA 4980
	ATAGTGGGCC CTCGACAGC CCCCTCTGCC GCCTCCCCAC AGCCGCTCCA GGGGTGGCTG 5040
	GAGACGGGTG GCGCGCTGGA GACCATGCAG AGCGCCGTGA GTTCTCAGGG CTCTGCTCTT 5100
	CTGTCTGGT GTCACTTACT GTTCTGTCA GGAGAGCAGC GGGGCGAAGC CCAGGCCCTT 5160
10	TTTCACTCCC TCCATCAAGA ATGGGGATCA CAGAGACATT CCTCCGAGCC GGGGAGTTTC 5220
	TTTCTGCTT TCTTCTTTT GCTGTGTTT CTAAACAAGA ATCAGTCTAT CCACAGAGAG 5280
	TCCCACTGCT TCAGGTTCTT ATGGCTGGCC ACTGCACAGA GCTCTCCAGC TCCAAGACCT 5340
	GTGGTTTCCA AGCCCTGGAG CCAACTGCTG CTTTTTGAGG TGGCACTTTT TCATTGCTCT 5400
	ATTCCACAC TCCACAGTT CAGTGGCAGG GCTCAGGATT TCGTGGGTCT GTTTTCTTTT 5460
15	CTCACCGCAG TCGTCGCACA GTCTCTCTCT CTCTCTCCCC TCAAGTCTG CAACTTTAA 5520
	CAGCTCTGTC TAATCAGTGT CTCACACTGG CGTAGAAGTT TTTGTACTGT AAAGAGACCT 5580
	ACCTCAGGTC GCTGCTGCTT GTGTGGTTTG GTGTGTTTCC GCAAAACCCC TTTGTGCTGT 5640
	GGGGCTGGTA GCTCAGGTGG GCGTGGTCCAC TGCTGTCTAT AGTTGAATGG TCAGCGTTGC 5700
	ATGTGTCGAC CAACTAGACA TTCTGTGCCC TTAGCATGTT TGCTGAACAC CTTGTGGAAG 5760
20	CAAAAATCTG AAAATGTGAA TAAAATTATT TTGGATTTTG TAAAAAATA AAAAAAATA 5820
	AAAAAATA AAAAAATA 5880

Seq ID NO: C106 DNA Sequence

Nucleic Acid Accession #: NM_005562

Coding sequence: 90..3671

25	Coding sequence: 90..3671									
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30	AGACAGAGAC	TGAGCGGGCC	GGCACCGCCA	TGCTCTGGCT	CTGGCTGGGC	TGCTGCTCTT	120			
	GCTTCTCGCT	CCTCTCGCCC	GCAGCCCGGG	CCACTCCAG	GAGGGAAGTC	TGTGATTGCA	180			
	ATGGGAAGTC	CAGGCGAGT	ATCTTTGATC	GGGAACCTCA	CAGACAAACT	GGTAAATGGAT	240			
	TCGCTGCTCT	CACTGCAAT	GACAACTGAG	ATGGCATTCA	CTGCGAGAAG	TGCAAGAAATG	300			
	GCTTTTACCG	GCACAGAGAA	AGGGACCGCT	GTTTGCCCTG	CAATTGTAAC	TCCAAAGGTT	360			
35	CTCTTAGTGC	TCGATGTGAC	AACCTCTGAC	GGTGCAGCTG	TAAACCAGGT	GTGACAGGAG	420			
	CCAGATGCGA	CCGATGTCTG	CCAGGCTTCC	ACATGCTCAC	GGATGCGGGG	TGCACCCAAG	480			
	ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540			
	ACGCGGGCCG	CTGTGCTGCG	AAGCCAGCTG	TTACTGTGGA	ACGCTGTGAT	AGGTGTGATG	600			
	CAGGTTACTA	TAATCTGGAT	GGGGGGAACC	CTGAGGGCTG	TACCCAGTGT	TTCTGCTATG	660			
40	GGCATTACGC	CAGCTGCCGC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720			
	TTCAATCAAGA	TGTGTATGGC	TGGAAAGGCTG	TCCAAAGAAA	TGGGTCTCTCT	GCAAAAGCTCC	780			
	AAATGGTACA	GGSCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840			
	TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGCCTGTCTCT	900			
	TTGACTACCG	TGTGACAGAA	GGAGGCGAGC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960			
45	GTGCTGTGCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020			
	TCACCAAGAC	TTACACATTG	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080			
	TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140			
	CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTCA	GCCCCCGCTG	1200			
	CTCTGGAGC	CCGACAGACC	TGGGTGGAAC	AGTGTATATG	TCCTGTTGGG	TACAAGGGGC	1260			
50	AAATCTGCCA	GGATTTGTCT	TCTGGCTACA	AGAGAGATTG	AGCGAGACTG	GGGCCTTTTG	1320			
	GCACCTGTAT	TCCTGTAAAC	TGTCAAGGGG	GAGGGGCTG	TGATCCAGAC	ACAGGAGATT	1380			
	GTATATTCAG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCCAAT	GGTTTCTACA	1440			
	ACGATCCGCA	GACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAACCGG	TTCAGCTGCT	1500			
	CAGTATGCCA	GGAGACGGAG	GAGGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTCACCGGTG	1560			
55	CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGACCC	CTTTGGTGAA	CATGGCCCGC	1620			
	TGAGGCGCTG	TCAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680			
	GTGACCGGCT	GACAGCGAGC	TGTTTGAAGT	GTATCCACAA	CACAGCCGCG	ATCTACTGCG	1740			
	ACCAATGCAA	AGCAGGCTAC	TTGGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAGTGTG	1800			
	GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTGGAAGT	GATGGCACCT	1860			
60	GTGTTTGCAA	GCCAGGATTG	GGTGGCCCCA	ACTGTGAGCA	TGGAGCATTC	AGCTGTCCAG	1920			
	CTTGCTATAA	TCAAGTGAAG	ATTCAAGATG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAATGG	1980			
	AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040			
	GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTCAG	2100			
	AAGGTGCTAG	CAGATCCCTT	GGTCTCCAGT	TGGCCAAAGT	GAGGAGCCAA	GAGAACAGCT	2160			
65	ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	GATTCCGGCT	CTGGGAAGTC	2220			
	AGTACCAGAA	CCGAGTTCCG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280			
	CAGAAAGTGA	AGCTTCTCTG	GGAAACACTA	ACATTCTGCT	CTCAGACCAC	TACGTGGGGC	2340			
	CAAAATGGCT	TAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAAG	2400			
	CAGCCAGTAA	CATGGAGCAA	CTGACAAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460			
70	CACGTGTGGC	CAAGGCCCTG	CATGAAGGAG	TGGGAAGCGG	AAGCGGTAGC	CCGGACGGTG	2520			
	CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAAACCA	GTCCCTGGCC	CAGCAGTTGA	2580			
	CAAGGGAGGC	CACTCAAGCG	GAAATTTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640			
	TCCTTGATTG	AGTGTCTCG	CTTCAGGAGG	TCAGTGATCA	GTCCCTTCAG	GTGGAAGAAG	2700			
	CAAGAGGAT	CAAAACAAAA	GCGGATTACT	TCCTCAAGCT	GGTAACCGCT	CATATGGATG	2760			
75	AGTTCAAGCG	TACACAAAAG	AATCTGGGAA	ACTGGAAGA	AGAAGCACAG	CAGCTCTTAC	2820			
	AGAAATGAAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880			
	AAAGCAGAGC	ACAAGAGACA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTTGAGAGCA	2940			
	TCCTTAAAAA	CCTCAGAGAG	TTTGACCTCG	AGGTGGACAA	CAGAAAAGCA	GAAAGCTGAAG	3000			
	AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060			
80	AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAAATGGG	3120			
	CCGGGGAGGC	CCTGGAATAT	TCCAGTGAGA	TTGAACAGGA	GATTGGGAGT	CTGAACCTGG	3180			
	AAGCCAAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAATA	GGGACTGGCC	TCTCTGAAGA	3240			
	GTGAGATGAG	GGAAGTGGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300			
	TGGATGCAAT	ACAGATGGTG	ATTACAGAAG	CCCGAAGAGT	TGATACCAGA	GCCCAAGAAC	3360			
	CTGGGGTTAC	AATCCAAGAC	ACATCAACA	CATTAGACGG	CCTCTGCTAT	CTGATGGACC	3420			

5	AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAAGCTT	TCCCGAGCCA	3480
	AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCAGCTC	3540
	AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
	AGAACTTGG	GAACATTAGG	GACAACCTGC	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
	AGCAACAGTG	AAGCTGCCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
	GGCTCGGGAG	CCATGTCTATG	TGAGTGGGTG	GGATGGGGAC	ATTGGAACAT	GTTTAATGGG	3780
	TATGCTCAGG	TCAACTGACC	TGACCCCAAT	CCTGATCCCA	TGGCCAGGTG	GTTGTCTTAT	3840
	TGCACCATAC	TCCTTGCTTC	CTGATGCTGG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
10	ATGATCAAGG	ATCTGGAGCCC	CAAAGAATAG	ACTGGATGGA	AAGACAACT	GCACAGGCAG	3960
	ATGTTTGCTT	CATAATAGTC	GTAAGTGGAG	TCCTGGAAAT	TGGCAAGTG	CTGTTGGGAT	4020
	ATAGTCAACT	TATTCTTTGA	GTAATGTGAC	TAAAGGAAAA	AACCTTGACT	TTGCCAGGC	4080
	ATGAAATCTT	TCCTAATGTC	AGAACAGAGT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
	ACTATTGCCT	CATATTGTCC	TCTGCAAGCT	TCTTGCTGAT	CAGAGTTCCT	CCTACTTACA	4200
15	AGCCAGGGTG	TGAACATGTT	CTCCATTTTC	AAGCTGGAAG	AAGTGAGCAG	TGTTGGAGTG	4260
	AGGAACTGTA	AGGAGGCCCC	ATTGAGAGCT	ATGGTGCTTG	CTGGTGCTG	CCACCTTCAA	4320
	GTCTTGAGCC	TATGGCATGAC	ATCCTTTCTT	TTAATGATGC	CATGGCAACT	TAGAGATTGC	4380
	ATTTTATTA	AAGCATTTC	TACCAGCAAA	GCAAAATGTTG	GGAAAGTATT	TACTTTTTCG	4440
	GTTCCAAAGT	GATAGAAAA	TGTGGCTTGG	GCATTGAAAG	AGGTAAATTT	CTCTAGATT	4500
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	ATCTTATTTT	CTCAATCTCC	TCTCTCTTTC	CTCCACCCAT	AATAAGAGAA	TGTTCTACT	4620
	CACACTTCAG	CTGGGTCA	TCCATCCCTC	CATTCACTCT	TCCATCCATC	TTTCCATCCA	4680
	TTACTTCCAT	CCATCTCTCC	AACATATATT	TATTGAGTAC	CTACTGTGTG	CCAGGGGCTG	4740
	GTGGGACAGT	GGTGACATAG	TCTCTGCCCT	CATAGAGTTG	ATTGTCTAGT	GAGGAAGACA	4800
25	AGCATTTTGA	AAAAATAAAT	TTAAACTTAC	AAACTTTGTT	TGTCACAAGT	GGTGTATTAT	4860
	GCAATAACCG	CTTGTTTTCG	AACTCTTTTG	CTCAACAGAA	CATATGTTGC	AAGACCCCTC	4920
	CATGGGGGCA	CTTGAGTTT	GGCAAGGCTG	ACAGAGCTCT	GGGTTGTGCA	CATTTCTTTG	4980
	CATTCCAGCT	GTCACTCTGT	GCTTTCTAC	AACGTATTGC	AACAGACTGT	TGAGTTATGA	5040
	TAACCCAGT	GGGAATTGCT	GGAGGAACCA	GAGGCACTTC	CACCTTGGCT	GGGAAGACTA	5100
30	TGGTGCTGCC	TGCTTCTGT	ATTTCTTGG	ATTTCTCTGA	AAGTGTTTTT	AAATAAAGAA	5160
	CAATTGTTAG	ATGCC					5175

Seq ID NO: C107 DNA Sequence
Nucleic Acid Accession #: NM_021101
Coding sequence: 221..856

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	GCAGGGGCTCC	CCGCGCTTAAC	TTCTCTCGCG	GGGCCCCAGC	ACCTTCGGGA	GTCCGGGTTG	180
	CCCACTTCTGA	AACCTCTCGC	CTTCTGCACC	TGCCACCCCT	GAGCCAGCGC	GGGCGCCCGA	240
	GCGAGTCATG	GCCAAOCGGG	GGCTGCAGCT	GTTGGGCTTC	ATTCTCGCCT	TCCTGGGATG	300
	GATCGGCGCG	ATCGTCAGCA	CTGCCCTGCC	CCAGTGGAGG	ATTACTCTCT	ATGCGGCGCA	360
45	CAACATCTGT	ACCGCCACAG	CCATGTACGA	GGGGCTGTGG	ATGTCTCTGG	TGTGCGCAGG	420
	CACCGGGCAG	ATCCAGTGCA	AAGTCTTTGA	CTCCTTGCTG	AATCTGAGCA	GCACATTGCA	480
	AGCAACCCGT	GCCTTGATGG	TGGTTGGCAT	OCTCTGGGA	GTGATAGCAA	TCTTTGTGGC	540
	CACCGTTGGC	ATGAAGTGTA	TGAAGTGCTT	GGAAGACGAT	GAGGTGCAGA	AGATGAGGAT	600
	GGCTGTCAAT	GGGGGCGCGA	TATTTCTTCT	TGCAGGCTCG	GCTATTTTAG	TTGCCACAGC	660
50	ATGGTATGGC	AATAGAATCG	TTCAAGAATT	CTATGACCCT	ATGACCCAG	TCAATGCCAG	720
	GTACGAAATT	GGTCAGGCTC	TCTTCACTGG	CTGGGCTGCT	GCTTCTCTCT	GCCTTCTGGT	780
	AGGTGCGCTA	CTTTGCTGTT	CCTGTCCCG	AAAAACAACC	TCTTACCCAA	CACCAAGGCC	840
	CTATCCAAAA	CCTGCACCTT	CCAGCGGGAA	AGACTACGTG	TGACACAGAG	GCAAAAGGAG	900
	AAAAATCATGT	TGAACAAAC	CGAAAAATGGA	CATTGAGATA	CTATCATTAA	CATTAGGACC	960
55	TTAGAAATTT	GGGTATTGTA	ATCTAAAGTA	TGTTATTACA	AAACAAACAA	ACAAACAAAC	1020
	AACCCATGTG	TTAAATATCT	CAGTGCTAAA	CATGGCTTAA	TCTTATTTTA	TCTTCTTTCC	1080
	TCAATATAGG	AGGGAAGATT	TTTCCATTG	TATTAETGCT	TCCCATTTAG	TAATCATACT	1140
	CAAAATGGGG	AAGGGTGCT	CCTTAAATAT	ATATAGATAT	GTATATATAC	ATGTTTTTCT	1200
	ATTAATAATA	GCCAGTAAAA	AAAAAAAAAA	AAAAAA			1237

Seq ID NO: C108 DNA Sequence
Nucleic Acid Accession #: AF508964.1
Coding sequence: 98..1531

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	CTTATCCCGG	GAAGTGTCTG	TTATCTGGGG	TTTTCTGGTA	GATGTGGGCG	GTGTTTGGAG	2520
45	GCTGTACTAT	ATGAAGCCTG	CATATACTGT	GAGCTGTGAT	TGGGAAACAC	CAATGCAGAG	2580
	GTAACCTCTA	GGCAGCTAAG	CAGCAACCTCA	AGAAAAATG	TTAAATTAAT	GCTTCTCTTC	2640
	TTACAGTAGT	TCAAAATACAA	AACGAAATG	AAATCCCAT	GGATTGTACT	TCTCTTCTGA	2700
	AAAGTGTGCT	TTTTGACCCCT	ACTGGACATT	TATTGACTTA	ATTGCTCTCT	TTTATTAATA	2760
	TTGACCTGCA	AAGTTAAAAA	AAAATTTAAG	TTGAGAACAG	GTATAAGTGC	ACACTGAATA	2820
50	GTCTAATCTA	CATGTAACAC	ATATTTTAGT	GTGATTTTCT	ATACTCTAAT	CAGCACTGAA	2880
	TTCAAGGGGT	TTGACTTTTT	CATCTATAAC	ACAGTGACTA	AAAGAGTTAA	GGGTATATAT	2940
	ACCATCATT	TGGGACTTGG	TAGTATTATT	AAAAGTTTAT	TTCCCTTCACT	GTCAATAAAA	3000
	GTCCAAATGT	TTAGCTTAGG	TCTGAGAGTC	AAACAATGTT	AAGGATGTG	TTAAAGTTCC	3060
	TTAGCCAGCA	AAACAAAAA	AAACAAAAA	AACAAATGAA	AAACGTTTAA	AAAGAAGAGG	3120
55	AAGAAAAAAA	ACAAGAAACAA	GCAGCAACAG	CTGTTTGGTT	GGGGCTATAG	ATTTAAGTTA	3180
	GGCATAGTCA	ATTTCAGAAT	AACTAAGAGT	GGATATATG	CATATGGTGA	AATTATAACC	3240
	TTGCCCTTTT	TTAATTGCCCT	TCTGCGATCC	ACCTGCTTTT	TAGAAGTCTG	COGAGTGAGA	3300
	AGGCCACAGT	ATCTCATGCT	GTTTGCATTA	CAGAACTGCA	GCTTTTCTAC	TCTGAAAAGG	3360
	CCTGGGAGCA	GAATGGCTGG	CCTGCTGTGA	GCAGGAGAGG	AGATTCTAAG	AAGGATAGTC	3420
60	CCCCCTACAA	CATACTGTCA	TACTGCTGGG	TTTTCATGGG	TAGGAAAGCT	TGTCTGACC	3480
	CCAGCAGCAA	AGAGGTGGCA	GGTGGCTAAT	GAATATATGC	TTTATAATGT	CCTTCTTCAT	3540
	TGCTGAGAGG	GCAGCCTTAG	AGCTGTGGAT	TTCTGCATCC	CCCCTGAGTC	TGACCCATGG	3600
	ACACCTGTTT	CATTCACTTT	AGCATCACAG	TGACCTTTGT	ATGCTCTGTT	CAGTCTGTGT	3660
	CAGGCAGTAT	GCTTGTCTGT	AAGAGAGGTT	TGGCTATCCC	CACCCACCCC	CACCCACCCC	3720
65	TGTTCCCTTT	TTATCAGGAG	GACTTCAGAG	CCAGGCCTGC	AGCATTTTGT	TTGAAAACAC	3780
	AATCAGCTCT	GACAGTTAGA	CATGCACACA	GACGCCATAG	CTGGATTGGA	AACATTGATG	3840
	TTTTAAAAAT	TTAATTTTTT	TGGAATAGT	TGCACAAATG	CTGCAATTTA	GCTTTAAGGT	3900
	TCTATAGATT	TTTAACTAGT	CCAACACAGT	CAGAAACATT	GTTTGAATC	CTCTGTAAAC	3960
	CAAGGCATTA	ATCTTAATAA	ACCAGGATCC	ATTAGGTAC	CACCTGATAT	AAAAAGGATA	4020
70	TCCATAATGA	ATATTTTATA	CTGCATCCTT	TACATTAGCC	ACTAAATACG	TTATTGCTTG	4080
	ATGAAGACCT	FTACAGAAAT	CCTATGGATT	GCAGCATTTT	ACTTGGCTAC	TTCATACCCA	4140
	TGCCCTTAAAG	AGGGGCGAGT	TCTCAAAGGC	AGAAACATGC	CGCCAGTTCT	CAAGTTTTC	4200
	TCCTAACTCC	ATTGGAATGT	AAGGGCAGCT	GGCCCCCAAT	GTGGGGAGGT	CCGAACATT	4260
	TCTGAATTCC	CATTTTCTTG	TTGCGGCTTA	AATGACAGTT	TCTGTCTATTA	CTTAGATTCC	4320
75	GATCTTTCCC	AAAGGTGTTG	ATTTACAAAG	AGGCCAGCTA	ATAGCAGAAA	TCAATGACCT	4380
	GAAAGAGAGA	TGAATTTCAA	GCTGTGAGCC	AGGCAGGAGC	TCAGTATGGC	AAAGGTTCTT	4440
	GAGAATCAGC	CATTTGGTAC	AAAAAGGATT	TTTAAAGCTT	TTATGTTATA	CCATGGAGCC	4500
	ATAGAAGGCG	TATGGATTGT	TTTAAAGCTA	TTTAAAGCTG	TTCCAGACCC	AAAAAGGAAA	4560
	AATAAAAAAA	AAGGAATATT	TGTATCCCAAC	AGCTAGAAGG	ATTGCAAGGT	AGATTTTTGT	4620
80	TTTAAATGAG	AGAGAAGTGG	ACAGATAAGG	CCATTAAATA	TATCAAGAGT	CAGTTGACAT	4680
	CTCTAGGGA	ATGATGAAAA	CAGCAGGCTA	T			4711

Seq ID NO: C111 DNA Sequence
Nucleic Acid Accession #: NM_130830.1
Coding sequence: 1..1746

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	GGGGCAGCGA	TTGTGGCGGT	GCCCCACCCCT	CTGCCCTGGA	AGGCCATGAG	CCTGCAGATC	180
	CTCAACACGC	ACATCACTGA	ACTCAATGAG	TCCCCGTTC	TCAATATCTC	AGCCCTCATC	240
	GCCCTGAGGA	TTGAGAAGAA	TGAGCTGTGG	CGCATCACGC	CTGGGGCCTT	CCGAAACCTG	300
10	GGCTCGCTGC	GCTATCTCAG	CCTCGCCAAC	AACAAGCTGC	AGGTCTTGCC	CATCGGCTC	360
	TTCCAGGGCC	TGGACAGCCT	TGAGTCTCTC	CTTCTGTCCA	GTAACCAAGT	GTTCAGATC	420
	CAGCGGCCCC	ACTTCTCCCA	GTGCAGCAAC	CTCAAGGAGC	TGCAGTTGCA	CGGCAACCAC	480
	CTGGAATACA	TCCCTGACGG	AGCCTTCGAC	CACCTGGTAG	GACTCAOGAA	GCTCAATCTG	540
	GGCAAGAATA	GCCTCACCCA	CATCTCACCC	AGGGTCTTCC	AGCACTGGG	CAATCTCCAG	600
15	GTCTCCGGC	TGTATGAGAA	CAGGCTCACG	GATATCCCCA	TGGGCACTTT	TGATGGGCTT	660
	GTTAACTGTC	AGGAACCTGG	TCTACAGCAG	AACCAAGATT	GACTGCTCTC	CCCTGGTCTC	720
	TTCCACAACA	ACCAACCTCT	CCAGAGACTC	TACCTGTCCA	ACAACCAAT	CTCCAGCTG	780
	CCACCCAGCA	TCTTCATGCA	GCTGCCCCAG	CTCAACCGTC	TTACTCTCTT	TGGGAATTC	840
	CTGAAGGAGC	TCTCTCTGGG	GATCTTGGGG	CCCATGCCCA	ACCTGCGGGA	GCTTTGGCTC	900
20	TATGACAACC	ACATCTCTTC	TCTACCCGAC	AATGTCTTCA	GCAACCTCCG	CCAGTTGCAG	960
	GTCTCTGATC	TTAGCCGCAA	TCAGATCAGC	TTCACTCTCC	CGGGTGCCTT	CAACGGGCTA	1020
	ACGGAGCTTC	GGGAGCTGTC	CCTCCACACC	AACGCACTGC	AGGACCTGGA	CGGGAATGTC	1080
	TTCCGCAATG	TGGCCAACTC	CGAGAACATC	TCCCTGCAGA	ACAATGSCCT	CAGACAGCTC	1140
	CCAGGGAATA	TCTTCGCCAA	CGTCAATGGC	CTCATGGCCA	TCCAGCTGCA	GAACAACCAG	1200
25	CTGGAGAACT	TGCCCTCTCG	CATCTTCGAT	CACCTGGGGA	AACCTGTGTA	GCTGCGGCTG	1260
	TATGACAATC	CCTGGAGGTG	TGACTCAGAC	ATCCTTCCCG	TCCGCAACTG	GCTCCTGCTC	1320
	AACCAAGCTA	GGTTAGGGAC	GGACACTGTA	CCTGTGTGTT	TACGCCACAG	CAATGTCCGA	1380
	GGCCAGTCCC	TCAATTATCAT	CAATGTCAAC	GTGTCTGTTC	CAGGCTCCA	TGTCCCTGAG	1440
	GTGCTCTAGT	ACCCAGAAAC	ACCATGGTAC	CCAGACACAC	CCAGTTACCC	TGACACCACA	1500
30	TCCGTCTCTT	TACCACTGTA	GCTAACCAAG	CCGTGGAAG	ACTCACTGTA	TCTGACTACC	1560
	ATTGAGTCCA	CTGATGACCG	CAGCGTTTGG	GGCATGACCC	AGGCCACAG	CGGGCTGGCC	1620
	ATTGCGGCA	TGTAAATTGG	CATTGTGCCC	CTGGCTGTCT	CCTGGCTGCG	CTGCGTGGC	1680
	TGTTGCTGCT	GCAAGAAGAG	GAGCCAAGCT	GTCTGATGTC	AGATGAAGGC	ACCCAATGAG	1740
	TGTTAA						1746

Seq ID NO: C112 DNA Sequence
 Nucleic Acid Accession #: NM_002658.1
 Coding sequence: 77..1372

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	CCCCGACCTC	GCCACCATGA	GAGCCCTGCT	GGCGCGCCTG	CTTCTCTGCG	TCCTGTGCTG	120
	GAGCGACTCC	AAAGGCAGCA	ATGAACCTCA	TCAAGTTCCA	TGGAACCTGTG	ACTGTCTAAA	180
45	TGGAGGAACA	TGTGTGTCCA	ACCAAGTACTT	CTCCAACATT	CATGTGTGCA	ACTGCCCAAA	240
	GAAATTCCGA	GGGCAGCACT	GTGAAATAGA	TAAATCAAAA	ACCTGTCTATG	AGGGGAATGG	300
	TCACTTTTAC	CGAGGAAAGG	CCAGCACTGA	CACCATGGGC	CGGCCCTGCC	TGCCCTGGAA	360
	CTCTGCCACT	GTCCCTCAGC	AAACGTACCA	TGCCACAGA	TCTGATGCTC	TTCACTGTGG	420
	CCTGGGGAAA	CATAATTACT	GCAGGAACCC	AGACAACCGG	AGGGAGCCCT	GGTGTCTATG	480
50	CGAGGTGGGC	CTAAAGCCGC	TTGTCCAAGA	GTGCATGGTG	CATGACTGCG	CAGATGGAAA	540
	AAAGCCCTCC	TCTCTCCAG	AAGAATTAAA	ATTTCAGTGT	GGCCAAAAGA	CTCTGAGGCC	600
	CGCTTTAAG	ATTATTGGGG	GAGAATTAC	CACCATCGAG	AACCAAGCCCT	GGTTTGGGCG	660
	CATCTACAGG	AGGCACCGGG	GGGGCTCTGT	CACCTACGTG	TGTGGAAGCA	GCCTCATCAG	720
	CCCTTGCTGG	GTGATCAGCG	CCACACACTG	CTTCATTGAT	TACCCAAAGA	AGGAGGACTA	780
55	CATCGTCTAC	CTGGGTGCTC	CAAGGCTTAA	CTCCAACACG	CAAGGGGAGA	TGAAGTTTGA	840
	GGTGGAAAC	CTCATCTCAC	ACAAGGACTA	CAGCGCTGAC	ACGCTTGCTC	ACCACAAOCA	900
	CATTGCGCTG	TGAAAGATCC	GTTCGAAGGA	GGGCAGGTGT	GGCAGCCAT	CCCGACTAT	960
	ACAGACCATC	TGCCTGCCCT	CGATGTATAA	CGATCCCCAG	TTTGGCACAA	GCTGTGAGAT	1020
	CACCTGGCTT	GGAAAAGAGA	ATTCTACCGA	CTATCTCTAT	COGGAGCAGC	TGAAAATGAC	1080
60	TGTTGTGAAG	CTGATTTC	ACCGGAGTGG	TCAGCAGCCC	CACACTACCG	GCTCTGAAGT	1140
	CACCAACCAA	ATGCTATGTG	CTGCTGACCC	CCAATGGAAA	ACAGATTCTC	GCCAGGGAGA	1200
	CTCAGGGGGA	CCCTCGTCT	GTTCCTCCA	AGGCCGATG	ACTTTGACTG	GAATTGTGAG	1260
	CTGGGGCCGT	GGATGTGCC	TGAAGSACAA	GCCAGGCGTC	TACACGAGAG	TCTCACACTT	1320
	CTTACCTCG	ATCCGAGTC	ACACCAAGGA	AGAGAATGGC	CTGGCCCTCT	GAGGGTCCCC	1380
65	AGGGAGGAAA	CGGGCACAC	CCGCTTCTT	GCTGGTTGTC	ATTTTTCAG	TAGAGTCATC	1440
	TCCATCAGCT	GTAAGAAGAG	ACTGGGAAGA	TAGGCTCTGC	ACAGATGGAT	TTGCTGTGG	1500
	CACCAACGAC	TGAAACGACA	ATAGCTTTAC	CCTCACGGAT	AGGCCTGGGT	GCTGGCTGCC	1560
	CAGACCTCT	GGCCAGGATG	GAGGGGTGGT	CCTGACTCAA	CATGTTACTG	ACCAGCAACT	1620
	TGTCTTTTTC	TGGACTGAAG	CCTGCAGGAG	TTAAAAAGGG	CAGGGCATCT	CCTGTGCATG	1680
70	GGCTCGAAGG	GAGAGCCAGC	TCCCCCGACC	GGTGGGCATT	TGTGAGGCC	ATGGTTGAGA	1740
	AATGAATAAT	TTCCCAATTA	GGAAGGTAA	GCAGCTGAGG	TCTCTTGAGG	GAGCTTAGCC	1800
	AATGTGGGAG	CAGCGGTTTG	GGGAGCAGAG	ACACTAACGA	CTTCAGGGCA	GGGCTCTGAT	1860
	ATTCCATGAA	TGTATCAGGA	AATATATATG	TGTGTGTATG	TTTGCACACT	TGTTGTGTGG	1920
	GCTGTGAGTG	TAAAGTGTGAG	TAAAGCTGG	TGTCTGATTG	TTAAGTCTAA	ATATTTCCTT	1980
75	AAACTGTGTG	GACTGTGATG	CCACACAGAG	TGGTCTTTCT	GGAGAGGTTA	TAGGCTCACTC	2040
	CTGGGGCCCT	TGGGTCCCC	CAGTGCAGAG	TGCCTGGGAA	TGTACTTATT	CTGCAGCATG	2100
	ACCTGTGACC	AGCATGTGCT	CAGTTTCACT	TTCAATAGA	TGTCCTTTTC	TTGGCCAGTT	2160
	ATCCCTTCTT	TTTAGCCTAG	TTTATCCAAT	CCTCACTGGG	TGGGGTGGAG	ACCACCTCCTT	2220
	ACACTGAATA	TTTATATTTC	ACTATTTTTA	TTTATATTTT	TGTAATTTTA	AATAAAGAGT	2280
80	ATCAATAAAA	TGTGATTTTT	CTGA				2304

Seq ID NO: C113 DNA Sequence
 Nucleic Acid Accession #: XM_087254.1
 Coding sequence: 47..2332

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5	ATGTTCAATT	AATGGCATGA	AATACCAAGA	AATTAATGGT	AGACTTGTAC	CCGAAGGACC	120
	AACACCAGAC	TCTTCAGAAG	GAAACTTATC	TTATCTTAGT	AGTTTATCCC	ATCTTAACAA	180
	CTTATCCCAT	CTTACAACCA	GTTCTCTTTT	CAGAACCCAGT	CCTGAAAATG	AAACTGAACT	240
	AAITAAAGAA	CATGATCTCT	TCTTTAAAGC	AGTCAGTCTC	TGTCACACTG	TACAGATTAG	300
	CAATGTTCAA	ACTGACTGCA	CTGGTGAATG	TCCCCTGGCA	TCCAACCTGG	CACCATCGCA	360
10	GTGGAATGAT	TATGCATCTT	CACCAGATGA	AAAGGCTCTA	GTAGAAGCTG	CTGCAAGGAT	420
	TGGTATTGTG	TTTATTGGCA	ATTCTGAAGA	AACTATGGAG	GTTAAAACTC	TTGGAAAACT	480
	GGAAAGGTAC	AAACTGCTTC	ATATTCTGGA	ATTGATTCTA	GATCGTAGGA	GAATGAGTGT	540
	AATTTGTCAG	GCACCTTCAG	GTGAGAAGTT	ATTATTGGCT	AAAGGAGCTG	AGTCATCAAT	600
	TCTCCCTAAA	TGTATAGGTG	GAGAAATAGA	AAAAACCAGA	ATTCTATGTAG	ATGAATTTCG	660
15	TTTGAAGGGG	CTAAGAACTC	TGTGTATAGC	ATATAGAAAA	TTTACATCAA	AAGAGTATGA	720
	GGAAATAGAT	AAAGCATAT	TTGAAGCCAG	GACTGCCCTG	CAGCAGCGGG	AAGAGAAATT	780
	GGCAGCTGTT	TTCCAGTTCA	TAGAGAAAGA	CCTGATATTA	CTTGGAGCCA	CAGCAGTAGA	840
	AGACAGACTA	CAAGATAAAG	TTCCGAGAAC	TATTGAAGCA	TTGAGAAATG	CTGGTATCAA	900
	AGTATGGTGA	CTTACTGGGG	ATAAACATGA	AACAGCTGTT	AGTGTGAGTT	TATCATGTGG	960
20	CCATTTTCAT	AGAACCATGA	ACATCCTTGA	ACTTATAAAC	CAGAAATCAG	ACAGCGAGTG	1020
	TGCTGAACAA	TTGAGGCAGA	TTGCCAGAAG	AATTACAGAG	GATCATGTGA	TTGAGCATGG	1080
	GCTGGTAGTG	GATGGGACCA	GCCTATCTCT	TGCACCTCAG	GAGCATGAAA	AACTATTAT	1140
	GGAAAGTTGC	AGAAATTTGT	CAGCTGTATT	ATGCTGTCTG	ATGGCTCCAC	TGCAGAAAGC	1200
	AAAAGTAATA	AGACTAATAA	AAATATCACC	TGAGAAACCT	ATAACATTGG	CTGTTGGTGA	1260
25	TGGTGTCAAT	GACGTAAAGA	TGATACAAGA	AGCCCATGTT	GGCATAGGAA	TCATGGGTAA	1320
	AGAAGGAAGA	CAGGCTGCAA	GAACACGTGA	CTATGCAATA	GCCAGATTTA	AGTTCTCTCT	1380
	CAAAATGCTT	TTTGTTCATG	GTCAATTTTA	TTATATTAGA	ATAGCTACCC	TTGTACAGTA	1440
	TTTTTTTTAT	AAGAATTTGT	GCTTTATCAC	ACCCAGTTT	TTATATCAGT	TCTACTGTTT	1500
	GTTTTCTCAG	CAACATTTGT	ATGACAGCGT	GTACCTGACT	TTATACAATA	TTTGTTTTAC	1560
30	TTCCCTACCT	ATTCTGATAT	ATAGTCTTTT	GGAAACAGAT	GTAGACCTTC	ATGTGTTTACA	1620
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	TCITTTATGG	ACCATCCTGG	GCTTCAGTCA	TGCCCTTATT	TTCTTTTTTG	GATCCTATT	1740
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	TGGCCTTTTG	GTCTTCACAG	TCATGGTTAT	TACAGTCACA	GTAAAGATGG	CTCTGGAAAC	1860
35	TCATTTTGGG	ACTTGGATCA	ACCATCTCGT	TACCTGGGGA	TCTATTATAT	TTTATTTTGT	1920
	ATTTTCTTTG	TTTATGGAG	GGATTCTCTG	GCCATTTTGG	GGCTCCGAGA	ATATGTATT	1980
	TGTGTTTATT	CAGCTCCTGT	CAAGTGGTTC	TGCTTGGTTT	GCCATAATCC	TCATGGTTGT	2040
	TACATGCTTA	TTTCTTGATA	TCATAAAGAA	GCTCTTTGAC	CGACACCTCC	ACCCTACAAG	2100
40	TACTGAAGAG	GCACAGCTTA	CTGAAACAAA	TGCAGGTATC	AAGTGCTTGG	ACTCCATGTG	2160
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	CAACGACAGG	AGCATCTTGA	CTCTCTCCAC	AATGGACTCA	TCTACTTGT	AAAGGGGCGG	2340
	TAGTACTTTG	TGGAGGCCAG	TTCACTCCT	TTCTTAAAT	TCAGTGTGAT	CACCTGTGTA	2400
45	ATGGCCACAC	TAGCTCTGAA	ATTAAATTTCC	AAATCTTTG	TAGTAGTTCA	TACCCACTCA	2460
	GAGTTATAAT	GGCAACCAAA	CAGAAAGCAT	TAGTACAAGC	CCCTCCCAAC	ACCCTTAATT	2520
	TGAATCTGAA	CATGTTAAAA	TTTGAGAATA	AAGAGACATT	TTTCTATCT	TTGCTGGTT	2580
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	TTTAATATAA	ATGTAGAAAA	AAGAGAGAAA	TCTTAGTAAA	GAGTATTTTT	TAGTATTAGC	2700
50	TTGATTATTG	ACTCTTCTAT	TTAAATCTGC	TTCTGTAAAT	TATGCTGAAA	GTTTGCTTGG	2760
	AGAACTCTAT	TTTTTTATTA	GAGTTATATT	TAAAGCTTTT	CATGGGAAAA	GTTAATGTGA	2820
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	TTTACAGAGC	AAATTAGGAG	AATCATTTCC	AACCATTAAT	TACTGAGTAA	TGGGGAGTAA	2940
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55	CAAGGGTATA	TCATATATAC	AAATCAGGAA	TCAGGTCCGT	TCACCGAACT	TCAAAATTGAT	3060
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60	TATGTTTAA	TATACAAATC	AGAATAGTAT	GGTAATTAA	ATGAATACAA	AAAGAGAGGC	3360
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	CTCAGTAGAG	TACTAGGTGG	GAGGATATGG	AAATTTGCTC	ATAAAATCTC	TTATAAAACG	4260
75	TGCATATAAC	AAAATGACAC	CCAGTAGGCC	TGCATTACAT	TTACATGACC	GTGTTTATTT	4320
	GCCATCAAA	AAACTGAGTA	CTGACACCAG	ACAAAGACTC	CAAAATCATA	AAATAGCCCTA	4380
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GCTGCTTTAA GTGACTCAGC ACCCTGCGCTC AGCTTCAGCA GGCGTAGGCT CACCCGSGGC 4980
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Seq ID NO: C114 DNA Sequence
Nucleic Acid Accession #: XM_087461.1
Coding sequence: 236..1138

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Nucleic Acid Accession #: XM_051522.4
Coding sequence: 127..1215

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Seq ID NO: C116 DNA Sequence
Nucleic Acid Accession #: NM_000350.1
Coding sequence: 82..6903

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Coding sequence: 278..2806

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	GGGCTTGCAG	TTGGCAGAAG	GGTCCCCGGC	CCAGAGCCAG	CGGGGCCGTG	CTGAGACGGC	60
	GTACGTGCC	TGCGTGAAGT	CGTGGCGGCG	GCGCGTGGCG	TAGGGGAGTG	GGCGGTGAGG	120
	CCTGGTCCAC	GTGCGTCCCT	TCCCGGGACC	CCCGCAGCTT	GGCGCCACGC	GGCTACGTGA	180
	GCCAAGGCAC	CGGATGTCC	GCGCCCTCT	CCGAGTGACA	AGTCCCGGCC	TCCGTTCCCG	240
35	CAGTGCCCGC	AGCCTCGGCC	GGCTCCACG	CATTGCCATG	GTGACTGTGG	GCAACTACTG	300
	CGAGGCCGAA	GGGCCCGTGG	GTCCCGCCTG	GATGCAGGAT	GGCTGAGTTC	CCTGCTTCTT	360
	CTTCACTCTC	GTGCGCTCGA	CGCGGATGGC	TCTAGGGACT	CTGGCTTGG	TGCTGGCTCT	420
	TCCCTGCAGA	CGCCGGGAGC	GGCCCGCTGG	TGCTGATTGG	CTGCTTGGG	GGCCCGGCC	480
	TGCGATCTCT	CCCTACGTGC	TGCAGCTGCT	TCTGGCCACA	CTTCAGGCGG	CGCTGCCCTT	540
40	GGCCGGCCTG	GCTGGCCGGG	TGGGCACTGC	CGGGGGGCC	CCACTGCCAA	GCTATCTACT	600
	TCTGGCTTCC	GTGCTGGAGA	GTCTGGCCGG	CGCCTGTGGC	CTGTGGCTGC	TTGTCTGTGA	660
	GCGGAGCCAG	GACCGGCAGC	GTCTGGCAAT	GGGCATCTGG	ATCAAGTTCA	GGCAGAGCCC	720
	TGGTCTCCTG	CTCCTCTGGA	CTGTGGCGTT	TGCAGCTGAG	AACTTGGCCC	TGTTGTCTTG	780
	GAACAGGCCA	CAGTGGTGGT	GGGCAAGGGC	AGACTTGGGC	CAACAGGTTT	AGTTTAGCCT	840
45	GTGGGTGCTG	CGGTATGTGG	TCTCTGGAGG	GCTGTTTGTG	CTGGGTCTCT	GGGCCCTCTG	900
	ACTTCGTCCC	CAGTCTTATA	CATTGCAGGT	TCATGAAGAG	GACCAAGATG	TGGAAGAGAG	960
	CCAGTCTCGG	TCAGCAGGCC	AACAGTCTAC	CTGGCGAGAT	TTTGGCAGGA	AGCTCGCCTT	1020
	CCTGAGTGGC	TACCTGTGGC	CTCGAGGAGG	TCCAGCTCTG	CAGCTGGTGG	TGCTCATCTG	1080
	CCTGGGGCTC	ATGGGTTTGG	AACGGGCACT	CAATGTGTTG	GTGCCTATAT	TCTATAGGAA	1140
50	CATTGTGAAC	TTGCTGACTG	AGAAGGCACC	TTGGAACCTC	CTGGCCTGGA	CTGTTACCAAG	1200
	TTACGTCTTC	CTCAAGTTCC	TCCAGGGGGG	TGGCACTGGC	AGTACAGGCT	TGCTGAGCAA	1260
	CTCGGCGACC	TTCTGTGGA	TCCGGGTGCA	GCAGTTCAAG	TCTCGGCGGG	TGGAGCTGCT	1320
	CATCTTCTCC	CACCTGCACG	AGCTCTCACT	GCGCTGGCAC	CTGGGGCGCC	GCACAGGGGA	1380
	GGTGCTGGGG	ATCGCGGATC	GGGGCACATC	CAGTGTCA	GGGCTGTCTA	GCTACCTGGT	1440
55	GTTCAATGTC	ATCCCCACGC	TGGCCGACAT	CATCATTGGC	ATCATCTACT	TCAGCATGTT	1500
	CTTCAAGGCC	TGGTTTGGCC	TCATTGTGTT	CCGTGTGATG	AGTCTTTTAC	TCACCCCTGAC	1560
	CATTGTGTCT	ACTGAGTGGG	GAACCAAGTT	TCGTGTGTCT	ATGAACACAC	AGGAGAACGC	1620
	TACCCGGGCA	CGAGCAGTGG	ACTCTCTGCT	AAACTTCGAG	ACGGTGAAGT	ATTACAAAGC	1680
	CGAGAGTTAC	GAAGTGGAAC	GCTATCGAGA	GGCCATCATC	AAATATCAGG	GTTTGGAGTG	1740
60	GAAGTCGAGC	GCTTCACTGG	TTTTACTAAA	TCAGACCCAG	AACTGTGTGA	TTGGGCTCGG	1800
	GCTCTCTGCC	GGCTCCCTGC	TTTGCGCATA	CTTTGTCACT	GAGCAGAAGC	TACAGGTTGG	1860
	GGACTATGTG	CTCTTTGGCA	CCTACATTAT	CCAGCTGTAC	ATGCCCTTCA	ATTGGTTTGG	1920
	CACCTACTAC	AGGATGATCC	AGACCAACTT	CATTGACATG	GAGAACATGT	TTGACTTGCT	1980
	GAAAGAGGAG	ACAGAAGTGA	AGGACCTTCC	TGGAGCAGGG	CCCCTTGGCT	TTTCAAGAGG	2040
65	CCGTATTGAG	TTTGAGAAAG	TGCACITCAG	CTATGCCGAT	GGGCGGAGGA	CTCTGCAGGA	2100
	CGTGTCTTTC	ACTGTGATGC	CTGGACAGAC	ACTTGCCTTG	GTGGGGCCAT	CTGGGGCAGG	2160
	GAAGAGCACA	ATTTTGCGCC	TGCTGTTTGG	CTTCTAAGAC	ATCAGCTCTG	GCTGCATCCG	2220
	AATAGATGGG	CAGGACATTT	CACAGGTGAC	CCAGGCCCTCT	CTCCGGTCTC	ACATTGGAGT	2280
	TGTGCCCCAA	GACACTGTCC	TCTTTAATGA	CACCATGGCC	GACAATATCC	GTTACGGCCG	2340
70	TGTCACAGCT	GGGAATGATG	AGGTGAGAGC	TGCTGCTCAG	GCTGCAGGCA	TCCATGATGC	2400
	CATTATGGCT	TTCCCTGAAG	GGTACAGGAC	ACAGGTGGGC	GAGCGGGGAC	TGAAGCTGAG	2460
	CGGCGGGGAG	AAGCAGCGCG	TGGCCATTGC	CGCACCATC	CTCAAGGCTC	CGGCATCAT	2520
	TCTGTGTGAT	GAGGCAACCT	CAGCGCTGGA	TACATCTAAT	GAGAGGGCCA	TCCAGGCTTC	2580
	TCTGGCCAAA	GTCTGTGCCA	ACCGCACACC	CATCGTAGTG	GCACACAGGC	TCTCAACTGT	2640
75	GGTCAATGCT	GACCAGATCC	TGCTCATCAA	GGATGGCTGC	ATCGTGAGGA	GGGGACGACA	2700
	CGAGGCTCTG	TGTGTCGAG	GTGGGGTGTG	TGCTGACATG	TGGCAGCTGC	AGCAGGGACA	2760
	GGAGAAAGCC	TCTGAAGACA	CTAAGCCTCA	GACCATGGAA	CGGTGACAAA	AGTTTGGCCA	2820
	CTTCCCTCTC	AAAGACTAAC	CCAGAAGGGA	ATAAGATGTG	TCTCCTTTCC	CTGGCTTATT	2880
80	TCATCTGTGT	CTTGGGGTAT	GGTGCTAGCT	ATGTTAAGGG	AAAGGGACCT	TTCCGAAAAA	2940
	CATCTTTTGG	GGAAATAAAA	ATGTGACTG	TGAAAAAAA	AAAAAAA	AAA	2993

Seq ID NO: C119 DNA Sequence
Nucleic Acid Accession #: NM_000676
Coding sequence: 333..1331

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	CCCCGGCGG	GGCGGAAC	TGGGCTCGGG	CGAGTGGGTG	GTGCTCCGCC	CAGCCCGAGA	120
	CGGGCGGGCG	CGCGGGCCAA	TGGGTGCGGC	CTCTTGGCGG	CGGGGGGGCC	CGACCCGTGG	180
	GTCCCGGCCA	CCAGCGCCCC	AGCCCCGAGG	CTCAGAAAGG	GCAGGCGGAG	GCGCGGTCCG	240
	GGCGCTATGG	CCATGCCCCG	CGGGTCTCAC	GCGGCTGCCC	CTCGCCCGGC	GCGCCTTCGG	300
10	TAGGGGGCGC	CCGGGGCCCA	GCTGGCCCGG	CCATGCTGCT	GGAGACACAG	GACGCGCTGT	360
	ACGTGGCGCT	GGAGCTGGTC	ATCGCCGGGC	TTTCGGTGGC	GGGCAACGTG	CTGGTGTGCG	420
	CGCGGTGGG	CACGGCGAAC	ACTCTGCAGA	CGCCCAACAA	CTACTTCCTG	GTGTCCCTGG	480
	CTCGGGCCGA	CGTGGCCGTG	GGGCTCTTCG	CCATCCCTTT	TGCCATACCC	ATCAGCCTGG	540
	GCTTCTGCAC	TGACTTCTAC	GGCTGCTCTT	TCCTCGCCTG	CTTCGTGCTG	GTGCTCACGC	600
15	AGAGCTCCAT	CTTCAGCCTT	CTGGCCGTGG	CAGTGCAGAG	ATACCTGGCC	ATCTGTGTTC	660
	CGCTCAGGTA	TAAAGATT	GTACCGGGA	CCCGAGCAAG	AGGGGTCAAT	GCTGTCTCTT	720
	GGGTCTTGG	CTTTGGCATC	GGATTGACTC	CATTCTCTGG	GTGGAACAGT	AAAGACAGTG	780
	CCACCAACAA	CTGCACAGAA	CCCTGGGATG	GAAACACGAA	TGAAGCTGCG	TGCCTTGTGA	840
	AGTGTCTCTT	TGAGAATGTG	GTCCCCATGA	GCTACATGGT	ATATTTCAAT	TTCTTTGGGT	900
20	GTGTTCTGCC	CCCACTGCTT	ATAATGCTGG	TGATCTACAT	TAAGATCTTC	CTGGTGGCCT	960
	GCAGGCAGCT	TCAGCGCACT	GAGCTGATGG	ACCACTCGAG	GACCACCCCTC	CAGCGGGAGA	1020
	TCCATGCAGC	CAGTCACTG	GCCATGATTG	TGGGGATT	TGCCCTGTGC	TGGTTACCTG	1080
	TGCATGCTGT	TAACTGTGTC	ACTCTTTTCC	AGCCAGCTCA	GGGTAAAAAT	AAGCCCAAGT	1140
	GGGCAATGAA	TATGGCCATT	CTTCTGTGAC	ATGCCAATTC	AGTTGTCAAT	CCCATTGTCT	1200
25	ATGCTTACCG	GAACCGAGAC	TTCCGCTACA	CTTTTCACAA	AATTATCTCC	AGGTATCTTC	1260
	TCTGCCAAGC	AGATGTCAAG	AGTGGGAATG	GTACGGCTGG	GGTACAGCCT	GCTCTCGGTG	1320
	TGGGCTATG	ATCTAGGCTC	TGCGCTCTTC	CAGGAGAAAG	TACAAATCCA	CAAGAAACAA	1380
	AGAGGACAGC	GCTGGTTTTT	ATTGTGAAAG	ATAGCTACAC	CTCAACAAGG	AATGGACTGC	1440
	CTCTCTTGAG	CACCTCCCTG	GAGCTACCAC	GTATCTAGCT	AATATGTATG	TGTCTAGTGT	1500
30	AGGCTCCAA	GATTGACAAA	TATATTTATG	ATCTATTTCAG	CTGCTTTTTC	TGTGTGGAGT	1560
	ATGCCCAACG	CTTGAATGGA	TTCTAACAGA	CTCTTTTGTG	TTTAAAGATC	TGCCTTGTTC	1620
	ATGGTGGAAA	ATTACTGAAA	CTATTTTACT	GTGAAACAGT	GTGAACATTT	ATAATGCAAA	1680
	TACTTTTTAA	CTTAGAGGCA	ATGGAAAAAT	AAAAGTTGAC	TGTACTAAAA	ATG	1733

Seq ID NO: C120 DNA Sequence
Nucleic Acid Accession #: NM_052932
Coding sequence: 217..786

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	CGCCCTATT	GGTCAATCGG	GGGGCAAGCG	GCGGGAGGGG	AAACGTGCGC	GGCGGAAGGG	120
	GAGCGGAGC	CGGCGCCGGC	TGCGCAGAGG	AGCCGCTCTC	GCCGCGCCCA	CCTCGGCTGG	180
	GAGCCCAAGA	GGCTGCGGCA	TCCTGCCCTC	GGAAACAATG	GACTCGGCGC	GCGAGGTGCT	240
45	TGGGCGGCGC	TGCTCTCTGG	GACGCTGCAG	GTGCTAGCGC	TGCTGGGGGG	CGCCCATGAA	300
	AGCGCAGCCA	TGGCGGAGAC	TCTCCAACAT	GTGCCCTCTG	ACCATACAAA	TGAAACTTCC	360
	AACAGTAGTG	TGAAACCAAC	AACCTCAGTT	GCCTCAGACT	CCAGTAATAC	AACGGTCAAC	420
	ACCATGAAC	CTACAGCGGC	ATCTAATACA	ACAACACCAG	GGATGCTCTC	AACAAATATG	480
	ACTTCTACCA	CCTTAAAGTC	TACACCCAAA	ACAACAAGTG	TTTCACAGAA	CACATCTCAG	540
50	ATATCAACAT	CCACAATGAC	CGTAACCCAC	AATAGTTCAG	TGACATCTGC	TGCTTCATCA	600
	GTAACAATCA	CAACAATCTAT	GCAATCTGAA	GCAAGAAAGG	GATCAAAATT	TGATACTGGG	660
	AGCTTTGTGT	GTGGTATTGT	ATTAACGCTG	GGAGTTTAT	CTATTCTTTA	CATTGGATGG	720
	AAAATGTATT	ACTCAAGAAG	AGGCATTGCG	TATCGAACCA	TAGATGAACA	TGATGCCATC	780
	ATTTAAGGAA	ATCCATGGAC	CAAGGATGGA	ATACAGATTG	ATGCTGCCCT	ATCAATTAAT	840
55	TTTGGTTTAT	TAAATAGTTT	AAACAATATT	CTCTTTTGA	AAATAGTATA	AACAGGCCAT	900
	GCATATAAGT	TACAGTGTAT	TACGTAAATA	TGTAAAGATT	CTTCAAGGTA	ACAAGGGTTT	960
	GGGTTTGTGA	ATAAACATCT	GGATCTTATA	GACCGTTTAT	ACAAATGGTT	TAGCAAGTTC	1020
	ATAGTAAGAC	AAACAAGTCC	TATCTTTTTT	TTTTTGGCTG	GGGTGGGGGC	ATTGGTCACA	1080
	TATGACCAGT	AATTGAAAGA	CGTCATCACT	GAAAGACAGA	ATGCCATCTG	GGCATACAAA	1140
60	TAAGAAAGTT	GTACAGCAC	TCAGGATTTT	GGGTATCTTT	TGTAGCTCTG	ATAAAGAACT	1200
	TCAGTGCTTT	TCAGAGCTGG	ATATATCTTA	ATTACTAATG	CCACACAGAA	ATTATACAA	1260
	CAAACTAGAT	CTGAAGCATA	ATTTAAGAAA	AACATCAACA	TTTTTTGTGC	TTTAAACTGT	1320
	AGTAGTTGTT	CTAGAAACAA	AATACTCCAA	GAAAAAGAAA	ATTTTCAAT	AAAACCCAA	1380
	ATAATAGCTT	TGCTTAGCCC	TGTTAGGAT	CCATTGGAGC	ATTAAGGAGC	ACATATTTT	1440
65	ATTAACCTCT	TTTGAGCTTT	CAATGTTGAT	GTAATTTTGG	TTCTCTGTGT	AATTTAGGTA	1500
	AACCTGCACT	TTTAACATAA	TAAATGTTTA	AAGACTTAGT	TGTCAGTATT	AAATAATCCT	1560
	GGCATTATAG	GGAAAAAACC	TCCTAGAAGT	TAGATTATTT	GCTACTGTGA	GAATATTGTC	1620
	ACCATGGA	GTTACTTTAG	TTCTATTAA	TTTAATTTTA	TATTTTGTGA	ATATTTTAAG	1680
	AACCTGADAG	CTGCTTTCAA	TATCTAGAAA	TTTTTAATG	AGTGTAAACA	CACCTAATCT	1740
70	TAAGAAAGAG	AACCGCTTGT	ATGATTTTCA	AAAGAACATT	TAGAATTCTA	TAGAGTCAAA	1800
	ACTATAGCGT	AATGCTGTGT	TTATTAAGCC	AGGGATTGTG	GGACTTCCCC	CAGGCAACTA	1860
	AACTGCGAG	ATGAAATGCG	TATATTTTCT	TTCTGCACT	GTGATATTA	CTCAGATTG	1920
	GGGAAATGAC	ATTTTATATC	TAAACAAC	ACCAAAATAT	TTTGAATAA	ATTCTTAGAA	1980
	AGTTTGTAGA	GGAATTTTAT	GAGAGGACAT	TTCTCTCTTC	CTGATTGTGA	TATTCCTCA	2040
75	AATCCCTCT	CTTACTCCAT	GCTGAAGGAG	AAGTACTCTC	AGATGCATTA	TGTTAATGGA	2100
	GAGAAAAAGC	ACAGTATTGT	AGAGACACCA	ATATTAGCTA	ATGTATTTTG	GAGTGTTTTC	2160
	CATTTACAG	TTTATTTTCC	AGCACTCAAA	ACTCAGGGTC	AAGTTTAAAC	AAAAGAGGTA	2220
	TGTAGTCACA	GTAAATACTA	AGATGGCATT	TCTATCTCAG	AGGGCCAAAG	TGAATCACAC	2280
	CAGTTTCTGA	AGGTCTTAAA	AATAGCTCAG	ATGTCCTAAT	GACATGTCAC	CTACATTTAA	2340
80	TAGGAGTACA	ATAAAACTGT	TGTCAGCTTT	TGTTTTACAG	AGAACTGTAG	ATATTAAGAA	2400
	TTTTGAAATG	GATCATTTCT	ACTTGCTGTG	CATTTTAAAC	AATAATCTGA	TGAATATAGA	2460
	AAAAAATGAT	CCAAAAATATG	GATATGATTG	GATGTATGTA	ACACATACAT	GGAGTATGGA	2520
	GGAAATTTTC	TGAAAAATAC	ATTTAGATTA	GTTTAGTTTG	AAGGAGAGGT	GGGCTGATGG	2580
	CTGAGTTGTA	TGTTACTAAC	TTGGCCCTGA	CTGGTTGTGC	AACCATTTGT	TCAATTTCTT	2640
	GCAAAATGTA	GTTAAGATAT	ACTTTATCT	AATGAAGGCC	TTTTAAATTT	GTCCACTGCA	2700

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TTCTTGGTAT TTCACACTT CAAGTCAGTC AGAACTTGGT AGACCGACCT GAAGTTTCTT 2760
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CATCAATTGC CTTGAAAGTT TCCTCTGCAT TGGGTTTGAA GTAGTTIAGT TATGTCTTTT 2880
TCTCTGATG TAAGTAGTAT AATTGTGTAC TTTCAAAATAC CCGTACTTTG AATGTAGGTT 2940
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TTGGACCATA TTTCTTAAGC AAAAAAAAT GCTCAGTTT GCTTGCAATC CTGAGAATG 3060
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Seq ID NO: C121 DNA Sequence
 Nucleic Acid Accession #: NM_004195
 Coding sequence: 1..726

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1 ATGGCACAGC ACGGGGCGAT GGGCGCGTTT OGGGCCCTGT GCGGCGCTGC GCTGCTGTGC 60
2 CGCTCAGCC TGGGT CAGCG CCCACCGGG GGTCCCGGGT GCGGCCCTGG GCGCTCTCTG 120
3 CTGGGACGG GAACGGACGC GCGCTCTGTC OGGGTTTACA CGACCGCTGT CTGCGCGGAT 180
4 TACCGGGCG AGAGTGTCTG TTCGAGTGG GACTGCATGT GTGTCCAGCC TGAATTCAC 240
5 TGCAGAGACC CTGCTGCAC GACCTGCCGG CACCACCTTT GTCCCCCAGG CCAGGGGGTA 300
6 CAGTCCACGG GGAATTCAG TTTGGCTTC CAGTGTATCG ACTGTGCCTC GGGGACCTTC 360
7 TCGGGGGGCC ACGAAGGCCA CTGCAAACTT TGGACAGACT GCACCCAGTT CCGGTTTCTC 420
8 ACTGTGTTC CTGGGAACAA GACCCACAAC GCTGTGTGCG TCCCAAGGTC CCGCGCGCA 480
9 GAGCGCTTG GGTGGCTGAC CGTCTCTCTC CTGGCGGTGG CCGCTCTGCT CCTCTCTCTG 540
10 ACCTGGCCCG AGCTGTGACT GCACATCTGG CAGCTGAGGA GTCACTGCAT GTGGCCCGCA 600
11 GAGACCCAGC TGCTGTCTGA GGTGCGCGCG TCGACCGAAG ACGCCAGAAG CTGCCAGTTC 660
12 CCGAGGAAG AGCGGGGCGA GCGATCGGCA GAGGAGAAG GCGGCTGGG AGACCTGTGG 720
13 GTGTGA 726
  
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Seq ID NO: C122 DNA Sequence
 Nucleic Acid Accession #: AK091896.1
 Coding sequence: 28..1572

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3 ATGCGCTTCC TGGGGCCAC GCTGCTGGAC CTGCGCTGTC AGACGCACAG CTGCTGCCCC 180
4 CAGATCTCTT GGGTCTTCTT CTGCGAGCAG CTCTGCCCTCC TGCTGGGCGG CCGCCTCGGG 240
5 GGGCTCTTCA AAAGGACCTT GGGCCAGTCA CTATGGGCCC TGTTCACTCT CTCTCTGGCC 300
6 ATCTCCCTGG TGTGTGCGT CATCCCTTTC TGCGCGACCG TGAAGGTGCT GGCCTCAGTC 360
7 ATGGCGCTGG CCGGCTTGGC CATGGGCTGC ATCGACACCG TGGCCAAAT GCAGCTGGTA 420
8 AGGATGTACC AGAAGGACTC GGCGCTCTTC CTCCAGGTGC TCCATTCTT CTGCGGCTTT 480
9 GGTGCTCTGC TGAGCCCCCT TATTGCTGAC CCTTTCCTGT CTGAGGCCAA CTGCTTGCCT 540
10 GCCAATAGCA CGGCCAACAC CACCTCCCGA GGCCACCTGT TCCATGTCTC CAGGGTGTCT 600
11 GGCCAGACCC ACGTAGATGC CAAGCCTTGG TCCAACCAAG CGTTCACAGG GCTGACTCCA 660
12 AAGGACGGGG CAGGAGCCCG AGTGTCTTAT GCCTTCTGGA TCATGGCCCT CATCGATCTT 720
13 CCAGTGCCCA TGGCTGTGCT GATGCTGTCT TCCAAGGAGC GGCTGCTGAC CTGCTGTCCC 780
14 CAGAGGAGGC CCTGCTTCTT GTCTGCTGAT GAGCTTGCTT TGGAGACACA GCCTCTGAG 840
15 AAGGAAGATG CCTCTCACT GCCCCCAAG TTTCAGTCAC ACCTAGGCA TGAGGACCTG 900
16 TTCAGCTGCT GCCAAGGAA GAACCTCAGA GGAGCCCTT ATTCTTCTT TGCCATCCAC 960
17 ATCAGCGGCG CCTGTGACT GTTCATGACG GATGGGTGA CCGGTGCCCTA TCCGCTTTC 1020
18 GTGTACAGCT ATGCTGTGGA GAAGCCCTTG TCTGTGGGAC ACAAGTGGC TGGCTACCTC 1080
19 CCCAGCCTCT TCTGGGCTT CATCACACTG GGCCGGCTCC TCTCCATTCC CATATCTTCA 1140
20 AGAATGAAGC CGGCCACCAT GGTTTTTCATC AACGTGTTG GCGTGGTGGT GACGTTCTCT 1200
21 GTGCTGCTTA TTTTCTCCTA CAACGTCTGC TTCTGTTCG TGGGACCGGC AAGCCTGGGC 1260
22 CTGTTTCTCA GCAGCACCTT CCCAGCATG CTGGCTTACA OGGAGGACTC GCTGCACTAC 1320
23 AAAGGCTGTG CAACCAAGT GCTGTGACA GGGGAGGAG TTGGCGAGAT GGTGCTGCAG 1380
24 ATGCTGTTTG GTTCGATATT CCAGGCTCAG GCAGCTATA GTTCTCTGGT CTGTGGCTG 1440
25 ATCTTTGGTT GTCTGGCTTT TACCTTCTAT ATCTTGCTCC TGTTTTCCA CAGGATGCAC 1500
26 CCTGACTCC CATCAGTTCC TACCCAAGAC AGATCAATTG GAATGGAATA CTCTGAGTGC 1560
27 TACCAGAGGT AAACTGGGT GAAGAAGGCA AGAGAAGACT TTCGCTCTC TGATCACCAG 1620
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29 AAGTCTTCTC CACTAAAATC TGGTTGGGTA GAGGAAATTA AATTGAGTCC TGGTACCTGG 1740
30 TCAAAATCAT TAGAAGTTTA CCTGGCTTCT CAAGTTATCT TCTTCCCTGG TTCAGACTGT 1800
31 TGGTAAGAGC TGTCCAGATA CCCAGATGGG AAGGAAGGAG ACAGCGCGGC GCTTCACTCC 1860
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34 TTAAGCAAAA CAAGCTGCAA GTTATTCCTT GCATGCTCA AAGGATTTTC GTGCTTTTCA 2040
35 CTTAATAGTC CAAAGTCTCT TAAATCTCTG CTGCAGATAT CAATAGCTTA TCTATATTCT 2100
36 CAAACACCAA AAGGAAAAAT TGAATCTTGC TCTCTTGGT ATACTAATGT AGTGGTATGC 2160
37 TAAGCTGGCT CATACCAACT TAGAAAAGCT GATTGTAAAA TTTTCATTTT GACAGCTGGT 2220
38 TATTAAATGC AGCCATTATT AAAAATCAAA TCATACAAAC TTATAATTAA ATCAATTACA 2280
39 TTTAAACAA AGGTAATAAA TATTCAAAGC ATATCACTTC CT 2322
  
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Seq ID NO: C123 DNA Sequence
 Nucleic Acid Accession #: NM_002203.2
 Coding sequence: 43..3588

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	GGGGCCGGCG	CGCTGCGCGT	GCTGCTGGTG	TTAGCGCTCA	GTCGAAGCAT	TTTAAATTGT	120
	TGTTTGGCCT	ACAAATGTTG	TCTCCAGAA	GCAAAATAT	TTTCCGGTCC	TTCAAGTGAA	180
5	CAGTTTGGGT	ATGCAGTGCA	GCAGTTTATA	AATCCAAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCTCGGA	GTGGCTTTCC	TGAGAACCGA	ATGGGAGATG	TGTATAAATG	TCCTGTTGAC	300
	CTATCCACTG	CCACATGTGA	AAAACATAAT	TTGCAAACTT	CAACAAGCAT	TCCAAATGTT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCTCA	CCAGGAACAT	GGGAACATGA	420
	GGTTTTCTCA	CATGTGTGTC	TCTGTGGSCA	CAGCAATGTG	GGAAATCAGTA	TTACACAAAG	480
10	GGTGTGTGTT	CTGACATCAG	TCCTGATTTT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
	CAGCCCTGCC	CTTCCCTCAT	AGATGTTGTG	GTTGTGTGTG	ATGAATCAAA	TAGTATTAT	600
	CCTTGGGATG	CAGTAAAGAA	TTTTTTGGAA	AAATTGTATC	AAGGCCCTGA	TATAGGCCCC	660
	ACAAAGACAC	AGGTGGGGTT	AATTCAGTAT	GCCAAATATC	CAAGAGTTGT	GTTTAACTTG	720
	AACACATATA	AAACCAAGA	AGAAATGATT	GTAGCAACAT	CCCAGACATC	CCAATATGGT	780
15	GGGACCTCA	CAACACATT	CGGAGCAATT	CAATATGCAA	GAAATATGCT	CTATTGACGA	840
	GCTTCTGGTG	GGCGACGAAG	TGCTACGAAA	GTAATGGTAG	TGTAACTGAA	CGGTGAATCA	900
	CATGATGATG	CAATGTTGAA	AGCTGTGATT	GATCAATGCA	ACCATGACAA	TATAGTGAGG	960
	TTTGGCATAG	CAGTCTTGGG	GTACTTAAAC	AGAAACGCCC	TTGATACTAA	AAATTTAATA	1020
	AAAGAAATA	AAGCGATGCG	TAGTATTCCA	ACAGAAAGAT	ACTTTTTCAT	TGTGTCTGAT	1080
20	GAAGCAGTCA	TACTAGTAAA	GGCTGGGACA	TTAGGAGAAC	AAATTTTCAG	CATTGAAGGT	1140
	ACTGTTCAAG	GAGGAGACAA	CTTTCAGATG	GAAATGTGAC	AAGTGGGATT	CAGTGCAGAT	1200
	TACTCTTCTC	AAAATGATAT	TCTGATGCTG	GGTGCAGTGG	GAGCTTTTGG	CTGGAGTGGG	1260
	ACCATGTGCC	AGAAGACATC	TCAATGGCCAT	TTGATCTTTC	CTAAACAAGC	CTTTGACCAA	1320
	ATTCTGCAGG	ACAGAAATCA	CAGTTTCATAT	TTAGGTTACT	CTGTGGCTGC	AATTTCTACT	1380
25	GGAGAAAGCA	CTACATTTGT	TGCTGGTGGT	CCTCGGGCAA	ATTATACCGG	CCAGATAGTG	1440
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70	ACAGGTTTTT	TCAATTTATG	CTGCTCATCC	AAAGTTGCCA	CAGATGATAC	TTCCAAGTGA	4140
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75	TGTGCCAGAT	GAAGAAAAAG	GAGGAAATTT	CCTTTCTCTT	TAGGAGGACA	CAACAGTTCT	4440
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 Coding sequence: 103..1101

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Seq ID NO: C125 DNA Sequence
 Nucleic Acid Accession #: NM_004154
 Coding sequence: 309..1295

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80
 Seq ID NO: C126 DNA Sequence
 Nucleic Acid Accession #: NM_007197
 Coding sequence: 18..1763

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	TGATGGGCCA	CGAGAAACAG	CGGAGGCAG	CCATCCAGTT	GCACGAGTTC	GCGCCGCTGG	240
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	TCAAGTGCTC	CCCGATTATG	GAGCAGTTCA	ACTTCAAGTG	GCCCCGACTCC	CTGGACTGCC	420
	GGAAACTCCC	CAACAAGAAC	GACCCCAACT	ACCTGTGCAT	GGAGGCGCCC	AACAACGGCT	480
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	CGGCTTCTGT	GCTCATTCCT	CTGGCCTGCT	ACCTGGTCT	CGGACGCTCC	TTCTATCTCT	1260
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	ACAAGCTGGA	GAAGCTCATG	GTGGGTATCG	GGCTCTTCTC	TGTGTCTGAT	ACCGTCCCGG	1380
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	CGGCTCTCAT	CCCGCGGTG	GAGATCTTCA	TGGTGAAGAT	CTTTATGCTG	CTGGTGGTGG	1560
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35	AAGCTCTCTC	AGTGAAGTAG	CCTCTTGTGT	AACATAATTG	TGGTAAAGTA	GTTGATTGAT	2040
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Nucleic Acid Accession #: NM_005761.1
Coding sequence: 250..4956

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	CTCCGTGTGC	GCGCGCTGGA	GCGCGCGTGC	CGCGCGCGCG	CCCTGCGCGG	GGGCGGCCCC	240
60	CCGAGCCCGA	TGGAGGTCTC	CCGAGGGAAG	GCGCGCGCGC	GCCCCCGCGG	CCCGCGAGCG	300
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	AAAGGAACCA	GTACCTGTGA	TAAGGATGTG	ATCAGGTTA	GCCATGTGCT	AAATGACACC	2400
	CACATGAAAT	TCTCTCTTCC	ATCAAGCCGG	AAAGAAATGA	AGGATGTGTG	TATCCAGTTT	2460
	GATGGTGGGA	ACTGCTCTTC	TGTGGGATCC	TTATCTCTACA	TTGCTCTGCC	ACATTGTTCC	2520
	CTTATATTTT	CTGCTACCA	CTGGATCAGT	GGTGGTCAAA	ATATAACCAT	GATGGGCAGA	2580
15	AATTTTATG	TAATTGACAA	CTTAATCATT	TCACATGAAT	TAAAGGAAA	CATAAATGTC	2640
	TCTGAATATT	GTGTGGCGAC	TTACTGCGGG	TTTTTAGCCC	CCAGTTTAAA	GAGTTCAAAA	2700
	GTGCGCAGCA	ATGTCCTGCT	GAAGCTGAGA	GTACAAGACA	CCTACTTGGA	TTGTGGAAAC	2760
	CTGCAATATC	TGGAGGACCC	CAGATTCAAG	GGGTATCGGG	TGGAATCCGA	GGTGGACACA	2820
	GAACCTGGA	TGAAATTTCA	AAAAGAAAAT	GACAACTTCA	ATATTTCCAA	AAAAGACATT	2880
20	GAATTTACTC	TCTTCAATGG	GGAAAATGGG	CAATTAATTT	GCAGTTTGA	AAATATTACT	2940
	AGAAATCAAG	ATCTTACCAC	CATCCTTTGC	AAAATTAAG	GCATCAAGAC	TGCAAGCACC	3000
	ATTGCCAATC	CTTCTAAGAA	AGTTCGGGTC	AAGCTGGGAA	ACCTGGAGCT	CTACGTCGAG	3060
	CAGGAGTCAG	TTCTTCCAC	ATGGTATTTT	CTGATTGTGC	TCCTCTGCTT	GCTAGTGATT	3120
	GTCAATTTTG	CGGCGGTGGG	GGTGACCAAG	CACAAATCGA	AGGAGCTGAG	TGCAAAACAG	3180
25	AGTCAACAC	TAGAATTTGCT	GGAAAGCGAG	CTCGGAAAG	AGATACGTGA	CGGCTTGTCT	3240
	GAGCTGCAGA	TGGATAAATT	GGATGTGGTT	GATAGTTTGT	GAACGTGTC	CTTCTTGTAC	3300
	TACAAACATT	TTGCTCTGAG	AACCTTCTTC	CCTGAGTCAG	GTGGCTTCAC	CCACATCTTC	3360
	ACTGAAGATG	TGCATAACAG	AGACGCCAAC	GACAAAGATG	AAAGCTCTAC	AGCTTTGGAT	3420
	GGCCTTAATC	GTAATAAAG	CTTCTCTGTT	ACTGTCTATC	ACACCTCTGA	AAAGCAGAA	3480
30	AACCTTCTCT	TGAAGACAG	GTGCTGTGTT	GCCTCTCTCC	TAAACATGTC	ACTGCAAAAC	3540
	AAGCTGTGCT	ACCTGACCAG	CATCCTAGAG	GTGCTGACCA	GGGACTTGAT	GGAAACAGTG	3600
	AGTAACATGC	AGCCGAAACT	CATGCTGAGA	CGCAGGAGT	CGTCTGTGGA	AAAACCTCTC	3660
	ACAAACTGGA	TGTCGGTCTG	CCTTCTGGA	TTTCTCGGG	AGACTGTGCG	AGAGCCCTTC	3720
	TATTTGCTGT	TGAGGACTCT	GAACCCAGAA	ATTAACAGG	GTCCCGTGGG	TGTAATCACT	3780
35	TGCAAAAGCC	TGTACACACT	TAATGAAGAC	TGGCTGTGTT	GGCAGTTTCC	GGAAATTCAGT	3840
	ACTGTGGCAT	TAAACGTGCT	CTTTGAAAA	ATCCCGGAAA	ACGAGAGTGC	AGATGTCTGT	3900
	CGGAATATTT	CAGTCAATGT	TCTCGACTGT	GACACATTG	GCCAAGCCAA	AGAAAAGATT	3960
	TTCCAAGCTG	TCTTAAGCAA	AAATGGCTCT	CCTTATGGAC	TTCACTTAA	TGAAATTTGTT	4020
	CTTGAGCTCT	AAATGGGCAC	ACGACAGAAA	GAACCTCTGG	ACATCGACAG	TTCTCTCGTG	4080
40	ATTCTTGAAG	TGGAATTCAC	CAAGCTAAAC	ACCATTGGCC	ACTATGAGAT	ATCAATGGA	4140
	TCCACTATAA	AAGCTTTTAA	GAAGATAGCA	AATTTTACTT	CAGATGTGGA	GTACTCGGAT	4200
	GACCACTGCC	ATTTGATTTT	ACCAGATTG	GAAGCAATTC	AAGATGTGCA	AGGAAAGAGA	4260
	CATCGAGCTG	TGTCAGAGTT	CAAAAGTAA	GAAATGTATC	TGACAAAGCT	GCTGTGACCC	4320
	AAGGTGGCAA	TTCAATCTGT	GCTTGAAAA	CTTTTATGAA	GCATTGTGAG	TTTACCCAAC	4380
45	AGCAGAGCTC	CATTTGCTAT	AAAATACTTT	TTTGACTTTT	TGGACGCCCA	GGCTGAAAA	4440
	AAAAAATCA	CAGATCTGTA	CGTCTGATAC	ATTTGAAAA	CAACAGGCT	TCTCTTGGC	4500
	TTCTGGGTAA	ACATCCTGAA	GAACCTCTAG	TTTGTCTTTG	ACATTAAAGAA	GACACCAAT	4560
	ATAGACGGT	GTGCTCTTGT	GATTGCCAG	GCATTCTG	ATGCAATTTT	TCTCAGAGAG	4620
	CAGCAACTAG	GGAGGAGAGC	ACCAACTAAT	AAGCTTCTCT	ATGCCAAGGA	TATCCCAACC	4680
50	TACAAAGAG	AAGTAAATC	TTATTACAA	GCAATCAGG	ATTGCTCTCC	ATTGTCTATC	4740
	TCAGAAATGG	AAGAATTTT	AACCTAGGAA	TCTAAGAAAC	ATGAAAATGA	ATTTAATGAA	4800
	GAGTGGCCCT	TGACAGAAAT	TTACAAATAC	ATCGTAAAT	ATTTGTATGA	GATTTCTAAT	4860
	AAACTAGAAA	GAGAACGAGG	GCTGGAAGAA	GCTCAGAAAC	AACCTCTGCA	TGTAAAAGTC	4920
	TTATTTGATG	AAAAGAGAA	ATGCAAGTGG	ATGAAGCAC	TCTGGGCTCT	GGCTTAATCT	4980
55	GGCAAGTTTC	TTCAAGCAG	TTGGAGCAG	AATGGCTGCT	TGAGCTACTC	TGTGTGCTTA	5040
	ATTTGTGTT	TGCACATAGG	TTCCACTTTG	GGCAGCTGCT	TTTTAAGAGA	CCAAGGCACA	5100
	TGCACAGCTT	TTAGAAAGCA	A				5121

Seq ID NO: C128 DNA Sequence

Nucleic Acid Accession #: NM_002185.1

Coding sequence: 23..1402

60	1	11	21	31	41	51	
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65	TTTACTTCAA	ATCGTTTCTG	GAGAAAGTGG	CTATGCTCAA	AATGGAGACT	TGGAAGATGC	120
	AGAACTGGAT	GACTACTCAT	TCTCATGCTA	TAGCCAGTTG	GAAGTGAATG	GATCGCAGCA	180
	TTCACTGACC	TGTGCTTTTG	AGGACCCAGA	TGTCAACACC	ACCAATCTGG	AATTTGAAAT	240
	ATGTGGGGCC	CTCGTGGAGG	TAAAGTGCCT	GAATTTCAAG	AACTACAAG	AGATATATTT	300
	CATCGAGACA	AAGAAATCT	TACTGATTGG	AAAGAGCAAT	ATATGTGTGA	AGGTTGGAGA	360
70	AAAGAGTCTA	ACCTGCARAA	AAATAGACCT	AACCACTATA	GTAAACCTG	AGGCTCCTTT	420
	TGACCTGAGT	GTCACTATC	GGGAAGGAGC	CAATGACTTT	GTGGTGACAT	TTAATACATC	480
	ACACTTGCAA	AGAAGTATG	TAAAAGTTT	AATGCATGAT	GTAGCTTACC	GCCAGGAAAA	540
	GGATGAAAA	AAATGGAGCG	ATGTGAATTT	ATCCAGCACA	AAGCTGACAC	TCTTCAGAG	600
	AAAGCTCCAA	CCGGCAGCAA	TGTATGAGAT	TAAAGTTGGA	TCCATCCCTG	ATCACTATTT	660
75	TAAAGGCTTC	TGAAGTGAAT	GGAGTCCAAG	TTATTACTTC	AGAACTCCAG	AGATCAATAA	720
	TAGCTCAGGG	GAGATGGATC	CTATCTTACT	AACCATCAGC	ATTTTGAGTT	TTTTCTCTGT	780
	CGCTCTGTTG	GTCACTCTGG	CCTGTGTGTT	ATGGAAAAAA	AGGATTAAGC	CTATCGTATG	840
	GCCAGTCTC	CCGATCATA	AGAAGACTCT	GGAACATCTT	TGTAAAGAAC	CAAGAAAAAA	900
80	TTTAAATGTG	AGTTTCAATC	CTGAAAGTTT	CCTGGACTGC	CAGATTCTAA	GGGTGGATGA	960
	CATTCAAGCT	AGAGATGAAG	TGGAAGGTTT	TCTGCAAGAT	ACGTTTCTCT	AGCAACTAGA	1020
	AGAATCTGAG	AAAGCAGAGG	TTGGAGGGGA	TGTGCAGAGC	CCCAACTGCC	CATCTGAGGA	1080
	TGTAGTCTGC	ACTCCAGAAA	GCTTTGGAAG	AGATTCTATC	CTCACATGCC	TGGCTGGGAA	1140
	TGTAGTGCA	TGTAGCGCCC	CTATTCTCTC	CTCTCCAGG	TCCCTAGACT	GCAGGGAGAG	1200
	TGGCAAGAA	GGGCTCATG	TGTACCAGGA	CCTCCTGCTT	AGCCTTGGGA	CTACAAACAG	1260

5 CACGCTGCC CCTCCATTTT CTCTCCAATC TGGAACTCTG ACATTGAACC CAGTTGCTCA 1320
 GGGTCAGCCC ATTCTTACTT CCCTGGGATC AAATCAAGAA GAAGCATATG TCACCATGTC 1380
 CAGCTTCTAC CAAAACCACT GAAGTGTAAG AAACCCAGAC TGAACCTACC GTGAGCGACA 1440
 AAGATGATTT AAAAGGGGAA TCTAGAGTTC CTAGTCTCCC TCACAGCACA GAGAAGACAA 1500
 AATTAGCAAA ACCCCACTAC ACAGTCTGCA AGATTCTGAA ACATTGCTTT GACCACTCTT 1560
 CCTGAGTTCA GTGGCACTCA ACATGAGTCA AGAGCATCTT GCTTCTACCA TGTGGATTGG 1620
 GTCACAAGGT TTAAGGTGAC CCAATGATTC AGCTATTT 1658

10 Seq ID NO: C129 DNA Sequence
 Nucleic Acid Accession #: NM_002722.1
 Coding sequence: 15..302

15 1 11 21 31 41 51
 ACTCTGDACT CCGGATGGCT GCCGCACGCC TCTGCCCTCTC CCTGTGCTCTC CTGTCCACCT 60
 GCGTGGCTCT GTTACTACAG CCCTGCTGCG GTGCCCAAGG AGCCCCACTG GAGCCAGTGT 120
 ACCCAGGGGA CAATGCCACA CCAGAGCAGA TGGCCCAAGT TGCAGCTGAT CTCGTAGAT 180
 ACATCAACAT GCTGACCAAG CCTAGGTATG GGAAGAGACA CAAAGAGGAC ACGTGGCCCT 240
 TCTCGAGTGT GGGGTCCCGG CATGCTGCTG TCCCCAGGGA GCTCAGCCCG CTGGACTTAT 300
 20 AATGCCACCT TCTGTCTCTC ACGACTCCAT GAGCAGGCGC AGCCAGCTC TCCCTCTGTC 360
 ACCCTTGGCT CTGGCCAAAG CTGTCTCCCT GCTCCACAC AGGCTCAATA AAGCAAGTCA 420
 AAGCC 425

25 Seq ID NO: C130 DNA Sequence
 Nucleic Acid Accession #: NM_032545.1
 Coding sequence: 47..718

30 1 11 21 31 41 51
 AAATGATCT TCAATGCACT AAGAGAAGGA GACTCTCAAA CCAAAAATGA CTGGAGGCA 60
 CCATGTCAGG CTCTGTGTTA CCGTCAGTTT GGCATTACAG ATCACTCAAT TGGGAAACAG 120
 CTATCAAGGA GAGAAACATA ACGGCGGTAG AGAGGAAGTC ACCAAGTTG CCACTCAGAA 180
 GCACCGACAG TCACCGCTCA ACTGGAACCTC CAGTCATTTC GGAGAGGTGA CTGGGAGCGC 240
 CGAGGGCTGG GGGCGGAGG AGCCGCTCCC TACTTCCCGG GCTTTGGGAG AGGGTGGCTC 300
 35 CGCGCGGCGG CCGTGTCTGA GGAACGGCGG TACCTGCGTG CTGGGCGACT TCTGCGTGTG 360
 CCGGGCCAC TTACCGCGCC GCTACTGCGA GCATGACCAG AGGCGCAGTG AATGCGGCGC 420
 CTTGAGACAC GAGGCTGGA CCCTCCGCGC CTGCCACCTC TGCAGGTGCA TCTTGGGGCG 480
 CTTGCACTGC CTCCCTCTCC AGACGCTGGA CCGCTGTGAC CCGAAAGACT TCCTGGCCCTC 540
 CCACGCTCAC GGGCGGAGCG CCGGGGGCGC GCCCAGCCTG CTACTCTTGC TGCCCTGCGC 600
 40 ACTCTGTCAC CGCTCTCTGC GCCCGGATGC GCCCGCGCAC CTTGCGTCCC TGGTCCCTTC 660
 CGTCTCCAG CGGGAGCGGC GCCCCTGCGG AAGGCCGGGA CTTGGGCATC GCCTTTAATT 720
 TTCTATGTTG TAAATAATAG ATGTGTTTAG TTTACCGTAA GCTGAAGCAC TGGGTGAATA 780
 TTTTATTTGG GTAATAAATA TTTTCATGAA AGCGCCAAAA AAAAAAAAAA AAAAAAAAAA 840
 AAAAAA 846

45 Seq ID NO: C131 DNA Sequence
 Nucleic Acid Accession #: NM_006533.1
 Coding sequence: 72..467

50 1 11 21 31 41 51
 AGGGAGAGAG GGAGGGGAGG AAATTGGAGA CCCCAGCACC CCCTTGCTCA CTCTCTTGCT 60
 CACAGTCCAC GATGGCCCGG TCCCTGGTGT GCCTTGGTGT CATCATCTTG CTGTCTGGCT 120
 TCTCCGACAC TGGGTCTCAG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
 55 CGGACCAAGG GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
 CCGACTGCGG ATTCTGACC ATTCACCGGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
 AGGGCGGTGG CGGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360
 CTGCTGCGCT GGGCTATTTC CCGAGTAGCA TTGTCCGAGA GGACCAAGAC CTGAAACCTG 420
 GCAAGTCTGA TGTGAAGACA GACAAATGGG ATTTCTACTG CCAGTGAGCT CAGCCTACCG 480
 60 CTGCGCCCTGC CGTTTCCCTT CCTTGGGTTT ATGCAAAATC AATCAGCCCA GTGCAAAC 538

65 Seq ID NO: C132 DNA Sequence
 Nucleic Acid Accession #: AB064272
 Coding sequence: 1..708

70 1 11 21 31 41 51
 ATGACACAAG TCACAGAAAA GTCCACAGAA CACCCAGAAA AGACCAAGTC AACCACAGAG 60
 AAAACCAAA GAACCCACGA AAGCCCTACG CTATACTCAG AGAAGACCAT ATGCACCAA 120
 GGGAAAAACA CACCACTCCC AGAAAAGCCT ACAGAAAACC TGGGGAACAC CACACTGACC 180
 ACTGAGACCA TAAAGCCCCC AGTAAAGTCC ACAGAAAACC CAGAAAAAAC AGCAGCAGTC 240
 CAAAGACTA TAAACCTTC AGTCAAGTTC ACAGGAGACA AATCTCTCAC TACTACTCT 300
 TCTCATCTAA ATAAACTGTA AGTTACTCAT CAGGTGCCCA CTGGTCTCTT CACCTCAT 360
 ACATCTAGAA CGAAGCTGAG TTCTATCACA TCAGAAAGCCA CAGGAAACGA GAGCCATCCA 420
 75 TACCTCAATA AAGATGGCTC ACAGAAAGGT ATCCAGCTG GACAGATGGG AGAGAATGAT 480
 TCATTCCCTG CATGGGCCAT AGTTATTGTG GTCTTGGTGG CTGTGATTCT CCTCTGGTG 540
 TTCTTGGCC TGATCTTCTT GGTCTCCTAT ATGATGCGGA CACGCGGCAC ACTAACCCAG 600
 AACACCCAGT ACAATGATGC AGAGGATGAG GGTGGCCCCA ATTCTACCC GGTCTACCTG 660
 80 ATGGAGCAGC AGAATCTTGG CATGGGCCAG ATCCCTTCCC CAGGTTGA 708

Seq ID NO: C133 DNA Sequence
 Nucleic Acid Accession #: NM_080870.1
 Coding sequence: 3..710

1 11 21 31 41 51
 5 AGATGACACA AGTCACAGAA AAGTCCACAG AACACCCAGA AAAGACCAG TCAACCCAG 60
 AGAAAAACCA AAGAACCCCA GAAAAGCCTA CGCTATACTC AGAGAAGACC ATATGCACCA 120
 AAGGGAAAAA CACACCAGTC CCAGAAAAGC CTACAGAAAA CCTGGGGAAC ACCCACTGA 180
 CCACTGAGAC CATAAAGGCC CCAGTAAAGT CCACAGAAAA CCCAGAAAAA ACAGCAGCAG 240
 TCACAAAGAC TATAAAACCT TCAGTCAAGG TCACAGGAGA CAAATCTCTC ACTACTACCT 300
 10 CTCTCATCTT AAATAAAACT GAAGTTACTC ATCAGGTGCC CACTGGTTCT TTCACCCCTCA 360
 TTACATCTAG AAGCAAGCTG AGTTCTATCA CATCAGAAGC CACAGGAAAC GAGAGCCATC 420
 CATACTCTAA TAAAGATGGC TCACAGAAAG GTATCCACGC TGGACAGATG GAGAGAAATG 480
 ATTCAATCCC TGCATGGGCC ATAGTTATTG TGGTCCCTGG GGCCTGTGAT CTCCCTCTCG 540
 TGTTCCTTGG CCTGATCTTC TTGGTCTCCT ATATGATGCG GACACGCCGC ACACCTAACCC 600
 15 AGAACACCCA GTACAATGAT GCAGAGGATG AGGGTGGCCC CAATTCCTAC COGGTCTACC 660
 TGATGAGACA GCAGAATCTT GGCATGGGCC AGATCCCTTC CCCACGGTGA TCTTGGAGTA 720
 GGGGCCGAGC CCTGGCTCTT CCATGCTCTG CCCCCTTCTT GGAATGAGGA COGGACTCAC 780
 AATTTCTATT TCCGGGACTA CAGGAAGGGC AGAGAATACT GACGGTTACC AGTATTAACC 840
 CTTCACTCTG TCTTGAAACT GGTGGGGGAA TGAGGTGATA AGCAAGGAGG GTGTAAGTTT 900
 20 AGGGACACAA GAAGAAAGAA TGAATAATAC GAGCAGACAT TCTCTGTAGA AGGTAATGGT 960
 CTGAGAAATGA AAAGGTGTTT GATGGACATG TTGTGGGGGC ACCAATGCAG AACACTGCAC 1020
 TGAGTCTCTAA AGGAAGGACA GGAAGCCTAT AGGCAATGCC CCAAGCTGAC TTGTGAGTGG 1080
 GGTATTATGG GAAAGGGAGG GACTGAGGGC AGAGTCTCTG GGTTCAGGA CAGCATTATG 1140
 TTATTTCCAT TCACATATAC TTAAGAGTTT GTGTGTAAC AGGCTCATCT CTGAGTTCTC 1200
 25 AGGACCCCTG CCCCCACCCC CATTTTTTTA ATGAAAAAAA AAAACAAAAA AAACGGATCC 1260
 AAGAAGAAAA GAGAAATTAT TTCTCTCTCC ACTCTCTCCA TGCCCTGGAG AAAAAAAGT 1320
 CCAGAAGAAA CATAAATAT CTCTCATCTA CATGGTTGCT TCCCTCTCTC CCCAAATCCC 1380
 TTAGTTTTCC TAAATGTCTA CAGTGGACGC CCTGTTGGTT TGGCTTGCTG GGTGTGGGT 1440
 GGCACGCAAA GGAGGGGATT TTTATTTGGC CAGCAGTCTC ACCCACTGAT CTCCACCCCA 1500
 30 GACCTTCCCT GATTGGTGTG TCAGCATTTA TTTTCTGTCT TCTTCCACCA AAAGCCAGCT 1560
 GTAGCTTTAT CTGTAATAAG TTACCCATCT TCTCTACTGT CCCCATTCTC TCTCTCCCA 1620
 CCTTCAACCC AGATTCAAGT TTCTCTCTT GTAGGCATTI CATCTGTGTG TGTTTCTGG 1680
 ATTTCTCTCT TCTCTCTTA TGGCCATTTC ACCTTATTAC TGATGGGTA GAGGGGAAA 1740
 35 AGGAGATGA TGATGATAGT TTCTTCTGT CTATTGACCT TTTTATAAT AAAGTATAAC 1800
 ATGTT 1805

Seq ID NO: C134 DNA Sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..10674

40 1 11 21 31 41 51
 45 ATGTGGCCTC GCCTGGCCTT TTGTGCTGG GGTCTGGGCG TGTCTTGGGG CTGGGCGACC 60
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 GGGGCCCCCG GGAGTATCCC CGCGCGCGCC GCTCTGGGCG ACGAAGCGGC GGGGAGCAGA 180
 GTGGAGCGGC TGGGCCAGGC GTTCCGGGGA CGCGTGCGGC TGCTGCGGGA GCTCAGCAG 240
 CGCCTGGAGC TTGTCTTCTT GGTGGATGAT TGGTCCAGCG TGGGCGAAGT CAACTTCCGC 300
 AGCGAGCTCA TGTTCGTCCG CAAAGCTGCTG TCCGACTTCC CCGTGGTGCC CAGCGCCACG 360
 50 CGCGTGCGCA CTGTGACCTT CTGTGCCAAG AACTACGTGG TGCGCGCGGT CGATTACATC 420
 TCCACCCGCC CGCGCGCCA GCACAAGTGC GCGCTGTCTC TCCAAGAGAT CCGTGCCATC 480
 TCTAOCGAG GTGGCGGCAC CTACACCAAG GCGCCTTCC AGCAAGCGCG CAATAATCTT 540
 CTTCTATGCTA GAGAAAACTC AACAAAAATT GTATTCTCA TCACTGATGG ATATTCCAAT 600
 GGGGAGAGAC CTAGACCAAT TGCAGCGTCA CTGCGAGATT CAGGAGTGGG GATCTTCACT 660
 55 TTGGCATAAT GGCAGGGGAA CATTGAGAG CTGAATGACA TGGCTTCCAC CCCAAGAGAG 720
 GAGCACTGTT ACCGTCTAGA CAGTTTGAAG GAATTGAGG CTTTAGCTCG CCGGCGATTG 780
 CATGAAGATC TACCTTCTGG GAGTTTATT CAAGATGATA TGGTCCACTG CTATATCTT 840
 TGTGATGAAG GCAAGGACTG CTGTGACCGA ATGGGAAGCT GCAAAATGGG GACACACACA 900
 GGCCATTITG AGTGATCTG TGAAGAGGGG TATTACGGGA AAGGTCTGCA GTATGAATGC 960
 60 ACAGCTTGCC CATCGGGGAC ATACAAACCT GAAGGCTCAC CAGGAGGAAT CAGCAGTTGC 1020
 ATTCCATGTC CTGATGAAAA TCACACTCTC CCACCTGGAA GCACATCCCC TGAAGACTGT 1080
 GTCTGCAGAG AGGGATACAG GGCATCTGGC CAGACCTGTG AACTGTGCCA CTGCCCTGCC 1140
 CTGAAGCCTC CGAAAAATGG TTACTTTATC CAAAACACTT GCAACAACTA CTTCAATGCA 1200
 GCCTGTGGGG TCCGATGTCA CCCTGGATTG GATCTTGTGG GAAGCAGCAT CATCTTATGT 1260
 65 CTACCCAATG GTTTGTGGTC CGGTTGAGAG AGCTACTGCA GAGTAAGAAC ATGTCTCAT 1320
 CTCGCGCAGC CGAAACATGG CCACATCAGC TGTCTACAA GGGAAATGTT ATATAAGACA 1380
 ACATGTTTGG TTGCTGTGTA TGAAGGTTAC AGACTAGAAG GCAGTGATAA GCTTACTTGT 1440
 CAAGGAACA GCGAGTGGGA TGGGCCAGAA CCGCGGTGTG TGGAGCGCCA CTGTTCCACC 1500
 TTTAGATGTC CCAAGATGAT CATCATATCC CCCCACAACT GTGGCAAGCA GCCAGCCAAA 1560
 70 TTGGGACGA TCTGCTATGT AAGTTGCGGC CAAGGGTTCA TTTTATCTGG AGTCAAAGAA 1620
 ATGCTGAGAT GTACCACTTC TGGAAAAATG AATGTGCGAG TTCAGGCAGC TGTGTGTAAA 1680
 GACGTGAGG CTCTCAAAAT CAACTGTCTC AAGGACATAG AGGCTAAGAC TCTGGAACAG 1740
 CAAGATTCTG CCAATGTTAC CTGGCAGATT CCAACAGCTA AAGACAACCT TGGTGAAGAG 1800
 GTGTGAGTCC AGTTTCATCC AGCTTTCACC CCACCTTACC TTTTCCAAAT TGGAGATGTT 1860
 75 GCTATGATAT ACACGGCAAC TGACCTATCC GGCAACAGG CCAGCTGCAT TTTCCATATC 1920
 AAGGTATTAT ATGCAGAAC ACCTGTCTAT GACTGGTGCA GATCTCCACC TCCGCTCCAG 1980
 GTCTGGAGA AGGTATATGC CGCAAGCTGG GATGAGCCTC AGTTCTCAGA CAACTCAGGG 2040
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 ATAGTACAGT ATACAGCCAC TGACCCCTCA GGCATAAACA GGACATGTGA TATCCATATT 2160
 80 GTCTAAAAAG GTTCTCCCTG TGAAATTCCA TTCACACCTG TAAATGGGGA TTTTATATGC 2220
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 GCATTTGAGA CGACCTCGGG AAAAAATGGT CCATCATTTT GTAGTGATGC AGAGGACATT 2520

	GACTGCAGAC	TGGAGGAGAA	CCTGACC ^{AA}	AAATATTGCC	TAGAATATAA	TTATGACTAT	2580
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	TACGATGACT	TCTGTGACAC	TGTGCAAGAA	ACAGCCACAA	GCATCGGCAA	TGCCAAGTCC	2700
5	TCACGGATTA	AAAGAAAGTGC	CCCATTTATCT	GACTATAAAA	TTAAGTTAAT	TTTTAACATC	2760
	ACAGCTAGTG	TGCCATTACC	CGATGAAAGA	AATGATACCC	TTGAATGGGA	AAATCAGCAA	2820
	CGACTCCTTC	AGACATTGGA	AACTATCACA	AATAAACTGA	AAAGGACTCT	CAACAAAGAC	2880
	CCCATGTATT	CCTTTACAGT	TGCATCAGAA	ATACTTATAG	CCGACAGCAA	TTCATTAGAA	2940
	ACAAAAAAGG	CTTCCCCCTT	CTGCAGACCA	GGCTCAGTGC	TGAGAGGGCG	TATGTGTGTC	3000
10	AATTGCCCTT	TGGGAACCTA	TTATAATCTG	GAACATTTCA	CCTGTGAAAG	CTGCCGGATC	3060
	GGATCCTATC	AAGATGAAGA	AGGGCAACTT	GAGTGCAGCG	TTTGGCCCTC	TGGGATGTAC	3120
	ACGGAAATATA	TCCATTCAAG	AAACATCTCT	GATTGTAAAG	CTCAGTGTAA	ACAAGGCACC	3180
	TACTCATACA	GTGGACTTGA	GACTTGTGAA	TCGTGTCCAC	TGGGCACCTA	TCAGCCAAAA	3240
	TTTGGTTCCT	GGAGCTGCCT	CTCGTGTCCA	GAAAAACACT	CAACTGTGAA	AAGAGGAGCC	3300
15	GTGAACATTT	CTGCATGTGG	AGTTCCTTGT	CCAGAAGGAA	AATTCTCGCG	TTCGGGTTA	3360
	ATGCCCTGTC	ACCCATGTCC	TCGTGACTAT	TACCAACCTA	ATGCAGGGAA	GGCCTTCTGT	3420
	CTGGCCTGTC	CCTTTTATGG	AACTACCCCA	TTCTGTGGT	CCAGATCCAT	CACAGAATGC	3480
	TCAACTTCAG	TTCTGAATAT	TACTATTTTC	GGTGGATTGG	GGCATCTGGA	GTGTGTTAAAT	3540
	TGTCCTTCTG	AGGTTTTCCT	TGAATGCTTC	TTTAAACCTT	GCCACAATAG	TGGAACTGCT	3600
20	CAGCAACTTG	GGCGTGGTTA	TGTTTGTCTC	TGTCACCTTG	GATATACAGG	CTTAAAGTGT	3660
	GAAACAGACA	TGATGAGTGT	CAGGCCACTG	CCTTGCCCTA	ACAAATGGAGT	TTGTAAAGAC	3720
	CTAGTTGGGG	AATTCAATTG	TGAGTGCCCA	TCAGGTTACA	CAGGTGACGC	GTGTGAAGAA	3780
	AATATAAATG	AGTGTAGCTC	CAGTCCCTGT	TTAAATAAAG	GAATCTGTGT	TGATGGTGTG	3840
	GCTGGCTATC	GTGTCACATG	TGTGAAAAGG	TTTGTAGGGC	TGCATTGTGA	AACAGAAGTC	3900
25	AATGAATGCC	GTGCAAAACC	ATGCTTAAAT	AATGCAGTCT	GTGAAGACCA	GGTTGGGGGA	3960
	TTCTTGTGCA	AATGCCACCC	TGGATTTTGG	GGTACCCGAT	GTGGAAGAA	CGTGGATGAG	4020
	TGTCCTCAGT	AGCCATGCAA	AAATGGAGCT	ACCTGTAAAG	ACGGTGCCAA	TAGCTTCAGA	4080
	TGCCCTGTGTG	CAGCTGGCTT	CACAGGATCA	CAGTGTGAAT	TGAACATCAA	TGAATGTGAG	4140
	TCTAATCCAT	GTGAAATACA	GGCCACCTGT	GTGGATGAAT	TAAATTCATA	CAGTTGTAAA	4200
30	TGTCAGCCAG	GAATTTTCAGG	CAAAAGGTGT	GAAACAGAAC	AGTCTACAGG	CTTAAACCTG	4260
	GAATTTTGAAG	TTTCTGGCAT	CTATGGATAT	GTCAATGCTAG	ATGGCATGCT	CCCATCTCTC	4320
	CATGCTCTAA	CCTGTACCTT	CTGGATGAAA	TCTCTGACG	ACATGAACTA	TGGAACACCA	4380
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	TCTGATTGCC	CAGCTTAGG	AGGGTCAGTG	CCTCATCTGA	GAACCTGCATC	TGAAGATTTA	4920
	AAGCCAGGTT	CCAAAGTCAA	TCTGTTCTGT	GATCCAGGCT	TCCAGCTGGT	CGGGAACCTC	4980
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	TTCTGTACAG	ATAATGGGAG	CTGGAACGGC	GTTCACCAT	CCTGCCTTGA	TGTGATGAG	5220
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	CCCCCAGAG	GTCAAGACAT	GCCCCGTGT	ATAGCTCATT	TCTGTGAAAA	ACCTCCATCG	6240
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Seq ID NO: C135 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..390

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Seq ID NO: C136 DNA Sequence
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Coding sequence: 126..1745

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Seq ID NO: C137 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1761

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Seq ID NO: C138 DNA Sequence
Nucleic Acid Accession #: PGENESH predicted
Coding sequence: 1..2310

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25 Seq ID NO: C139 DNA Sequence
 Nucleic Acid Accession #: NM_004616.2
 Coding sequence: 180..893

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 45 TCTTGGCAA AAATTTGATT ATAGTTATTG GAATATCATT TGGACTGGCA GTTATTGAGA 840
 TACTGGGTTT GGTGTTTCT ATGGTCTGTG ATTGCCAGAT CGGGAACAAA TGAATCTGTG 900
 GATGCATCAA CCTATCGTCA GTCAAAACCC TTTAAATGT TGCTTTGGCT TTGTAATTT 960
 AAATATGTAA GTGCTATATA AGTCAGGAGC AGCTGTCTTT TTAATATGTC TCGCTAGCT 1020
 AGACCACAGA TATCTTCTAG ACATATTGAA CACATTAAAG ATTTGAGGGA TATAAGGGA 1080
 50 AATGATATGA ATGTGTAATT TTAATCAAAA TAAAGTTAAC TGTTTACGTT AAAAAAAA 1140
 AAAAAAAA AAAAAAAA 1159

55 Seq ID NO: C140 DNA Sequence
 Nucleic Acid Accession #: NM_004617.2
 Coding sequence: 232..840

60 1 11 21 31 41 51
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 AGCTGAAGCA ACTCCAAGGA CACAGTTTCA AGAAATTTGG TTCTCAGCCC CAAAATACTG 120
 ATTGAATTGG AGACAATTAC AAGGACTCTC TGCCCAAAAA CCCTTGAAGA GGCCCCGTGA 180
 AGGAGGCGAGT GAGGAGCTTT TGATTGCTGA CCTGTGTCGT ACCACCCGAC AATGTGCATC 240
 GGGGGCTGTG CCGATGTCCT GGGGGGGACC CTCAATCCCC TTGCTTTTTT TGGCTTCTGT 300
 GCTAACATCC TGTATTTTT TTCTGGAGGA AAAGTGATAG ATGACAACGA CCACCTTTCC 360
 65 CAAGAGATCT GGTTTTTCGG AGGAATATTA GGAAGCGGTG TCTTGATGAT CTTCCTGTG 420
 CTGGTGTCTT TGGGCTTGAA GAACAATGAC TGCTGTGGGT GCTGCGGCAA CGAGGGCTGT 480
 GGGAAAGCAT TTGCGATGTT CACCTCCAGC ATATTGTCTG TGGTTGGATT CTGGGAGCT 540
 GGATACTGTT TTATCATCTC AGCCATTTC AATCAACAAG GTCTTAAATG CCTCATGGCC 600
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 70 AACAAGTGCC GAGAGCCTCT CAATGTGGTT CCTTGAATC TGACCTCTCT CTCCATCCTG 720
 CTGGTCTGTG GAGGAATCCA GATGGTCTC TGCGCCATCC AGGTGGTCAA TGGCCTCTGT 780
 GGGACCTCT GTGGGAGCTG CCAGTGTGTG GGTGCTGTG GGGGAGATGG ACCCGTTTAA 840
 ACCTCGAGGA TGAGCTGTCT AGACTCTACA GCATGACGAC TACAATTTCT TTTTATAAAA 900
 CTCTCTCTCT TCTTGAATTT ATTAATTTCT ATCTGCTTCC TAGCTGATAA AGCTTAGAAA 960
 75 AGGCAGTTAT TCCTTCTTTC CAACAGCTT TGCTCGAGTT AGAATTTTGT TATTTTCAAA 1020
 TAAAAAATAG TTTGGCCACT TAACAAATTT GATTTATAAA TCTTTCAAT TAGTTCCTTT 1080
 TTAGAATTTA CCAACAGGTT CAAAGCATAC TTTTCATGAT TTTTATATA CAAATGTAAA 1140
 ATGTATAAAG TCATATGTAC TGCCATACTA CTCTTTTGA TATAAAGATG TTTATATCTT 1200
 TGGAGTGTTC ACATAAATCA AAGGAAGAAA GCACATTTAA AATGAGAAAC TAAGACCAAT 1260
 80 TTCTGTTTTT AAGAGGAAAA AGAATGATTG ATGTATCCTA AGTATTGTTA TTTGTGTCT 1320
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 GGGTCTTTT ATGTATGTGA AATTAAACC TGAATTCAGA GGTAACTG 1428

Seq ID NO: C141 DNA Sequence
 Nucleic Acid Accession #: NM_002381.2

Coding sequence: 64..1524

1	11	21	31	41	51	
5	AAATCCGAGC	CTCGCGTGGG	CTCCTGGCCC	CCGACGGACA	CCACCAGGCC	CACGGAGCCC 60
	ACCATGCCGC	GCCCGGCCCC	CGCGCGCCGC	CTCCCGGGAC	TCCCTCTGCT	GCTCTGGCCG 120
	CTGCTGCTGC	TGCCCTCCGC	CGCCCCCGAC	CCCGTGGCCC	GCCCGGGCTT	CCGGAGGCTG 180
	GAGACCCGAG	GTCCCGGGGG	CAGCCCTGGA	CGCCGCCCTT	CTCCTGCGGC	TCCCGACGGC 240
	GCGCCCGCTT	CGCGGACCCAG	CGAGCCTGGC	CGCGCCCGCG	GTGCAGGTGT	TTGCAAGAGC 300
10	AGACCTTGG	ACCTGGTGT	TATCATTGAT	AGTTCTCGTA	GCGTAGCGCC	CCTGGAATTC 360
	ACCAAGTGA	AAACTTTTGT	CTCCCGGATA	ATCGACACTC	TGGACATTGG	GCCAGCCGAC 420
	ACGCGGGTGG	CAGTGGTGAA	CTATGCTAGC	ACTGTGAAGA	TGAGTTTCCA	ACTCCAGGCC 480
	TACACAGATA	AGCAGTCCCT	GAAGCAGGCT	GTGGGTGAAA	TACACCCCTT	GTCAACAGGC 540
	ACCATGTGAG	GCTAGCCAT	CCAGACAGCA	ATGGAACGAG	CCTTCACAGT	GGAGGCAGGG 600
15	GCTCGAGAGC	CCTCTTCTAA	CATCCCTAAG	GTGGCCATCA	TTGTTACAGA	TGGGAGGCC 660
	CAGGACCCAG	TGAATGAAGT	GGCGGCTCGG	GCCCAAGCAT	CTGGTATTGA	GCTCTATGCT 720
	GTGGGGTGG	ACGCGGAGAA	CATGGCGTCC	CTCAAGATGA	TGGCCAGTGA	GCCCTAGAG 780
	GAGCATGTTT	TCTACGTGGA	GACCTATGGG	GTCAATTGAA	AACTTTCTCT	TAGATTCCAG 840
	GAAACCTTCT	GTGGCTGGA	CCCTGTGTG	CTTGGAAAC	ACCAATGCCA	GCACTGTG 900
20	ATCAGTATG	GGGAGGCCAA	GCACCACTGT	GAGTGTAGCC	AAGGATACAC	CTTGAATGCC 960
	GACAGAAAA	CGTGTTCAGC	TCTTGATAGG	TGTGCTCTTA	ACACCCACGG	ATGTGAGCAC 1020
	ATCTGTGGA	ATGACAGAA	TGGCTCTTAT	CATTGTGAGT	GCTATGAAGG	TTATACCTTG 1080
	AATGAAGACA	GGAAACTTGG	TTCAGCTCAA	GATAAATGTG	CTTTGGGTAC	CCATGGGTGT 1140
	CAGCACATTT	GTGTGAATGA	CAGAACAGGG	TCCCATCATT	GTGAATGCTA	TGAGGGCTAC 1200
25	ACTCTGAATG	CAGATAAAAA	AACATGTTCA	GTCGGTGACA	AGTGTGCCCT	AGGCTCTCAT 1260
	GGTTGCCAGC	ACATTTGTGT	GAGTGATGGG	GCCGCATCCT	ACCACGTGTA	TTGCTATCCT 1320
	GGCTACACCT	TAAATGAGGA	CAAGAAAAACA	TGTTACAGCA	CTGAGGAAGC	ACGAAGACTT 1380
	GTTTCCACTG	AAGATGCTTG	TGGATGTGAA	GCTACACTGG	CATTCCAGGA	CAAGGTGAGC 1440
	TGATATCTTC	TCTAAGTTAT	GACTAAGTGA	GATGACATTT	TGGAGAAAGT	GAAATAAAT 1500
30	GAATATGGAC	AAATACATCG	TAAATTTGCT	CCAATTTCTC	ACCTGAAAT	GTGACAGCT 1560
	TGCTGTACTT	AATACTCATG	CATTCTTTTG	CACACCTGTT	ATTGCCAATG	TTCTGCTTAA 1620
	TAATTTGCCA	TTATCTGTAT	TAATGCTTGA	ATATTACTGG	ATAAATGTGA	TGAAGACTTT 1680
	CTGCAGAAAT	AGCATGATTT	TTCCAAGGAA	ATACATATGC	AGTACTTTAT	TAAAGCAAAA 1740
	CTTTAGTGTG	TCTAAGTTAT	GACTGTGAAA	TGATTGGTAG	GAAATAGAAAT	GAAAGTTTAA 1800
35	GTGTTTCTTT	ATCTACTAAT	TGAGCCATTT	AATTTTAAAA	TGTTTATATT	AGATAACCAT 1860
	ATTCACAATG	GAAACTTTAG	GTCTAGTTTC	TTTTGATAGT	ATTTATATAA	TAAATCAATC 1920
	TTATTACTGA	GAGTGCAAAAT	TGTACAAAGT	ATTTACACAT	ACAACTTCAT	ATAACTGAGA 1980
	TGAATGTAAT	TTTGAACCTG	TTAACACTTT	TTGTTTTTTG	CTTATTTTGT	TGGAGTATTA 2040
	TTGAAGATGT	GATCAATAGA	TTGTAATACA	CATATCTAAA	AATAGTTAAC	ACAGATCAAG 2100
40	TGAACATTAC	ATTGCCATTT	TTAATTCAAT	CTGGTCTTTG	AAAGAAATGT	ACTACTAAAG 2160
	AGCACTAGTT	GTGAATTTAG	GGTGTAAAC	TTTTTACCAA	GTACAAAAAT	CCCAATTTCA 2220
	CTTTATTATT	TTGCTTCAGG	ATCCAAGTGA	CAAAGTTATA	TATTTATAAA	ATTGCTATAA 2280
	ATCGACAAAA	TCTAATGTTG	TCTTTTAAAT	GTAGTGATC	CACCTGCCCT	AGCCTCCCAA 2340
	AGTGCTGGGA	TTACAGGCTT	GAAAGTCTAA	CTTTTCTTAA	CTTATATATT	TGATACATAT 2400
45	AATTCCTTTG	GCTTTGAAAC	TTGCAACTTT	GAGAACAAAA	CAGTCCCTTA	AATTTTGCAC 2460
	TGCTCAATTC	TGTTTTTCGT	TTGCAATGTC	TTTAATATAA	TAAAGTTTAT	TACCTTTACA 2520
	TATTATCATG	TCTATTTTGG	ATGACTCATC	AATTTTGTCT	ATTAAAGATA	TTTCTTTAAA 2580
	TTAAAAA	AAAAA				2599

Seq ID NO: C142 DNA Sequence
Nucleic Acid Accession #: NM_016639.1
Coding sequence: 40..429

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	CGGTGCTGCG	GGCTCCTCGT	GCTGGGGCTC	TGGCTGGCGT	TGCTGCGCTC	CGTGGCGGGG 120
	GAGCAAGCGC	CAGGCACCGC	CCCTGCTGCC	CGCGGCAGCT	CCTGGAGCGT	GGACCTGGAC 180
60	AAGTGATGCG	ACTGCGCGTC	TTGCAAGGCG	CGACCGCACA	GCGACTTCTG	CCTGGGCTGC 240
	GCTGCGACAC	CTCCTGCCCC	CTTCGGGCTG	CTTTGGCCCA	TCCTTGGGGG	CGCTCTGAGC 300
	CTGACCTTCG	TGCTGGGGCT	GCTTTCTGGC	TTTTTGGTCT	GGAGACGATG	CGCAGGAGA 360
	GAGAAGTTCA	CAACCCCAT	AGAGGAGACC	GGCGGAGAGG	GCTGCCAGC	TGTGGCGCTG 420
	ATCCAGTGAC	AATGTGCCCC	CTGCCAGCGG	GGGCTCGCCC	ACTCATCATT	CATTCAATCA 480
65	TTCTAGAGCC	AGTCTCTGCC	TCCAGAGCGC	GGCGGAGGCC	AAGCTCTTCC	AACCAAGAG 540
	GGGGTGGGGG	GCGGTGAATC	ACCTCTGAGG	CCTGGGCCCA	GGGTTCAAGG	GAACCTTCCA 600
	AGGTGTCTGG	TTGCCCTGCC	TCTGGCTCCA	GAACAGAAAG	GGAGCCTCAC	GCTGGCTCAC 660
	ACAAAACAGC	TGACACTGAC	TAAAGAACTG	CAGCATTTGC	ACAGGGGAGG	GGGGTGCCT 720
	CCTTCTTATG	GACCTGGGGG	CCAGGCTGAC	TTGGGGGGCA	GACTTGACAC	TAGGCCCCAC 780
70	TCACTCAGAT	GTCTGAAAT	TCCACCACGG	GGGTCAACCT	GGGGGGTTAG	GGACCTATTT 840
	TTAACTACTG	GGGCTGGCCC	ACTAGGAGGG	CTGGCCCTAA	GATACAGACC	CCCCCACTC 900
	CCCAAGCGG	GGAGGAGATA	TTTATTTTGG	GGAGAGTTTG	GAGGGGAGGG	AGAATTTATT 960
	AATAAAGAA	TCTTTAACTT	TAAAAA	AAAAA		998

Seq ID NO: C143 DNA Sequence
Nucleic Acid Accession #: NM_001819
Coding sequence: 113..2146

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	CTCCGGTCCA	GCGGCCATCT	TCCCTTCGCG	ACAGGGGGCG	CGAGGGGGGG	CCATGCAGCC 120
	AACGCTGCTT	CTCAGCCTCC	TGGGAGCGGT	GGGGCTGGCG	GCTGTCAATT	CCATGCCAGT 180
	GGATAACAGG	AACCACAATG	AAGGAATGGT	GACTGCTGTC	ATCATTTAGG	TCTCTCAAAA 240

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AAGATTGTTA AGAGAGCCAG CTGATGCCCTC GGAAGCCCAC GAGTCTCTCCA GCAGGGGAGA 420
GGCAGGAGGCC CCAGGGGAGG AGGACATCCA AGGCCCAACA AAGGCAGACA CAGAGAAATG 480
GGCAGAGGGA GGGGGGACCA GCGGAGAGCG AGCGGATGAG CCCCAGTGGA GCCTCTATCC 540
CTCCGACAGC CAAATCTCTG AAGAAGTGAA GACACGCCAT TCTGAGAAGA GCCAGAGAGA 600
GGATGAGGAG GAGGAGGAGG GAGAGAACTA TCAAAAAGGG GAGCGAGGGG AAGATAGCAG 660
TGAAGAGAAA CACCTTGAAG AGCCAGGAGA GACACAAAAC GCTTTTCTCA ATGAAAGAAA 720
GCAGGCTTCA GCTATAAAAA AAGAGGAGTT AGTGGCCAGA TCGGAAACAC ATGCTGCCGG 780
GCATTCTCAG GAGAAAGACAC ATAGCCGAGA GAAGAGTAGC CAGGAGAGTG GAGAGGAGGC 840
AGGAGGCCAG GAGAAATCAC CCCAGGAGTC TAAAGGCCAA CCCCAGAGCC AGGAAGAATC 900
TGAGGAAGGT GAGGAAGATG CCACCTCTGA GGTGGACAAA CGACGCACGA GGCCAGACA 960
CCACCAGCGG AGGAGCAGGC CCGACAGGTC CTCTCAAGGA GGGAGTCTTC CCTCTGAGGA 1020
AAGGGGACAC CCCAGGAGG AATCTGAGGA GTCAAAACGTC AGCATGGCCA GTTTAGGGGA 1080
AAGAGGGGAC CACCATTCAA CCCACTACAG GGCTTCAGAG GAAGAACCTG AATATGGAGA 1140
AGAAATAAAG GGTATCCAG GGTCCAGGC CCTGAGGAC CTGGAGTGGG AGCGCTATAG 1200
GGGCAGAGGA AGTGAAGAAT ACAGGGCTCC AAGACCTCAG AGTGAGGAGA GTTGGGATGA 1260
GAGGAGCAAG AGAAACTACC CCAGCTTAGA GCTTGATAAG ATGGCACATG GATATGGTGA 1320
AGAAAGCTAG GAGAGAGGG GCCTTGAGCC GGGAAAGGGA CGCCATCACA GAGGCAGGGG 1380
AGGGGAGCCA CGTGCCTATT TCATGTCTGA CACCAGAGAA GAGAAAGGT TCTTGGGTGA 1440
AGGACACACG CGTGTCCAG AAAACCAGAT GGACAAAGCA AGGAGGCATC CACAAGGTGC 1500
GTGGAAGAG CTGACAGAA ATTATCTCAA CTACGGTGAG GAAGGAGCCC CAGGGAAGTG 1560
GCAGCAGCAG GGAGACCTGC AGGACACTAA AGAAAAAGG GAGGAAGCTA GOTTTCAGAA 1620
TAAACAATAT AGCTTCCATC ACACAGCTGA AAAGAGGAAG AGATTAGGGG AACTGTTCAA 1680
CCCACTACTA GACCTCTCC AGTGAAGAG CAGCCATTTT GAAAGAGAG ACAACATGAA 1740
TGACAAATTT CTGAGGGTG AGGAGGAAA TGAGCTGACC TTGAACGAGA AGAATTTCTT 1800
CCCAGAATAC AACTATGACT GGTGGGAGAA AAAGCCCTTC TCTGAGGATG TGAACCTGGG 1860
GTATGAAGAG AGAAACCTCG CCAGGGTCCC CAAGCTGGAC CTGAAAAGGC AATATGACAG 1920
GGTGGCCCAA CTGGACCAAG TCCTTCACTA CAGGAAGGAG TCAGCTGAGT TTCCAGACTT 1980
CTATGATTC CTGAGGCGCG TGAGCACCCA CCAGGAGGCA GAAATGAAA AGGACAGGGC 2040
TGACACAGCA GTCTCTGACG AGGACGAGAA AAAAGAACTC GAAAACTTGG CTGCAATGGA 2100
TTTGAAGCTA CAGAAGATAG CTGAGAAATT CAGCCAAAGG GGCTGACTGT CATTGGAGCG 2160
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ACCATTATA TACCAAGGG CAGAAAGTAG AACTTACTAT TCATTAAATG TTTGACACAA 2280
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TCTTTGGAAA AATGTTTGTG TCAGTTGGAA ATAATAAAG ATTCACTGA GACC 2454

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Seq ID NO: C144 DNA Sequence
Nucleic Acid Accession #: XM_093082.1
Coding sequence: 93..1988

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AGCCCAACTA TGTATTACAG ACATTGAGGT GGTACGGTG CCTATCTCT TCTGCTTCTT 180
GTGGGGCTCT AGCAGCTGTT CTTAGCACCA GTCACTGGCT CACTGAACTG GAATTTAGTG 240
AGACAAACTT GGAAGCTTCA GCTTTGAAAT TGCTCTATGG AGGCTTAAAA GATCCAAATT 300
GCAAAATACA GAAGCTCAAC TTGCAGTTTT CTTTATCTGT AACCGCTGCA AAACCTCCAG 360
TTGGAATGGT TGGAAATTGT TCTGGTTTCT CGGATCATT GGTGCAATCT CATTTTGGCT 420
ACTGTGAGGA CAGTTCCTTC AAATGTGATC TTTGTAAAGT GCTCTGGCCT TCCACCAGAG 480
TTGCTGCTGC AAAGGATTGT GGGAGTCTTA AGTCTCTCT ATCAGAAAGG CTGAACTGGG 540
CAGGAAGACT TGAGGCACTG GAGGAGGTTT TGGGGTTGGG GGTGCTTGTA CAGCCCGGTG 600
ACCCAGCATC TCAGGGTGGG GGGCATGTG AAAACTATGG GTCTTTTAGA GACTTGGTGG 660
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CCCTACAAGT TGTCTCTCCT TGCAAAATCT TCTCCTCAA ACTATTCTC TTTATTGATC 780
TGCCTAATTC TCCTGGTCAG GTTAGTGTGG TGCAAGTGAC CATCCCAGAC GOTTTOGTGA 840
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GAGAACAGCT TTCCATCCAG TGGTCTTTCT TCCATAAGAA GGAGATGGAG CCAATTTCTT 960
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AGCAGGCTGA ACTCCAGATT TACTTTTCTC AAGGTGGACA AGCTGTAGCC ATCGGGCAAT 1080
TTAAAGATCG AATTACAGGG TCCAACGATC CAGGTAATGC ATCTATCACT ATCTCGCATG 1140
TGCAAGCCAG AGACAGTGGG ATTTACATCT GCGATGTTAA CAACCCCACT GACTTTCTCG 1200
GCCAAACCA AGGCATCTCT AACGTCACTG TGTTAGTGAA ACCTTCTAAG CCCCTTTGTA 1260
GCGTTCAAGG AAGACCAGAA ACTGGCCACA CTATTTCCCT TTCTGTCTC TCTGGCTTG 1320
GAACACCTTC CCTGTGTAC TACTGGCATA AACTTGAGGG AAGAGACATC GTGCCAGTGA 1380
AAGAAACTT CAACCAACC ACCGGGATTT TGGTCATTGG AAATCTGACA AATTTTGAAC 1440
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TCACTTCTTC ACATCCAGAA GTTGAATCA TTGTTGGGGC CTTGATTGTT AGCCTGCTAG 1560
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GAGAAAGCGA AGCAATGCCA AGAGAAAGCG CTACCCAAC AGAAGTAAC CTACCATCTT 1740
CCATTCTATG GACTGGCCCT GATACCATCC AAGAACCACT CTATGAGCCA AGCCCTACTC 1800
AGGAGCTGCG CCCAGAGCCT GCCCCAGGAT CAGAGCCTAT GGCAGTGCTT GACCTTGACA 1860
TCGAGCTGGA GCTGGAGCCA GAAACGCACT CGGAATTGGA GCCAGAGCCA GAGCCAGAGC 1920
CAGAGTCAGA GCCTGGGGTT GTAGTTGAGC CCTTAAGTGA AGATGAAAAG GGAGTGGTTA 1988
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Seq ID NO: C145 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1242

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CTCATCTGCA	TCTACACCAC	CACCTGTGGC	TCCCGAGAAC	AGCTTTCCAT	CCAGTGGTCT	180
TTCTTCCATA	AGAAGGAGAT	GGAGCCAAAT	TCTTCTCCTT	GGGAGGAGGG	GAAGTGGCCA	240
GATGTTGAGG	CTGTGAAGGG	CACCTCTGAT	GGACAGCAGG	CTGAACCTCA	GATTTACTTT	300
TCTCAAGGTG	GACAAGCTGT	AGCCATCGGG	CAATTTAAAG	ATCGAATTAC	AGGGTCCAAC	360
GATCCAGGTA	ATGCATCTAT	CACATATCTG	CATATGCAGC	CAGCAGACAG	TGGAATTTAC	420
ATCTGCGATG	TTAAACAACCC	CCCAGACTTT	CTCGGCCAAA	ACCAAGGCAT	CCTCAACGTC	480
AGTGTGTTAG	TGAAACCTTC	TAAAGCCCTT	TGTAGCGTTC	AAGGAAGACC	AGAAACTGGC	540
CACACTATT	CCCTTTCTCT	TCTCTCTGCG	CTTGGAACAC	CTCCCTCTGT	GTACTACTGG	600
CATAAACTTG	AGGGAAGAGA	CATCTGTGCA	GTGAAAGAAA	ACTTCAACCC	AACCCCGGG	660
ATTTTGGTCA	TGGAAATCT	GACAAATTTT	GAACAAGGTT	ATTACCACTG	TACTGCCATC	720
AACAGACTTG	GCAATAGTTC	CTGCGAAATC	GATCTCACTT	CTTCACATCC	AGAAAGTTGA	780
ATCATTGTTG	GGGCTCTGAT	TGGTAGCCCTG	GTAGGTGCGG	CCATCATCAT	CTCTGTTGTG	840
TGCTGTGCAA	GAAATAAGAG	AAAAGCAAAG	GCAAAAGAAA	GAAATTTTAA	GACCATGCGG	900
GAACCTTGAGC	CAATGACAAA	GATAAAACCA	AGGGGAGAAA	GCGAAGCAAT	GCCAAGAGAA	960
GACGCTACCC	AACTAGAAGT	AACCTTACCA	TCTTCCATTC	ATGAGACTGG	CCCTGATACC	1020
ATCCAAGAAC	CAGACTATGA	GCCAAGCCCT	ACTCAGGAGC	CTGCCCCAGA	GCGTGCCTCA	1080
GGATCAGAGC	CTATGGCAGT	GCCTGACCTT	GACATCGAGC	TGGAGCTGGA	GCCAGAAACG	1140
CAGTCGGAAT	TGGAGCCAGA	GCCAGAGCCA	GAGCCAGAGT	CAGAGCCTGG	GGTTGTAGTT	1200
GAGCCCTTAA	GTGAAGATGA	AAAGGGAGTG	GTTAAGGCAT	AG		1242

Seq ID NO: C146 DNA Sequence
 Nucleic Acid Accession #: NM_003020.1
 Coding sequence: 29..664

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CCCTGACCGG	GTCTCAGAAG	CAGATATCCA	GAGGCTGCTT	CATGGTGTTA	TGGAGCAATT	180
GGGCATTGCG	AGGCCCCGAG	TGGAATATCC	AGCTCACCAG	GCCATGAATC	TTGTGGGCCC	240
CCAGAGCAAT	GAAGGTGGAG	CTCATGAAGG	ACTTCAGCAT	TTGGGTCTCT	TTGGCAACAT	300
CCCCAACATC	GTGGCAGAGT	TGACTGGAGA	CAACATTCTC	AAGGACTTTA	GTGAGGATCA	360
GGGTACCCCA	GACCTCTCAA	ATCCCTGTCC	TGTTGGAAAA	ACAGATGATG	GATGTCTAGA	420
AAACACCCCT	GACACTGCAG	AGTTCACTCG	AGAGTTCCAG	TTGCACCAGC	ATCTCTTTGA	480
TCCGGAACAT	GACTATCCAG	GCTTGGGCAA	TGGAACAAG	AACTCCTTTT	ACGAGAAGAT	540
GAAGGGAGGA	GAGAGACGAA	AGCGGAGGAG	TGTCAATCCA	TATCTACAAG	GACAGAGACT	600
GGATAATGTT	GTGCAAAAGA	AGTCTGTCCC	CCATTTTTC	GATGAGGATA	AGGATCCAGA	660
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TGCAGGTGTA	AATGGAGTCC	CTGTGAATGA	CAGCATGTTT	CTTACATAGA	TAATTTATGA	780
TACAAGAGCAG	CTGTATGTAG	ATAGTGATAT	GTCTTCACAC	CGATGATTC	GCTTTTGTCT	840
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TGCAAGTTAA	AATGGTGCTC	GAGGTTGTAC	TATTTTGGCC	AAGTCTGTAG	AAAGCTGTCA	1020
TTTGATTTTG	ATTATGTAGT	TCATCCAGCC	CTTGGGCATT	GTTATACACC	AGTAAAGAA	1080
GCTGTACTCA	AGAGGAGGAG	CTGACACATT	TCACTTGGCT	GCGTCTTAAT	AAACATGAAT	1140
GCAAGCATTG	GC					1152

Seq ID NO: C147 DNA Sequence
 Nucleic Acid Accession #: NM_024021.2
 Coding sequence: 144..806

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ATTGAGACAC	CTTTTCTGCT	GCCATGACAA	CCATGCAAGG	AATGGAACAG	GCATGCCAG	180
GGGCTGGCCC	TGGTGTGCCC	CAGCTGGGAA	ACATGGCTGT	CATACATTCA	CATCTGTGGA	240
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ATGGAAGTAA	CCCTATTTC	GTGTATATCG	GGTACACAAT	TTGGGGGTCA	GTAATGTTTA	420
TTATTTTCAG	ATCCTTGTC	ATTGCAGCAG	GAATTAGAAC	TACAAAAGGC	CTGGTCCGAG	480
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CATTTAGCTT	GGGGTTTTAT	TCATTCCATC	ACCCCTTACT	TAACCTACTAT	GGCAACTCAA	600
ATAATTTGTA	TGGGACTATG	TCCATCTTAA	TGGGTCTGGA	TGGCATGGTG	CTCCTCTTAA	660
GTGTGCTGGA	ATTCTGCAAT	GCTGTGTCCC	TCTCTGCTT	TGGATGTAAA	GTGCTCTGTT	720
GTACCCCTGG	TGGGGTTGTG	TTAATTCTGC	CATCACATTC	TCATATGGCA	GAACAGCAT	780
CTCCACACCC	ACTTAATGAG	GTTTGAAGCC	ACCAAAAGAT	CAACAGACAA	ATGCTCCAGA	840
AATCTATGCT	GACTGTGACA	CAAGAGCCTC	ACATGAGAAA	TTACCAAGTAT	CCAACCTCGA	900
TACTGATAGA	CTTGTGATA	TTATTATTAT	ATGTAATCCA	ATTATGAAT	GTGTGTGTAT	960
AGAGAGATAA	TAAATTCAAA	ATTATGTTCT	CATTTTTTTC	CCTGGAACCT	AATAACTCAT	1020
TTCACTGGCT	CTTTATCGAG	AGTACTAGAA	GTTAAATTAA	TAAATAATGC	ATTTAATGAG	1080
GCAACAGCAC	TTGAAAGTTT	TTCATTATC	ATAAGAACTT	TATATAAAGG	CATTACATTG	1140
GCAAAATAAG	TTTGAAGACA	GAAGAGCAAA	AAAAAGATAT	TGTTAAATG	AGGCCTCCAT	1200
GCAAAACACA	TACTTCCCTC	CCATTTATTT	AACITTTTTT	TTCTCCTACC	TATGGGGACC	1260
AAAGTGTCTT	TTCTCTCAGG	AAGTGGAGAT	GCAATGGCCAT	CTCCCCCTCC	CTTTTCTCTT	1320
CTCCTGCTTT	TCCTTCCCCA	TAGAAAGTAC	CTTGAAGTAG	CACAGTCCGT	CCTTGCAATG	1380
GCACGAGCTA	TCATTTGAGT	AAAAGTATAC	ATGGAGTAAA	AATCATATTA	AGCATCAGAT	1440
TCAACTTATA	TTTTCTATT	CATCTTCTTC	CTTTCCCTTC	TCCACCTTTC	TACTGGGCAT	1500
AATTATATCT	TAATCATATA	TGGAATGTG	CAACATATGG	TATTTGTATA	ATACGTTTGT	1560
TTTTATTGCA	GAGCAAAAT	AAATCAAAAT	AGAAGCAATA	AAAAAAAAAA	AAAAAAAAAA	1619

Seq ID NO: C148 DNA Sequence
Nucleic Acid Accession #: NM_002091.1
Coding sequence: 56..502

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1	11	21	31	41	51	
AGTCTCTGCT	CTTCCCAGCC	TCTCCGGGCG	GCTCCAAGGG	CTTCCCGTCG	GGACCATGGG	60
CGGCAGTGAG	CTCCCGCTGG	TCTGCTGGC	GCTGGTCCTC	TGCTTAGCGC	CCCGGGGGCG	120
AGCGGTCCCG	CTGCCTGCGG	GCGGAGGGAC	CGTGTGACCC	AAGATGTACC	CGCGCGGCAA	180
CCACTGGGCG	GTGGGGCACT	TAATGGGGAA	AAAGAGCACA	GGGGAGTCTT	CTTCTGT TTC	240
TGAGAGAGGG	AGCCTGAAGC	AGCAGCTGAG	AGAGTACATC	AGGTGGGAAG	AAGCTGCAAG	300
GAATTGTGCT	GGTCTCATAG	AAGCAAAGGA	GAACAGAAAC	CACCCAGCCAC	CTCAACCCAA	360
GGCCTTGGGC	AATCAGCAGC	CTCGTGGGA	TTCAAGAGAT	AGCAGCAACT	TCAAAGATGT	420
AGGTTCAAAA	GGCAAAGTTG	GTAGACTCTC	TGCTCCAGGT	TCTCAACGTG	AAGGAAGGAA	480
CCCCCAGCTG	AACCAGCAAT	GATAATGATG	GCCTCTCTCA	AAAGAGAAAA	ACAAAACCCC	540
TAAGAGACTG	AGTTCTGCAG	GCATCAGTTC	TACGGATCAT	CAACAAGATT	TCCTTGTGCA	600
AAATATTGTA	CTATTCTGTA	TCCTTCAATC	TTGACTAAAT	TCGTGATTTT	CAAGCAGCAT	660
CTTCTGTTT	AACTTGTGTT	GCTGTGAACA	ATTGTGGAAG	AGAGTCTTCC	AATTAAATGCT	720
TTTTTATATC	TAGGCTACCT	GTTGTTTAGA	TTCAAGGCCC	CGAGCTGTTA	CCATTACAAA	780
TAAAAGCTTA	AACACAT					797

Seq ID NO: C149 DNA Sequence
Nucleic Acid Accession #: NM_012261.1
Coding sequence: 203..1045

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1	11	21	31	41	51	
GATTGTCTCT	GCCAGCAGCT	GTCGGTGCCG	CGCTCGACAC	CGAGTCTTAG	CTAGGCGCTC	60
ACAGAAATAG	CGCTCCCTCC	CTCCCCCTTC	TCTGTCCCCC	GCCTCTCGCT	CACCCCGGCC	120
CACTCCAGCG	GGGACTTTGA	GGGATTCCCT	CTCTGGCGGC	CTCTGCAGCA	GCACAGCCGG	180
CCTCATTCGG	GGCACTGCGA	GTATGGATCT	CCAAGGAAGA	GGGGTCCCCA	GCATCGACAG	240
ACTTCGAGTT	CTCCTGATGT	TGTTCCATAC	AATGGCTCAA	ATCATGGCAG	AACAAGAAAT	300
GGAAATCTC	TCAGGCCTTT	CACTAAACCC	TGAAAAAGAT	ATATTGTGGG	TGCGGGAAAA	360
TGGGACGACG	TGCTCATGGG	CAGAGTTTGC	AGCCAAATTT	ATTGTACCTT	ATGATGTGTG	420
GGCCAGCAAC	TACGTAGATC	TGATCACAGA	ACAGGCCGAT	ATCGCATTGA	CCCGGGGAGC	480
TGAGGTGAAG	GGCGCTGTG	GCCACAGCCA	GTGGAGCTG	CAAGTGTCTT	GGGTGGATCG	540
CGCATATGCA	CTCAAAATGC	TCTTTGTAAA	GGAAAGCCAC	AACATGTCCA	AGGGACCTTA	600
GGCGACTTGG	AGGCTGAGCA	AAGTGCAGTT	TGCTACGAC	TCCTCGGAGA	AAACCCACTT	660
CAGAGACGCA	GTCACTGCTG	GGAAGCACAC	AGCCAACTCG	CACCACTCTT	CTGCCCTTGGT	720
CACCCCGCT	GGGAAGTCTT	ATGAGTGTCA	AGCTCAACAA	ACCATTTTCA	TGGCCTCTAG	780
TGATCCGAG	AAGAAGGTCA	CCATGATCCT	GTCTGGGGTC	CACATCCAA	CTTTTGACAT	840
TATCTCAGAT	TTTGTCTTCA	GTGAAGAGCA	TAAATGCCCA	GTGGATGAGC	GGGAGCAACT	900
GGAAAGAAAC	TGCGCCCTGA	TTTGGGGGCT	CATCTGGGTC	CTCCTCATCA	TGGTAACACT	960
CGCGATTTAC	CACGTCCACC	ACAAAATGAC	TGCCAACGAG	GTGCAGATCC	CTCGGGACAG	1020
ATCCCATGAT	AAGCAGATGG	GCTAGAGGCC	GTTAGGCAGG	CACCCCTTAT	TCCTGTCTCC	1080
CCCACTGAGT	AGGTAGAAC	AACAAAAGCA	CTTTTCCATC	TTGTACAGCA	GATACACCAA	1140
CATAGCTACA	ATCAACAGG	CCTGGGTATC	TGAGGCTTGC	TTGGCTTGTG	TCCATGCTTA	1200
AACCCACGGA	AGGGGGAGAC	TCCTTGGGAT	TTGTAGGGTG	AAATGGCAAT	TATTTCTTCC	1260
ATGCTGGGGA	GGAGGGGAGG	AGGGTCTCAG	ACAGCTTTGG	TGCTCATGGT	GGCTTGGCTT	1320
TGACTCTCCA	AAGAGCAATA	AATGCCACTT	GGAGCTGTAT	CTGGCCCCAA	AGTTTAGGGA	1380
TTGAAACATG	GCTTCTTTGA	GGAGGAAACC	CTTTAGGTT	CAGAAGAATA	TGGGGTGCTT	1440
TGCTCCCTTG	GACACAGCTG	GCTTATCTTA	TACAGTTGTC	AATGCACACA	GAATACAAAC	1500
TCATGCTCCG	TGCAGCAAGA	CCCTGAAAG	TGATTCATGC	TTCTGCTCGG	CATTCTGCAT	1560
GTTTAGTGAT	TGCTTGGGA	ATGTTTCACT	GCTACCCGCA	TCCAGGACT	GCAGCACCAG	1620
AAAACGACTA	ATGTAACAT	GCAGAGTTGT	TTGGACTTCT	TCCTGTGCCA	GGTCCAAAGT	1680
GGGGACCTG	AAGAATCAAT	CTGTGTGAGT	CTGTTTTTCA	AAATGAAATA	AAACACACTA	1740
TTCTCTGCG						1749

Seq ID NO: C150 DNA Sequence
Nucleic Acid Accession #: NM_003226.1
Coding sequence: 2..226

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1	11	21	31	41	51	
GATGCTGGGG	CTGGTCTCTG	CCTTGCTGTC	CTCCAGCTCT	GCTGAGGAGT	ACGTGGGCCCT	60
GTCTGCAAAC	CAGTGTGCGG	TGCGGGCCAA	GGACAGGGTG	GACTGCGGCT	ACCCCATGTT	120
CACCCCAAG	GAGTGCACAA	ACCGGGGCTG	CTGCTTTGAC	TCCAGGATCC	CTGGAGTGCC	180
TTGGTGTTC	AAGCCCTTGA	CTAGGAAGAC	AGAAATGCACC	TTCTGAGGCA	CCTCCAGCTG	240
CCCTGGGAT	GCAGGCTGAG	CACCCCTTGC	CGGCTGTGAT	TGCTGCCAGG	CACTGTTTAT	300
CTCAGTTTTT	CTGTCCCTTT	GCTCCCGGCA	AGCTTTCTGC	TGAAAGTTCA	TATCTGAGC	360
CTGATGCTTT	AACGAATAAA	GGTCCCATGC	TCCACCCG			398

Seq ID NO: C151 DNA Sequence
Nucleic Acid Accession #: NM_002993.1
Coding sequence: 64..408

80

1	11	21	31	41	51	
GGCACGAGCC	AGTCTCCGCG	CCTCCACCCA	GCTCAGGAAC	CCGGAACCC	TCTCTTGACC	60
ACTATGAGCC	TCCGTCAGG	CCGCGCGGCC	CGTGTCCCGG	GTCTTGGGG	CTCTTGTGTC	120
GCGCTGCTCG	CGCTGCTGCT	CCTGCTGAAG	CCGCGCGGGC	CCCTCGCCAG	CGCTGTCTCT	180
GTCTCTGCTG	TGCTGACAGA	GCTGCGTTGC	ACTTGTTTAC	CGGTTACGCT	GAGAGTAAAC	240

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CCCAAAACGA TTGGTAAAT GCAGGTGTTT CCGGCAGGCC CGCAGTGCTC CAAGGTGGAA 300
GTGGTAGCCT CCTCGAAGAA CGGGAAGCAA GTTTGTCTGG ACCCGGAAGC CCCTTTTCTA 360
AAGAAAGTCA TCCAGAAAAA TTTGGACAGT GGAACAAGA AAAACTGAGT AACAAAAAAG 420
ACCATGCATC ATAAATTGTC CCAGTCTTCA GCGGAGCAGT TTTCTGGAGA TCCCTGGAOC 480
CAGTAAGAAT AAGAAGGAAG GGTGGTTTTT TTTCCATTTT CTACATGGAT TCCCTACTTT 540
GAAGAGTGTG GGGGAAAGCC TACGCTTCTC CCTGAAGTTT ACAGCTCAGC TAATGAAGTA 600
CTAATATAGT ATTTCCACTA TTTACTGTTA TTTTACCTGA TAAGTTATTG AACCCITTGG 660
CAATTGACCA TATTGTGAGC AAAGAATCAC TGGTTATTAG TCITTCATAG AATATTGAAT 720
TGAAGATAAC TATTGTATTT CTATCATACA TTCCTTAAAG TCTTACCGAA AAGGCTGTGG 780
ATTTCTGTATG GAAATAATGT TTTATTAGTG TGCTGTGAG GAGGTATACC TGTGTGTTCT 840
ACTCACTCTT CTCATAAAAT AGGAAATATT TTAGTTCTGT TTTCTGGGGG AATATGTTAC 900
TCITTACCCT AGGATGCTAT TTAAGTTGTA CTGTATTAGA ACCTGGGTGG TGTACATCCG 960
TTATCTGTGC AGAATATATT TCCTTATTCA GAATTTCTAA AAATTTAAGT TCTGTAAGGG 1020
CTAATATATT CTCTTCTAT GGTTTTAGAT GTTTGATGTC TCTTAGTAT GGCATAATGT 1080
CATGATTTAC TCATTAAACT TTGATTTTGT ATGCTATTTT TTCATATAG GATGACTATA 1140
ATTTCTGGTCA CTAATATATAC ACTTTAGATA GATGAAGAAG CCCAAAAACA GATAAATTCC 1200
TGATTGCTAA TTTACATAGA AATGTATTCT CTGTGTTTTT TAAATAAAG CAAAATTAC 1260
AATGATCTGT GCTCTGCAA GTTTTGAAAA TATATTGAA CAATTGCAAT ATAAATTCAT 1320
CAATTAGTCC TCAAAATATA TACAGCATTG CTAAGATTTT CAGATATCTA TTGTGGATCT 1380
TTTAAAGGTT TTGACCATT TGTATGAGG AATTATACAT GTATCACATT CACTATATTA 1440
AAATTGCACT TTTATTTTTT CCTGTGTGTC ATGTTGTTT TTGTTACTTG TATTGTCAAT 1500
TGGAGAAACA ATAAAGATT TCTAAACCAA AAAAAAAAAA AAAAAAA 1547
  
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25
 Seq ID NO: C152 DNA Sequence
 Nucleic Acid Accession #: NM_005242.2
 Coding sequence: 148..1341

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1 11 21 31 41 51
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TTTCTCTCGG TGCGTCCAGT GGAGCTCTGA GTTTCGAATC GGTGGCGGCG GATTCCCGCG 120
GCGCCCGCGG TCGGGGCTTC CAGGAGGATG CGGAGCCCCA GCGCGCGGTG GCTGCTGGGG 180
GCGGCCATCC TGCTAGCAGC CTCTCTCTCC TGCAGTGGCA CCATCCAAGG AACCAATAGA 240
TCCTCTAAGG GAAGAAGCCT TATTGGTAAG GTTGATGGCA CATCCACGT CACTGGAAAA 300
GGAGTTACAG TTGAACAGT CTTTCTGTG GATGAGTTTT CTGCATCTGT CCTCACTGGA 360
AAACTGCACA CGGTCTTCTC TCCAATTGTC TACACAATTG TGTGTTGGGT GGGTTTGCCA 420
AGTAACGGCA TGGCCCTGTG GGTCTTCTCT TTCCGAACTA AGAAGAAGCA CCTGCTGTG 480
ATTTACATGG CCAATCTGGC CTGCGCTGAC CTCTCTCTG TCATCTGGTT CCCCTTGAAG 540
ATTGCTATTC ACATACATGC CAACAACCTG ATTTATGGGG AAGCTCTTTG TAATGTGCTT 600
ATTGGCTTTT TCTATGGCAA CATGTACTGT TCATTCTCT TCATGACCTG CCTCAGTGTG 660
CAGAGGTATT GGTCTATCGT GAACCCCATG GGGCACTCCA GGAAGAAGCG AAACATTGCC 720
ATTGGCATCT CCCTGGCAAT ATGGCTGCTG ATCTGCTGG TCACCATCCC TTGTATGTC 780
GTGAAGCAGA CCATCTTCAT TCCTGCCCTG AACATCAGCA CCTGTCTGTA TGTTTTGCTT 840
GAGCAGCTCT TGGTGGGAGA CATGTTCAAT TACTTCTCT CTCTGGCCAT TGGGCTCTT 900
CTGTTCACAG CCTTCTCTAC AGCCTCTGCC TATGTGCTGA TGATCAGAA GCTGCGATCT 960
TCTGCCATGG ATGAAACTC AGAGAAGAAA AGGAAGAGGG CCATCAAAT CATTTGCTCT 1020
GTCTTGCCCA TGTACCTGAT CTGCTTCACT CTAAGTAACC TTCTGCTGTG GTTGCTATAT 1080
TTTCTGATTA AGAGCCAGGG CCAGAGCCAT GTCTATGCC TGTACATGT AGCCCTCTGC 1140
CTCTCTACCC TTAACAGCTG CATCGACCCC TTTGTCTATT ACTTTGTTTC ACATGATTTC 1200
AGGGATCATG CAAAGAACGC TCTCTTTTGC CGAAGTGTCC GCACTGTAAA GCAGATGCAA 1260
GTATCCCTCA TCTCAAAGAA ACACCTCCAG AATCCAGCT CTTACTCTTC AAGTTCAACC 1320
ACTGTTAAGA CTCTCTATTG AGTTTTCAG GTCTCAGAT GGAATTTGCA CAGTAGGATG 1380
TGGAACTCTT TTAATGTTAT GAGGACGTGT CTGTTATTTT CTAATCAAAA AGGTCTCACC 1440
ACATACCACC G 1451
  
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60
 Seq ID NO: C153 DNA Sequence
 Nucleic Acid Accession #: NM_003469.2
 Coding sequence: 92..1945

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GAAACGCGCC GAGAAGCTCG CCGGAGAAC GGGGAGGAAT ATGCTGTGGA GCTCCTCTGC 60
CATATAAACA AAAAGAGGAA ATCTTTTCAA CATGGCTGAA GCAAAGACCC ACTGGCTTGG 120
AGCAGCCCTG TCTCTTATCC CTTTAATTTT CCTATCTCT GGGGCTGAAG CAGCTTCATT 180
TCAGAGAAAC CAGCTGCTTC AGAAAGAAC AGACCTCAGG TTGGAATAAT TCCAAAAATT 240
TCCAGTCTCT GAAATGATCA GGGCTTTGGA GTACATAGAA AACCTCCGAC AACAAAGCTCA 300
TAAGGAAGAA AGCAGCCAG ATTATAATCC CTACCAAGGT GTCTCTGTCC CCCTTCAGCA 360
AAAAGAAAT GGCGATGAAA GCCACTTGCC CGAGAGGGAT TCACTGAGTG AAGAAGACTG 420
GATGAGAATA ATACTOGAAG CTTTGAGACA GGCTGAAAT GAGCCTCAGT CTGCACCAAA 480
AGAAAAAAG CCTATGCTCT TGAATTCAGA AAAGAACTTT CCAATGGACA TGAGTGATGA 540
TTATGAGACA CAGCAGTGGC CAGAAGAAA GCTTAAGCAC ATGCAATTCC CTCTATGTA 600
TGAAGAGAA TCCAGGGATA ACCCTTTTAA ACGCACAAAT GAAATAGTGG AGGAACAATA 660
TACTCTCTCA AGCCTTGCTA CATTTGAATC TGCTTCCAA GAGCTGGGGA AACTGACAGG 720
ACCAACCAAC CAGAAACGTG AGAGGATGGA TGAGGAGCAA AAACCTTATA GGAATGATGA 780
AGATGATATC TACAAGGCTA ATAACATTGC CTATGAAGAT GTGGTGGGGG GAGAAGACTG 840
GAACCCGATA GAGGAGAAAA TAGAGAGTCA AACCCAGGAA GAGGTGAGAG ACAGCAAGAA 900
GAATATAGGA AAAATGAAC AAATCAACGA TGAGATGAAA CGCTCAGGGC AGCTTGCCAT 960
CCAGGAAGAA GATCTTCGGA AAGAGAGTAA AGACCAACTC TCAGATGATG TCTCCAAAGT 1020
AATTGCTTAT TTGAAGAGT TAGTAAATGC TGCAGGAAGT GGGAGGTTAC AGAATGGGCA 1080
AAATGGGGAA AGGGCCACCA GGCCTTTTGA GAAACCTCTT GATTCTCAGT CTATTATCA 1140
GCTGATTGAA ATCTCAAGGA ATTACAGAT ACCCCAGAA GACTTAAATT AGATGCTCAA 1200
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CCTAGATGAC ATCTCAGAGG CTGACTTAGA CCATCCAGAC CTGTTCCAAA ATAGGATGCT 1320
  
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5	CTCCAAGAGT	GGCTACCCCTA	AAACACCTGG	TGCTGCTGGG	ACTGAGGCC	TACCAGACGG	1380
	GCTCAGTGTT	GAGGATATTT	TAAATCTTTT	AGGATGQAG	AGTGACAGCA	ATCAGAAAAC	1440
	GTGCTATTTT	CCCAATCCAT	ATAACCAGGA	GAAAGTTCTG	CCAAAGGCTCC	CTTATGGTGC	1500
	TGGAAGATCT	AGATCGAAC	AGCTTCCCAA	AGCTGCCTGG	ATTCCACATG	TTGAAAACAG	1560
	ACAGATGGCA	TATGAAAAAC	TGAACGACAA	GGATCAAGAA	TTAGGTGAGT	ACTTGGCCAG	1620
	GATGCTAGTT	AAATACCCCTG	AGATCATTAA	TTCAAACCAA	GTGAAGCGAG	TTCTGTGTC	1680
	AGGCTCATCT	GAAGATGACC	TGCAGGAAGA	GGACAAAT	GAGCAGGCCA	TCAAAGAGCA	1740
	TTTGAATCAA	GGCAGCTCTC	AGGAGACTGA	CAAGCTGGCC	CCGCTGAGCA	AAAGGTTCCT	1800
10	TGTGGGGCCC	CCGAAGAATG	ATGATACCCC	AAATAGGCAG	TACTGGGATG	AAGATCTGTT	1860
	AATGAAAGTG	CTGGAATACC	TCAATCAAGA	AAAGGCAGAA	AAGGGAAGGG	AGCATATTGG	1920
	TAAGAGAGCA	ATGGAATA	TGTAAGCTGC	TTTCATTAAT	TACCTACTT	TCAATCTCTC	1980
	CACCCCAAGC	AAATCCCAAC	ATTTCCTCTC	AGTGTGTTGA	CTTCTATCTT	GTTAAACATG	2040
	TAATATCTTT	AAATGATGTA	CAGGCAGATG	AAACCAAGTC	ACTGGGGAGT	CTGCTTCATT	2100
15	TCTCTGAGC	TGTTATCTTG	TGTATGGATA	TGTGTAATG	TTATGACTCC	TTGATAAAAA	2160
	ATTTATTATG	TCCATTATTC	AAGAAAGATA	TCTATGACTG	TGTTTAATAG	TATATCTAAT	2220
	GGCTGTGGCA	TGTGTTAGTC	TCACATATGA	TAAAAAAGTG	TCCTTAATTT	CTATTGAAAG	2280
	TTTTTAATAT	TTATTGAATT	ATTTTGTTC	TGTCTGTAGC	GTTTGTGGA	GTACTGGACC	2340
	AAAAAATAA	AGCATTATAA	ATATA				2365

Seq ID NO: C154 DNA Sequence
Nucleic Acid Accession #: NM_030955
Coding sequence: 327..5108

25	1	11	21	31	41	51	
	GAATTCGGG	AGCGGGCGG	CTGCGAGGCC	GCGGGCATG	CGGGAGGCG	AGGGGTGGGA	60
	CCGGGTGGCT	GCGCCATTTC	CACACCGGCC	GAAAGCGGAC	ACTGTCTAGCT	GAATCACTCC	120
	CCTTTTAGGA	GGAGGGAGGG	GGAAAAAGTG	TCTAGCTAAT	TTCTGCTTAA	AAAAGCAGAG	180
30	GAGATGCGGG	GTCAAGCTTTG	CAGTCGCTGC	CTTCTCGCGC	CTGACCATGC	ACCCCTGCAT	240
	CTTCTCTGCT	GGCACAGGGG	AGCGCTTTAT	TTCTGAGAGT	GAGGGCTAAA	ACTTTTTCAT	300
	CTTTTCTCTT	CCTCAACATC	TGAATCATGC	CATGTGCCCA	GAGGAGCTGG	CTTGCAAAAC	360
	TTTCCGTGTT	GGCTCAGCTC	CTTAACCTTG	GGGGCTTTTG	CTATGGGAGA	CAGCCTCAGC	420
	CAGGCCCGGT	TGCTTCCCGG	GACAGGAGGC	AAGAGCAATT	TATCAAGGGC	CTGCCAGAAT	480
35	ACCACTGGGT	GGGTCCAGTC	CGAGTAGATG	CCAGTGGGCA	TTTTTTGTCA	TATGGCTTGC	540
	ACTATCCCAT	CACGAGCAGC	AGGAGGAAGA	GAGATTGGA	TGGCTCAGAG	GACTGGGTGT	600
	ACTACAGAAT	TTCTCACGAG	GAGAAGGACC	TGTTTTTAA	CTTGACGGTC	AATCAAGGAT	660
	TTCTTTCCAA	TAGCTACATC	ATGGAGAGAA	GATATGGGAA	CCTCTCCCAT	GTTAAGATGA	720
	TGGCTTCCCT	TGCCCCCTCT	TGCCATCTCA	GTGGCACGGT	TCTACAGCAG	GGCACACAG	780
40	TTGGGAGCGC	AGCCCTCAGT	GCCTGCCATG	GACTGACTGG	ATTTTTCCAA	CTACCACATG	840
	GAGACTTTTT	CATTGAACCC	GTGAAGRAGC	ATCCACTGGT	TGAGGGAGGG	TACCACCCGC	900
	ACATCGTTTA	CAGGAGGCAG	AAAGTTCCAG	AAACCAAGGA	GCCAACTCTG	GGATTAAAGG	960
	ACAGTGTTTA	CATCTCCAG	AAGCAAGAGC	TATGGCGGGA	GAAAGTGGAG	AGGCACAACT	1020
	TGCCAAGCAG	AAGCCTCTCT	CGGCGTTCCA	TCAGCAAGGA	GAGATGGGTG	GAGACACTGG	1080
45	TGTTGGCCGA	CACAAAGATG	ATTGAATACC	ATGGGAGTGA	GAATGTGGAG	TCCTACATCC	1140
	TCACCATCAT	GAACATGGTC	ACTGGGTTGT	TCCATAACCC	AAGCATTGGC	AATGCAATTC	1200
	ACATTGTTGT	GGTTCGGCTC	ATTCTACTCG	AAGAAGRAGA	GCAAGGACTG	AAAATAGTTC	1260
	ACCATGACGA	AAAGACACTG	TCTAGCTTCT	GCAAGTGGCA	GAAGAGTATC	AATCCCAAGA	1320
	GTGACCTCAA	TCCTGTTTCT	CACGACGTGG	CTGTCTTCTT	CACCAAGAAAG	GACATCTGTG	1380
50	CTGGTTTCAA	TGCCCCCTGC	GAGACCCCTG	GCCTGTCTCA	CCTTTCAGGA	ATGTGTGAGC	1440
	CTCACCCGAG	TTGTAACATC	AATGAAGATT	CGGACTCCCT	TCTGGCTTTC	ACAAATGGCC	1500
	ATGAGCTAGG	ACACAGCTTC	GGCATCCAGC	ATGATGGGAA	AGAAAATGAC	TGTGAGCCCTG	1560
	TGGGCAGACA	TGCTGTACATC	ATGTCGCCGC	AGCTCCAGTA	CGATCCCAT	CCGCTGACAT	1620
	GGTCCAAAGT	CAGCGAGGAG	TACATCACCC	GCTTCTTGGG	CCGAGGCTGG	GGGTTCTGTG	1680
55	TTGATGACAT	ACCTAAAAAG	AAAGGCTTGA	AGTCCAAGGT	CATTGCCCCC	GGAGTGATCT	1740
	ATGATGTTCA	CCACCAAGTC	CAGCTACAAT	ATGACCCCAA	TGCTACCTTC	TGCCAGGAAG	1800
	TAGAAAAAGT	CTGCCAGACA	CTGTGGTGCT	CGTGAAGGG	CTTTTGTGCG	TCTAAGCTGG	1860
	ACGCTGTGCA	AGATGGTAACT	CAATGTGGTG	AGAAGAAGTG	GTGTATGGCA	GCAGAGTGCA	1920
	TCACAGTGGG	GAAGAAACCA	GAGAGCATTC	CTGAGGCTGG	GGGCCGCTGG	TCAACCTGGT	1980
60	CCCACTGTTT	CAGGACCTGT	GGGCTGGGAG	TCCAGAGGCG	AGAGAGGCTC	TGCAACAACC	2040
	CCGAGCCCAA	GTTTGGAGGG	AAATATTGCA	CTGGAGAAAG	AAAACGCTAT	CGCTTGTGCA	2100
	ACGTCCACCC	CTGTGCTTCA	GAGGCACCAA	CATTTCGGCA	GATGCAAGTC	AGTGAATTTG	2160
	ACACTGTCTC	TACAGAAGAT	GAACTCTACC	ACTGGTTTCC	CATTTTAAAC	CCAGCACATC	2220
	CTTGTGAGCT	CTACTGCCGA	CCCATAGATG	GCCAGTTTTC	TGAGAAAATG	CTGGATGCTG	2280
65	TCATTGATGG	TACCCCTTGC	TTTGAAGGCG	GCAACAGCAG	AAATGTCTGT	ATTAATGGCA	2340
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	AAGGATCTGG	TTATGTTGAC	ATTGGGCTCA	TTCCAAAAGG	AGCAAGGGAC	ATAAGAGTGA	2520
	TGGAATTTGA	GGGAGCTGGA	AACTTCTCTG	CCATCAGGAG	TGAAGATCCT	GAAAAATATT	2580
70	ACCTGAATGG	AGGGTTTATT	ATCCAGTGGG	ACGGGAACCTA	TAAGCTGGCA	GGGACTGTCT	2640
	TTCAAGTATGA	CAGGAAAGGA	GACCTGGAAA	AGCTGATGGC	CACAGTCCC	ACCAATGAGT	2700
	CTGTGTGGAT	CCAGCTTCTA	TTCCAGGTGA	CTAACCTTGG	CATCAAGTAT	GAGTACACAA	2760
	TCCAGAAAGA	TGGCCTTGAC	AAATGATTTG	AGCAGATGTA	CTTCTGGCAG	TACGGCCACT	2820
	GGACAGAGTG	CAGTGTGACC	TGCGGGACAG	GATTCGCGCG	CCAAACTGCC	CATTGTCAAT	2880
75	AGAAGGGCCG	CGGGATGGTG	AAAGCTACAT	TCTGTGACCC	AGAAACACAG	CCCAATGGGA	2940
	GACAGAAGAA	GTGCCATGAA	AAGGCTTGTG	CACCCAGGTG	GTGGGCAGGG	GAGTGGGAAG	3000
	CATGCTCGCG	GACATGCGGG	CCCCACGGGG	AGAAGAAGCG	AACCGTGCTG	TGCATCCAGA	3060
	CCATGGTCTC	TGACAGCAG	GCTCTCCGCG	CCACAGACTG	CCAGCACTGT	CTGAAAGCCCA	3120
	AGACCCCTCT	TTCTGTCAAC	AGAGACATCC	TGTGCCCTCT	GGAAGTGACA	GTGGGCAACT	3180
80	GGAGTGAGTG	TTCTGTTTCC	TGTGGTGGTG	GAGTGGGAT	TCGCAAGTGC	ACATGTGCCA	3240
	AGAACCATGA	TGAACCTTGC	GATGTGACAA	GGAAACCCAA	CAGCCGAGCT	CTGTGTGGCC	3300
	TCCAGCAATG	CCCTTCTAGC	CGGAGAGTTC	TGAAACCCAA	CAAGGCACT	ATTTCCAAATG	3360
	GAAAAAACCC	ACCAACACTA	AAGCCCGTCC	CTCCACTTAC	ATCCAGGCC	AGAATGCTGA	3420
	CCACACCCAC	AGGGCTGAG	TCTATGAGCA	CAAGCACTCC	AGCAATCAGC	AGCCCTAGTC	3480
	CTACCAAGTC	CTCCAAAGAA	GGAGACCTGG	GTGGGAAACA	GTGGCAAGAT	AGCTCAACCC	3540

AACCTGAGCT GAGCTCTGCG TATCTCATTT CCACTGGAAG CACTTCCCAG OCCATCCTCA 3600
 CTTCCTCAATC CTGAGCATT CAGCCAAAGTG AGGAAAAATGT TTCCAGTTCA GATACTGGTC 3660
 CTACCTCGGA GGGAGGCCCT GTAGCTACAA CAACAAGTGG TTCTGGCTTG TCATCTTCCC 3720
 5 GCAACCCAT CACTTGGCCT GTGACTCCAT TTTACAATAC CTTGACCAA GGTCCAGAAA 3780
 TGGAGATTCA CAGTGGCTCA GGGGAAGAAA GAGAACAGCC TGAGGACAAA GATGAAAGCA 3840
 ATCCTGTAAT ATGGACCAAG ATCAGAGTAC CTGGAATGA CGCTCCAGTG GAAAGTACAG 3900
 AAATGCCACT TGCACCTCCA CTAACACCAG ATCTCAGCAG GGAGTCCTGG TGGCCACCTT 3960
 TCAGCAGAGT AATGGAAGGA CTGCTCCCA GCCAAGGCC CACTACTTCC GAAACTGGGA 4020
 10 CACCCAGAGT TGAGGGGATG GTTACTGAAA AGCCAGCCAA CACTCTGCTC CCTCTGGGAG 4080
 GAGACCACCA GCCAGAACCC TCAGGAAAGA CGCAGAACCC TAACCACCTG AAACCTCCAA 4140
 ACAACATGAA CCAACAAAA AGTTCTGAAC CAGTCTGAC TGAGGAGGAT GCAACAAGTC 4200
 TGATTACTGA GGGCTTTTGT CTAAATGCCT CCAATTACAA GCAGCTCACA AACGGCCACG 4260
 GCTCTGCACA CTGGATGCTG GGAACCTGGA GCGAGTGTCT CACCACATGT GGCCTGGGGG 4320
 CCTACTGGAA AAGGGTGGAG TGCACCACCC AGATGGATTG TGACTGTGCG GCCATCCAGA 4380
 15 GACCTGACCC TGCAAAAAGA TGCCACTCC GTCCCTGTGC TGGCTGGAAA GTGGGAAACT 4440
 GGAGCAAGTG CTCCAGAAAC TGCAAGTGGG GCTTCAAGAT ACGCGAGATT CAGTGGCTGG 4500
 ACAGCCGGAAC CCACCGGAAC CTGAGGCCAT TTCACTGCCA GTTCTGGGCC GGCATTCTCT 4560
 CCCCATTGAG CTAGAGCTGT AACCCGAGC CCTGTGAGGC GTGGCAGGTG GAGCCTTGGA 4620
 GCCAGTGTCT CAGGTCTCTG GGAGGTGGAG TTCAGGAGAG AGGAGTGTTC TGTCCAGGAG 4680
 20 GCCTCTGTGA TTGACAAAA AGACCCACAT CCACCATGTC TTGCAATGAG CACCTGTGCT 4740
 GTCACTGGGC CACTGGGAAC TGGGACCTGT GTTCCACTTC CTGTGGAGGT GGCCTTCAGA 4800
 AGAGGATTGT CCAATGTGTG CCTCAGAGG GCAATAAAAC TGAAGACCAA GACCAATGTC 4860
 TATGTGATCA CAAACCCAGA CCTCCAGAAT TCAAAAAATG CAACAGCAGC GCCTGCAAGA 4920
 AAAGTGCAGA TTACTTTTGC ACTAAGACA AACTGTGAG CAGTTTCTGC CAGACACTGA 4980
 25 AAGCCATGAA GAAATGTTCT GTGCCACCG TGAGGGCTGA GTGTGCTTC TGTGTCCCC 5040
 AGACACACAT CACACACACC CAAAGGCAAA GAAGGCAACG GTTGCTCCAA AAGTCAAAAG 5100
 AACTCTAAGC CCAA 5115

Seq ID NO: C155 DNA Sequence
 Nucleic Acid Accession #: NM_001062.1
 Coding sequence: 76..1380

1 11 21 31 41 51
 35 GCTCTCATTA CCTTCTGCCC ATCACTTAAT AAATAGCCAG CCAATTCATC AACATTCTGG 60
 TACACTGTGT GAGAGATGAG ACAGTCACAC CAGCTGCCCC TAGTGGGGCT CTACTGTTT 120
 TCTTTTATTC CAAGCCAACT ATGOGAGATT TGTGAGGTAA GTGAAGAAAA CTACATCCGC 180
 CTAACCTCTC TGTGTAATAC AATGATCCAG TCAAACTATA ACAGGGGAAC CAGCGCTGTC 240
 40 AATGTTGTGT TGTCCCTCAA ACTTGTGGA ATCCAGATCC AAACCTGAT GCAAAAGATG 300
 ATCCAACAAA TCAATACAA TGTGAAAAGC AGATTGTGAG ATGTAAGCTC GGGAGAGCTT 360
 GCCTTGATTA TACTGGCTTT GGGAGTATGT CGTAACGCTG AGGAAAACCT AATATATGAT 420
 TACCACCTGA CTGACAGCT AGAAAAATAA TTCCAAGCAG AAATTGAAAA TATGGAAGCA 480
 CACAATGGCA CTCCCCTGAC TAACCTACTAC CAGCTCAGCC TGAGCGTTTT GGCCTTGTGT 540
 45 CTGTTCAATG GGAACCTACT AACCGCGAAA GTTGTCAACC ACTTCACTCC TGAATAATAA 600
 AACTATTATT TGGTAGCCA GTTCTCAGTA GATACTGGTG CAATGGCTGT CCTGGCTCTG 660
 ACCTGTGTGA AGAAGAGTCT AATAAATGGG CAGATCAAG CAGATGAAGG CAGTTTAAAG 720
 AACATCAGTA TTTATACAAA GTCACTGGTA GAAAAGATTG TGTCTGAGAA AAAAGAAAAAT 780
 GGTCCTATTG GAAACACATT TAGCAGGGA GAAGCCATGC AGGCCCTCTT TGTATCATCA 840
 50 GACTATTATA ATGAAAATGA CTGGAATTGC CAACAACTC TGAATACAGT GCTCACGGAA 900
 ATTTCTCAAG GAGCATTGAG TAATCCAAAC GCTGCAGCCC AGGTCTTACC TGCCCTGATG 960
 GGAAGACCTT TCTTGGATAT TAACAAAGAC TCTTCTTGG TCTCTGCTTC AGGTAACTTC 1020
 AACATCTCG CTGATGAGCC TATAACTGTG ACACCTCCTG ACTCACATC ATATATCTCC 1080
 GTCATTAATC CTGTGAGAA CAATGAAACA TATTTACCA ATGTCACTGT GCTAAATGGT 1140
 55 TCTGTCTTCC TCAGTGTGAT GGAGAAAGCC CAGAAAATGA ATGATACTAT ATTTGGTTTC 1200
 ACAATGGAGG AGCGCTCATG GGGGCCCTAT ATCACTGTGA TTCAGGGCCT ATGTGCCAAC 1260
 AATAATGACA GAACCTACTG GGAACCTCTG AGTGGAGGCG AACCACTGAG CCAAGGAGCT 1320
 GGTAGTTACG TTGTCCGCAA TGGAGAAAC TTGGAGGTTT GCTGGAGCAA ATACTAATAA 1380
 GCCCAAACTT TCCTCAGCTG CATAAAATCC ATTTGAGTGA GAGTCCATG TTTATTGTCC 1440
 60 TTATGCCCTC TTCTTCATTT ATCCAGTAC GAGCAGGAGA GTTAATAACC TCCCCTTCTC 1500
 TCTCTACATG TTCAATAAAA GTTGTGAAA GATTAAAC 1537

Seq ID NO: C156 DNA Sequence
 Nucleic Acid Accession #: NM_004591
 Coding sequence: 59..349

1 11 21 31 41 51
 65 CACTCCCAAA GAAGTGGGTA CTCAACACTG AGCAGATCTG TTCTTTGAGC TAAAAACCAT 60
 GTGCTGTACC AAGAGTTTGC TCCTGGCTGC TTTGATGTCA GTCTGTCTAC TCCACCTCTG 120
 70 CGGGGAATCA GAAGCAGCAA GCAACTTTGA CTGCTGTCTT GGATACACAG ACOGTATTCT 180
 TCATCTCTAA TTTATTGTGG GCTTCACAGC GCAGCTGGCC AATGAAGGCT GTGACATCAA 240
 TGCTATCATC TTTACACAAA AGAAAAAGTT GTCTGTGTGC GCAATCCAAA AACAGACTTG 300
 GGTGAATAT ATTGTGCGTC TCCTCAGTAA AAAAGTCAAG AACATGTAAA AACTGTGGCT 360
 75 TTTCTGGAAT GGAATTGGAC ATAGCCCAAG AACAGAAAGA ACCTTGCTGG GGTGAGGT 420
 TCACATGCA CATCATGGAG GGTTTAGTGC TTATCTAATT TGTGCTCAC TGGACTTGTG 480
 CAATTAATGA AGTTGATTC TATTGCATCA TAGTTTGTCT TGTTTAAGCA TCACATTAAA 540
 GTTAACTGT ATTTTATGTT ATTTATAGCT GTAGGTTTTG TGTGTTAGC TATTTAATAC 600
 TAAATTTCCA TAAGCTATTT TGGTTTAGTG CAAAGTATAA AATTATATTT GGGGGGGAAT 660
 80 AAGATTATAT GGACTTTCTT GCAAGCAACA AGCTATTTTT TAAAAAACT ATTTAACATT 720
 CTTTGTGTTA TATTGTTTG TCTCTAAAT TGTGTGAATT GCATTATAAA ATAAGAAAAA 780
 CATTAAATAG ACAATATT 799

Seq ID NO: C157 DNA Sequence
 Nucleic Acid Accession #: NM_013271.1

Coding sequence: 27..809

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1      11      21      31      41      51
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      CCGGGGGGGT CGGCTTTTGG GTGCTGCTGC TGTCTGGGCT GTTTCGGCCG CCCCCCGCGC 120
      TCTGCGCGCG GCCGGTAAAG GAACCCCGCG GCCTAAGCGC AGCGTCTCCG CCCTTGGCTG 180
      AGACTGGCGC TCCTCGCCGC TTCCGGCGGT CAGTGCCTCG AGGTGAGGCG GCGGGGGCGG 240
      TGCAGGAGCT GCGCGGGCGC CTGGCGCATC TGTGAGAGC CGAACGTGAG GAGCGGGCGC 300
10     GGGCCGAGGC GCAGGAGGCT GAGGATCAGC AGGCGCGCGT CCTGGCGCAG CTGCTGCGCG 360
      TCTGGGGGCG CCCCCGCAAC TCTGATCCGG CTCTGGGCGT GGAGCAGCAG CCGGACGCGC 420
      CTGCAGCGCA GCTGCTCGCG GCTCTGCTCC GCGCCCGCGT TGACCTTGCC GCCCTAGCAG 480
      CCCAGCTTGT CCGCGCGCCC GTCCCGCGCG CGGCGCTCCG ACCCGGCGCC CCGGTCTACG 540
      ACGAGGCGCC CGCGGGCGCG GATGCTGAGG AGGCAGGCGA CGAGACACCC GACGTGGACC 600
15     CCGAGCTGTT GAGGTACTTG CTGGGACGGA TTCTTGCGGG AAGCGCGGAC TCCGAGGGGG 660
      TGGCAGCCCC GCGCCGCTTC GCGCTGCGCG CCGACCAAGA TGTGGGCTCT GAGCTGCCCC 720
      CTGAGGGGCT GTCTGGGGCG CTGCTGCGTG TGAAACGCGT AGAGACCCCG GCGCCCCAGG 780
      TGCTGTACAG CCGCTCTCTG CACCTCTGAG CACTGCGCGG ATCCCGTGCA CCCTGGGACC 840
      CAGAAGTCCC CCGCGCATCC GCGCACCAAG ACTTCTCCCG GCCAGCACGT CCAAGAGCAAC 900
20     TTACCCGCGC CAGCCAGCCC TCTCACCAGA GGATCCCTAC CCCCCTGGCC ACAATAACAT 960
      GATCTGAGC 969
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Seq ID NO: C158 DNA Sequence
Nucleic Acid Accession #: NM_002245.2
Coding sequence: 183..1193

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1      11      21      31      41      51
30     |      |      |      |      |      |
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      GCGGGCGGGA GCCAGGCCCC GCGGGGGCGG GGGGCGGGCG GGCCAGAAGA GCGGCGGGCG 120
      CGCGCTCCCG CCGGTCTGCG GCGTTGGGCT TGGCTTTGGC TTTCGGCGCG GCGGTGAGGA 180
      AGATGCTGCA GTCCCTGGCC GGCAGCTGCT GCGTGGCGCT GGTGGAGCGG CACCGCTCGG 240
      CCTGTGCTCT CGGCTCTCTG GTGCTGGGCT ACTTGTCTTA CTGCTCTTC GGCGCAGTGG 300
      TCTTCTCTCT GGTGGAGCTG CCCTATGAGG ACCTGCTCGG CCAGGAGCTG CGCAAGCTGA 360
35     AGCGAGCTTT CTGGAGGAG CACGAGTGCC TGTCTGAGCA GCAGCTGGAG CAGTTCCTGG 420
      GCGGGGTGCT GGAGGCCGAG AACTACGCGG TGTGCGTGCT CAGCAACGCC TGGGCAACT 480
      GGAAGTGGGA CTTCACCTCC GCGCTCTTCT TCGCCAGCAC CGTGTCTCC ACCACAGGTT 540
      ATGGCACAAC CGTGCCCTTG TCAGATGGAG GTAAGGCCCT CTGCATCATC TACTCCGTCA 600
      TTGGCATTCC CTTCACCTCC CTGTTCTGTA CGGCTGTGGT CCAGCGCATC ACCGTGCAAG 660
40     TCACCCGCGC GCCGCTCTC TACTTCCACA TCCGCTGGGG CTCTCCAAG CAGGTGGTGG 720
      CCATCGTCCA TGCGGTGCTC CTGGGTTTGG TCATGTGTGC CTGCTTCTTC TTATCCCGG 780
      CCGCTGTCTT CTAGTCTCTG GAGGATGACT GGAACCTTCT GGAATCCTTT TATTTTGTG 840
      TTATTTCCCT GAGCACCATT GGCCTGGGGG ATTATGTGCC TGGGGAAGGC TACAATCAA 900
      AATTGAGGCT GCTCTATAAG ATTGGGATCA CGTGTACCT GCTACTTGGC CTTATTGCCA 960
45     TGTGAGTAGT TCTGGAACCC TTCTGTGAAC TCCATGAGCT GAAAAAATTC AGAAAAATGT 1020
      TCTATGTGAA GAAGGACAAG GACGAGGATC AGGTGCACAT CATAGAGCAT GACCAACTGT 1080
      CCTTCTCTCT GATCACAGAC CAGGCAAGTG GCATGAAAGA GGACCAAGAAG CAAAATGAGC 1140
      CTTTGTGGCG CACCCAGTCA TCTGCTGCGG TGGATGGCCC TGCAAAACCAT TGAGCGTAGG 1200
      ATTTGTTGCA TTATGCTAGA GCACCAAGGT CAGGCTGCAA GGAAGAGGCT TAAGTATGTT 1260
50     CATTTTATC AGAATGCAAA AGCGAAAAAT ATGTCACTTT AAGAAATAGC TACTGTTTGC 1320
      AATGCTCTAT TAAAAACAA CAAAAAAGA CACATGGAAC AAAGAAGCTG TGACCCGAGC 1380
      AGGATGTCTA ATATGTGAGG AAATGAGATG TCCACCTAAA ATTCATATGT GACAAAATTA 1440
      TCTGACCTTT ACATAGGAGG AGAATACTTG AAGCAGTATG CTGCTGTGGT TAGAAGCAGA 1500
      TTTTATACIT TTAAGTGAA ACTTTGGGGT TTGCATTTAG ATCATTTAGC TGATGGCTAA 1560
55     ATAGCAAAAT TTATATTAG AAGCAAAAAA AAAAAGCATA GAGATGTGTT TTATAAATAG 1620
      GTTTATGTGT ACTGGTTTGC ATGTACCCAC CCAAAATGAT TATTTTGGGA GAATCTAAGT 1680
      CAAACTGACT ATTTATAATG CATAGGTAAC CATTAACTAT GTACATATAA AGTATAAATA 1740
      TGTATTATAT CTGTACATAT GGTTTAGGTC ACCAGATCCT AGTGTAGTTC TGAACCTAAG 1800
      ACTATAGATA TTTTGTCTCT TTTGATTCTT CTTTATACTA AAGAATCCAG AGTGTCTACA 1860
60     ATAAAAAAG GGAATAAATA AACTTGAGAG TGAATAACCA T 1901
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Seq ID NO: C159 DNA Sequence
Nucleic Acid Accession #: NM_005472.1
Coding sequence: 93..404

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1      11      21      31      41      51
65     |      |      |      |      |      |
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      CCGAGTCTTC CCCCACCTCA ATCCCTGTTG CTATGGAGAC TACCAATGGA ACGGAGACCT 120
      GGTATGAGAG CCGTCAATGC GTGCTGAAGG CTCTAAATGC CACTCTTCAC AGCAATTTGC 180
      TCTGCGCGCC AGGGCCAGGG CTGGGGCCAG ACAACAGAC TGAAGAGAGG CCGGCCAGCC 240
      TACCTGGCGG TGATGACAA CTTACATGT ACATTCTCTT TGTCAATGTT CTATTGCTG 300
      TAACGTGGG CAGCTCATC CTGGGATACA CCGCTCCCG CAAAGTGGAC AAGCGTAGTG 360
75     ACCCTATCA TGTGTATATC AAGAACCCTG TGTCTATGAT CTAACACGAG AGGCGTGGGA 420
      CGGTGGAAGA CCAAGACACC TGGGGATTGC GTCTGGGGCC TCCAGAACTC TGCTGTGGAC 480
      TGATCAGGT CT 492
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Seq ID NO: C160 DNA Sequence
Nucleic Acid Accession #: NM_005245.1
Coding sequence: 187..13959

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1      11      21      31      41      51
80     |      |      |      |      |      |
      CTGGGCGGCC GGGCGCGGGG AGAGGGCGCG GGAGCGGCTC GTGCGGCGAG TACCATGCGG 60
```

	ACGCGCGAGC	CGGCGAGGC	CCCAGCAGGC	CCGTCCTGCG	TCGGGGGCGC	GCTGAGACGG	120
	CGGGTGAGCT	CCACGAGAGC	GCCGTGCGCA	CTTGGGCGCA	ACTTTGCGAT	TCCGACAGT	180
	TAAACAAATGG	GGAGACAATT	GGCTTTGCTC	CTGCTTCTGC	TCCTTCTCTT	CCACATTTT	240
5	GGAGACAGTG	ATGGCAGCCA	ACGACTTGAA	CAGACTCCTC	TGCAGTTTAC	ACACCTCGAG	300
	TACACGTCA	CGGTGCAGGA	GAACCTCTGCA	GCTAAGACTT	ATGTGGGGCA	TCCTGTCAAG	360
	ATGGGTGTTT	ACATTACACA	TCCAGCGTGG	GAAGTAAGGT	ACAAAATTTG	TTCCGAGAGC	420
	AGTGAAACCC	TGTTCAAAGC	TGAAGAGTAC	ATTCTCGGAG	ACTTTTGCTT	TCTAAGAATA	480
	AGGACCAAG	GAGGAAATAC	AGCTATTCTT	AATAGAGAAG	TGAAGGATCA	CTACACATTG	540
10	ATAGTGAAAG	CACTTGAAAA	AAATACTAAT	GTGGAGGCGC	GAACAAAGGT	CAGGGTGCAG	600
	GTGCTGSAATA	CAATGACTTT	GAGACCGTTA	TTCTCACCCA	CCTCATACAG	CGTTTCTTTA	660
	CCTGAAAACA	CAGCTATAAG	GACCAGTATC	GCAAGAGTCA	GCGCCACGGA	TGCAGACATA	720
	GGAAACCAACG	GGGAATTTTA	CTACAGTTTT	AAAGATCGAA	CAGATATGTT	TGCTATTCAC	780
	CCAACCAAGT	GTGTGATAGT	GTTAACTGGT	AGACTTGATT	ACCTAGAGAC	CAAGCTCTAT	840
15	GAGATGGAAA	TCCTCGCTGC	GGACCGTGGC	ATGAAGTTGT	ATGGGAGCAG	TGGCATCAGC	900
	AGCATGCGCA	AGCTAACGGT	GCACATCGAA	CAGGCCAATG	AATGTGCTCC	GGTGATAACA	960
	GCAGTGACAT	TGTCACCATC	AGAACTGGAC	AGGGACCCAG	CATATGCAAT	TGTGACAGTG	1020
	GATGACTGCG	ATCAGGGTGC	CAATGCTGAC	ATAGCATCTT	TAAGCATCGT	GGCAGGTGAC	1080
	CTTCTCCAGC	AGTTTGAAGC	AGTGAGGTCC	TTTCCAGGGA	GTAAGGAGTA	TAAAGTCAAA	1140
20	GCCATCGGTG	AGTTGATTG	GGACAGTCAT	CCTTTCGGCT	ACAACTCTAC	ACTACAGGCT	1200
	AAAGATAAAG	GAACCTCGCC	CCAGTTCTCT	TCTGTTAAAG	TCATTCAAGT	GACTTCTCCA	1260
	CAGTTCAAAG	CCGGGCGAGT	CAAGTTTGAA	AAGGATGTTT	ACAGAGCAGA	AATAAGTGAA	1320
	TTTGCTCCTC	CCAACACACC	TGTGCTCATG	GTAAGGCCCA	TTCTGCTTGA	TTCCCATTTG	1380
	AGGTATGTTT	TTAAAGGAGC	ACCTGGAAAA	GCTAAATTCA	GTTTAAATTA	CAACACTGGT	1440
25	CTCATTTCTA	TTTTAGAACC	AGTTAAAGGA	CAGCAGGCAG	CCCAATTTGA	ACTTGAAGTA	1500
	ACAACAAGTG	ACAGAAAAGC	GTCCACCAAG	GTCTTGTGTA	AAGTCTTAGG	TGCAATATAGC	1560
	AATCCCCCTG	AATTTACCCA	GACAGCGTAC	AAAGCTGCTT	TTGATGAGAA	CGTGCCCAT	1620
	GGTACTACTA	TCATGAGCCT	GAGTGCCGTA	GACCTGATG	AGGCTGAGAA	TGGGTACCTG	1680
	ACATACAGTA	TGCAAAATTT	AAATCATGTG	CCGTTTGCGA	TTGACCAATT	CACTGGTGCC	1740
30	GTGAGTACGT	CAGAAAACCT	GGACTACGAA	CTGATGCCCT	GGGTTTATAC	TCTGAGGATT	1800
	CGTGATCAG	ACTGGGCTT	GCCGTACCGC	CGGGAAGTCG	AAGTCTCTGC	TACAATTACT	1860
	CTCAATAACT	TGAATGACAA	CACACCTTTG	TTTGAGAAAA	TAAATTGTGA	AGGGACAATT	1920
	CCCAGAGATC	TAGGCGTGGG	AGAGCAATA	ACCCTGTTT	CTGCTATTGA	TGCAGATGAA	1980
	CTTCAGTTTG	TACAGTATCA	GATTGAAGCT	GGAAATGAAC	TGGATTGTTT	TAGTTTAAAC	2040
35	CCCACTCGG	GGGTATTGTC	ATTAAAGCGA	TCGCTAATGG	ATGGCTTAGG	TGCAAGGTTG	2100
	TCTTTCCACA	GTCTGAGAA	CACAGCTACA	GATGGAGAAA	ATTTTGCCAC	ACCATTATAT	2160
	ATCAACATAA	CAGTGGCTGC	CAGTCACAAG	CTGGTAAACT	TGCAGTGTGA	AGAGACTGGT	2220
	GTTGCCAAAA	GTGCGGAGGA	GAAGCTCCTG	CAGGCAATA	AATTACACAA	CCAGGGAGAG	2280
	GTGGAGGATA	TTTCTTCGGA	TTCTCACTCT	GTCAATGCTC	ACATACCGCA	GTTTAGAAGC	2340
40	ACTCTCCGA	CTCAATTTCA	GGTAAAGGAA	AACCAAGCTG	TGGGTTCCAG	TGTAATTTTC	2400
	ATGAACCTCA	CTGACCTTGA	CAGTGGCTTC	AATGGAAGAA	TGGTCTATGC	TGTTTCTGGA	2460
	GGAAATGAGG	ATAGTTGCTT	CATGATTGAT	ATGGAACAG	GAATGCTGAA	AATTTTATCT	2520
	CCCTCTGACC	GTGAAACAAC	AGACAAATAC	ACCCTGAATA	TTACCGTCTA	TGACCTTGGG	2580
	ATACCCAGGA	AGGCTCGGTG	GGGTCTTCTA	CATGTCGTGG	TTGTGATGTC	CAATGATAAT	2640
45	CCACCCCTG	TTTTCAGGGA	GAGCTATTTT	GTGGAAGTGA	GTGAAGACAA	GGAGGTACAT	2700
	AGTGAATCA	TCCAGGTTGA	AGCCACAGAT	AAAGACCTGG	GGCCCAACGG	ACACGTGACG	2760
	TACTCAATTC	TTACAGACAC	AGACACATTT	TCAATTGACA	GCGTGACGGG	TGTTGTTAAC	2820
	ATCGCACGCC	CTCTGGATCG	AGAGCTGCAG	CATGAGCACT	CCTTAAAGAT	TGAGGCCAGG	2880
	GACCAAGCCA	GAGAAGAGCC	TGAGCTGTTT	TCCACTGTGG	TTGTGAAAGT	ATCACTAGAA	2940
50	GATGTTAATG	ACAACCCACC	TACATTTATT	CCACCTAATT	ATCGTGTGAA	AGTCCGAGAG	3000
	GATCTTCCAG	AAGGAACCGT	CATCATGTGG	TTAGAAGCCC	ACGATCCTGA	TTTAGGTCAG	3060
	TCCTGTGAGG	TGAGATACAG	CCTTCTGGAC	CAGGAGGAAG	GAAACTTCGA	TGTGGATAAA	3120
	CTCAGTGGAG	CAGTTAGGAT	CGTCCAGCAG	TTGGACTTTG	AGAGAAGACA	AGTGATATA	3180
	CTCACTGTGA	GGGCCAAAGC	CAGGGGAAAG	CCAGTTTCTC	TGCTTCTTAC	TTGCTATGTT	3240
55	GAAGTTGAGG	TGGTTGATGT	GAATGAGAAC	CTGCACCCAC	CGGTGTTTTC	CAGCTTTGTG	3300
	GAAAAGGGGA	CAGTGAAGAA	AGATGCACCT	GTGTTTTCAT	TGGTAATGAC	GGTGTGCGCT	3360
	CATGATGAGG	AGCGCGGAAG	AGATGGGGAG	ATCGATACCT	CCATTAGAGA	TGGCTCTGGC	3420
	GTTGTTGTTT	TCAAAATAGG	TGAAGAGACA	GGTGTCTATG	AGAGCTCAGA	TGCACTGGAC	3480
	CGTGAATCGA	CTCCCAATTA	TTGGCTTAACA	GTCTTTGCAA	CCGATCAGGG	TGTCGTGCTC	3540
60	CTTTCATGTA	TCTTAGAGAT	CTACATAGAG	GTTGAGGATG	TCAATGACAA	TGCACACAG	3600
	ACATCAGAGC	CTGTTTATTA	CCCAGAAATC	ATGGAAAATT	CTCCTAAAGA	TGTATCTGTG	3660
	GTCCAGATCG	AGGCATTGGA	TCCAGATTGG	AGCTCTAATG	ACAGCTCAT	GTACAAAATT	3720
	ACAAGTGGAA	ATCCACAAGG	ATTCTTTTCA	ATACATCCTA	AAACAGGTCT	CATCACAACT	3780
	ACGTCAAGGA	AGCTAGACCG	AGAACAGCAA	GATGAACACA	TATTAGAGGT	TACTGTGACA	3840
65	GACAAATGTA	GTCCGCCCAA	ATCAACCAAT	GCAAGAGTCA	TTGTGAAAT	CCTTGATGAA	3900
	AATGACAACA	AACCTCAGTT	TCTGCAAAAG	TTCTACAAAA	TCAGACTCCC	TGAGCGGGAA	3960
	AAGCCAGACC	GAGAAAGAAA	TGCCAGACGG	GAGCGCTCT	ATCGGCTCAT	AGCCACCGAC	4020
	AAGGATGAGG	GCCCAATGTC	AGAAATCTCC	TACAGCATCG	AAGACGGGAA	TGAGCATGGC	4080
	AAATTTTTC	TGAAACCGAA	AACTGGAGTG	GTTTGTGTTA	AGAGGTTTTC	AGCAGCTGGA	4140
70	GAATATGATA	TTCTTTCAAT	TAAGGCAGTT	GACAATGGTC	GCCCTCAAAA	GTCACTCAAC	4200
	ACCAGACTCC	ATATTGAATG	GATCTCCAAG	CCCAACAGT	CCCTGGAGCC	CATTTCATTT	4260
	GAAGAATCAT	TTTTTACCTT	TACTGTGATG	GAAAGTGACC	CGTTGCTCA	CATGATTGGA	4320
	GTAATATCTG	TGGAGCCTCC	TGGCATACCC	CTTTGGTTTG	ACATCACTGG	TGGCAACTAC	4380
	GACAGTCACT	TGATGTGGA	CAAGGGAACT	GGAACCATCA	TTGTTGCCAA	ACCTCTTGAT	4440
75	GCAGAACAGA	AGTCAAACTA	CAACCTCACA	GTCCAGGCTA	CAGATGGAAC	CACCACTATC	4500
	CTCACTCAGG	TATTCATCAA	AGTAATAGAC	ACAAATGACC	ATCGTCTCTA	GTTTCTTACA	4560
	TCAAAATATG	AGTTGTGTTT	TCCTGAAGAT	ACAGCGCCAG	AAACAGAAAT	TTTGCAAAAT	4620
	AGTGCTGTGG	ATCAGGATGA	GAAAAACAAA	CTAATCTACA	CTCTGCAGAG	CAGTAGAGAT	4680
	CCAAGTGATC	TCAAGAAATT	TGCTTTGAT	CCTGCAACCG	GCTCTCTCTA	TACTTCTGAG	4740
80	AAACTGGATC	ATGAAGCTGT	TTCAACGACA	CACCTCAACG	TCAATGTACG	AGATCAAGAT	4800
	GTGCTGTAA	AAAGCAACTT	TGCAAGGATT	GTGGTCAATG	TCAGCGACAC	GAATGACCAC	4860
	GCCTCGTGGT	TCAACGCTTC	CTCTACAAA	GGGCGGGTTT	ATGAATCGGC	AGCCGTTGGC	4920
	TCACTTGTGT	TGCAAGTGAC	GGCTCTGGAC	AAGGACAAAG	GGAAAAATGC	TGAAGTGCTG	4980
	TACTCGATCG	AGTCAGGAAA	TATTGGAAT	ATTGGAAT	CTTTTATGAT	TGATCCTGTC	5040
	TTGGGCTCTA	TTAAACTGCG	CAAAGAATTA	GATCGAAGTA	ACCAAGCGGA	GTATGATTTA	5100

	ATGTTAAAG	CTACAGATA	GGGCAGTCCA	CCATGAGTG	AAATAACTTC	TGTGCGTATC	5160
	TTTGTACAA	TTGCTGACAA	CGCCTCTCCG	AAGTTTACAT	CAAAAGAATA	TTCTGTTGAA	5220
	CTTAGTGAAA	CTGTACAGCAT	TGGGAGTTTC	GTGCGGATGG	TTACAGCCCA	TAGTCAATCA	5280
5	TCAGTGGTGT	ATGAATAAA	AGATGGAAAT	ACAGGTGATG	CTTTTGATAT	TAATCCACAT	5340
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	CAGGATGAGA	ATGACAACGC	GCCAGTTTTT	ATGCAGGCAG	AATATACAGG	ACTCATTAGT	5520
	GAATCAGCCT	CAATTAACAG	CGTGGTCTTA	ACAGACAGGA	ATGTCCCACT	GGTGATTGCA	5580
10	GCAGCTGATG	CTGATAAAGA	CTCAATGCT	TTGCTTGAT	ATCACATTGT	TGAACCATCT	5640
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	CGTTTATTGT	CTGAGTATGC	AGCGAATGTA	ACAGTACATG	TAATTGACAT	TAATGACTGC	5820
	CCCCCTGTGT	TTGCCAAGCC	ATTATATGAA	GCATCTCTTT	TGTTACCAAC	ATACAAAGGA	5880
15	GTAAAGTCA	TCACAGTAAA	TGCTACAGAT	GCTGATTCAA	GTGCATTCTC	ACAGTTGATT	5940
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	GATGGCAGAT	TTGCCGGCCT	TACCTCTGTC	AAAAATTAATG	TGAAAGAAAG	CAAGAAAGT	6120
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20	GAAACATTAG	CTGTCAATTAC	TGCTAATTGG	AGTCCAATCA	ATGAGCCCTT	GTTTATCAC	6240
	ATCCTCAACC	CAGATGCGAG	ATTTAAATA	AGCGCACTT	CAGGGGTTCT	GTCAACCACT	6300
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25	GTGGGCCATG	TCATTGCTA	TGTCACGTCT	GTAGACAGAG	ACAGTGGCAG	AAACGGGGAA	6540
	GTGCATTACT	ACCTCAAGGA	ACATCATGAA	CACTTTCAA	TTGACCCCTT	GGGTGAAATT	6600
	TCACTGAAAA	AGCAATTTGA	GCTTGACACC	TTAAATAAAG	AATATCTTGT	TACAGTGGTT	6660
	GCAAAAGATG	GAGGGAACCC	GGCCTTTTCA	GCGGAAGTTA	TGTTTCCGAT	CACGTGCTAG	6720
	AATAAAGCCA	TGCCCTGTGT	TGAAAAACCT	TTTACAGTG	CAGAGATTGC	AGAGAGCATC	6780
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	ATTGAATCCT	TTGCCATTAA	CATGGAAACA	GGCTGGATTA	CAACTTTAAA	GGAACTTGAC	8820
	CATGAAAGA	GAGACAATTA	CCAGATTAAA	TGGTTGCAT	CAGATCATGG	TGAAAAGATC	8880
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	AAGGTATATG	TGAAGAAACC	TCTAGACAGG	GAAAAAGGG	ACAATTACCT	TCTTACTATC	9180
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	CTTCTCGACC	GAGAAACGAT	TTGAGGTTAC	ACGCTCACGG	TTCAAGCTTC	TGATAATGGC	10440
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	CCAAGATATT	TTGTGCATTT	GTTCACACTG	AATTTTGGTG	GTGTCAGTGC	CATTATCTAG	14400
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80 Seq ID NO: C161 DNA Sequence
Nucleic Acid Accession #: NM_014220.1
Coding sequence: 102..710

1 11 21 31 41 51
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	CCGAGTGCAC	TGAACCCAA	CACATTGTGG	AATGGAATGT	ATCTCTGTTT	TCTATCCTCT	600
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20	AGTTGCTTTT	TATAAGACCA	AGAAGGAGAA	AATCCGACAA	CCTGGAAAGA	TTTTTTGTGT	1140
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30 Seq ID NO: C162 DNA Sequence
Nucleic Acid Accession #: NM_003759.1
Coding sequence: 150..3257

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40	TGTTTAAACA	CAGTATTTTC	ACTTCTGSCAG	TCTCTCCTGC	TGCAGAAOGC	ATCCGATTCA	300
	TCTTGGGAGA	GGAGGATGAC	AGCCCAGCTC	CCCCCTAGCT	CTTCAOGGAA	CTGGATGAGC	360
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	AAACCAAGAA	ATCCAACTTT	CGGTCCCTGG	CTGACATTGG	GAAGACAGTC	TCCAGTGCAA	720
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	CTGAAGTTCC	TGTGCCCAAC	AGGTTCTTGT	TCATTTCTTT	AGGTCTCTAG	GGGAAAGCCA	1020
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80 Seq ID NO: C163 DNA Sequence
Nucleic Acid Accession #: NM_000958
Coding sequence: 389..1855

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	TTATGGATCA	GGCTGCTGCA	TACAAACCTT	GCATCTATT	ATGCAGCTTA	CCTAATCTCT	2580
	AGACTATTCT	GAGTAATGCT	TGCTTGCTAA	TGAATGTATA	GGAGACCA	TTGTAATTGT	2640
	TCTTAGATGA	TGAGTCCAT	GCAGTTCTT	AQAAATCGGT	CTCAGTGCAT	GCTGTGCTTT	2700
	TTCACTATTG	CTCTGGGTTA	TCTGGGAAGT	ATCAGGTCTT	GGGAGGCAAC	AGCATTAAAT	2760
40	GATAAGAAAA	GGAGACATTC	TGGCAAGGCC	AATCTGCTTA	AAGGCAAGT	CCAGAACCTG	2820
	GAACCTAGAG	GCTTTCTCT	CTGCACGAAA	AACAGGTAGT	TTGCAGTCTG	AGATATGGGA	2880
	GAGCTTTTAG	GCTACACAGC	AACCAAGGG	ACCTCTCAC	TTTGTCTGAG	CTTCAATCAG	2940
	GAAGCTATTT	GCTGGGCTCC	AGCAGATGAT	GAGATAATGA	GGTAGTGGGT	TTTTTATTAC	3000
45	TGTTCCATT	TGCAACATCC	TGCAACACCA	TCTTGGGAGA	CAAGAGCATT	ACCCAGCTTG	3060
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Seq ID NO: C166 DNA Sequence
Nucleic Acid Accession #: NM_000574.1
Coding sequence: 66..1211

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55	CCCGGCTGCT	GCTGCTGGTG	CTGTTGTGCC	TGCGGGCGGT	GTGGGGTGAC	TGTGGCCTTC	180
	CCCGAGATGT	ACCTAATGCC	CAGCCAGCTT	TGGAAGGCCG	TACAAGTTTT	CCCGAGGATA	240
	CTGTAAATAC	GTACAAATGT	GAAGAAAGCT	TTGTGAAAT	TCCTGGCGAG	AAGGACTCAG	300
	TGATCTGCGT	TAGGGGAGT	CAATGGTCTG	ATATTGAAGA	GTTCTGCAAT	CGTAGCTGCG	360
	AGGTGCCAAC	AAGGCTAAAT	TCTGCATCCC	TCAAAACAGC	TTATATCACT	CAGAATTATT	420
60	TTCCAGTCGG	TACTGTTGTG	GAATATGAGT	GCCGTCCAGG	TTACAGAGA	GAACCTTCTC	480
	TATCACCAAA	ACTAATCTGC	CTTCAGAAAT	TAAATGGTTC	CACAGCAGTC	GAATTTTGTG	540
	AAAAGAAATC	ATGCCCTAAT	CCGGGAGAAA	TACGAAATGG	TCAGATTGAT	GTACCAGGTG	600
	GCATATTATT	TGTTGCAACC	ATCTCTCTCT	CATGTAAAC	AGGGTACAAA	TTATTTGGCT	660
	CGACTTCTAG	TTTTTGTCTT	ATTTCAAGCA	GCTCTGTCCA	GTGGAGTGAC	CCGTTGCCAG	720
65	AGTGCAGAGA	AATTTATTGT	CCAGCACCAC	CACAAATTGA	CAATGGAATA	ATTCAAGGGG	780
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	TGATTGGAGA	GCACTCTATT	TATTGTACTG	TGAATAATGA	TGAAGGAGAG	TGGAGTGGCC	900
	CACCACTGTA	ATGCAGAGGA	AAATCTCTAA	CTTCAAGGT	CCCAACCA	GTTCAAGAAC	960
70	CTACCAAGTA	AAATGTTCCA	ACTACAGAAG	TCTCAACCA	TTCTCAGAAA	ACCACCAAAA	1020
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	TGCTGACTTA	GCCAAAGAG	AGTTAAGAG	AAAATACACA	CAAGTATACA	GACTGTTCCT	1260
	AGTTTCTTAG	ACTTATCTCG	ATATTGGATA	AAATAAATGC	AATTGTGCTC	TTCAATTAGG	1320
75	ATGCTTTTCA	TGCTTTTAAG	ATGTGTTAGG	AATGTCAACA	GAGCAAGGAG	AAAAAGGCA	1380
	GTCTCGGAAT	CACATTCTTA	GCACACCTAC	ACCTCTTGAA	AATAGAACAA	CTTCAGAAAT	1440
	TGAGAGTGAT	TCCTTTCTTA	AAAGTGTAAG	AAAGCATAGA	GATTGTGTCG	TATTTAGAAAT	1500
	GGGATCACGA	GGAAAGAGGA	AGGAAAGTGA	TTTTTTTCCA	CAAGATCTGT	AATGTTATTT	1560
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	TCCTTTGGCTG	TAAAGCATTT	TCATCTTTCC	TTGGGGTTGG	CAAAATATTT	TAAAGGTAAA	1740
	ACATGCTGGT	GAACCAAGGG	TGTTGATGGT	GATAAGGGAG	GAATATAGAA	TGAAGAGCTG	1800
	AATCTTCTCT	TGTTGCAAAA	ATAGAGTTTG	GAAAAAGCCT	GTGAAAGGTG	TCTTCTTTGA	1860
	CTTAATGTCT	TAAAAAGTAT	CCAGAGATAC	TACAATATTA	ACATAAGAAA	AGATTATATA	1920

TTATTCTGA ATCGAGATGT CCATAGTCAA ATTGTAAAT CTTATTCTTT TGTAAATATT 1980
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 GT 2102

Seq ID NO: C167 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2651

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Seq ID NO: C168 DNA Sequence
 Nucleic Acid Accession #: NM_003667.2
 Coding sequence: 49..2772

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 CCCCTGCCCA GTCTCCGCTT CCTGGAGGAG TTAAGTCTTG CGGGAACGCG TCTGACATAC 360
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 CATAGCAACA ATATCAGGTC GATACCTGAG AAAGCATTTG TAGGCAACCC TTCTCTTATT 900
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	TTAACTCACT	TAAAAATTAAC	AGGAAATCAT	GCCTTACAGA	GCTTGATATC	ATCTGAAAAAC	1440
	TTTCCAGAATC	TCAAGGTTAT	AGAAATGCCT	TATGCTTACC	AGTGCTGTGC	ATTGGAGTGG	1500
	TGTGAGAATG	CCTATAAGAT	TTCTAATCAA	TGGAATAAAG	GTGACAACAG	CAGTATGGAC	1560
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	TTCTGTGCTG	ACTTTGAGGA	AGACCTGAAA	GCCCTTCATT	CAGTGCAGTG	TTACCTTCC	1680
	CCAGGCCCTT	TCAAACCCCTG	TGAACACCTG	CTTGATGGCT	GGCTGATCAG	AATGGAGTGG	1740
10	TGGACCATAG	CAGTCTGGC	ACTTACTTGT	AATGCTTTGG	TGACTTCAAC	AGTTTTGAGA	1800
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15	TCTGTGAAAT	ATTCTGCAAA	ATTTGAAACG	AAAGCTCCAT	TTTCTAGCCT	GAAAGTAATC	2100
	ATTTTGTCTT	GTGCTCTGCT	GGCCTTGACC	ATGGCCGAG	TTCCCTGCT	GGGTGGCAGC	2160
	AAGTATGGGG	CCTCCCTCTT	CTGCCCTGCT	TTGCCCTTTG	GGGAGCCGAG	CACCATGGGC	2220
	TACATGGTGG	GCTCAATCTT	GCTCAATTCCT	CTTTGCTTCC	TCATGATGAC	CATTGCCTAC	2280
	ACCAAGCTCT	ACTGCAATTT	GGACAAGGGA	GACCTGGAGA	ATATTTGGGA	CTGCTCTATG	2340
20	GTAAAAACAC	TGCTCCCTGT	GCTCTTCAAC	AACCTGCATC	TAAACTGCC	TGTGGCTTTC	2400
	TGTCTCTCT	CCTCTTTAAT	AAACCTTACA	TTTATCAGTC	CTGAAGTAAT	TAAGTTTATC	2460
	CTTCTGGTGG	TAGTCCCACT	TCCTGCTATG	CTCAATCCCT	TTCTCTACAT	CTTGTTCAT	2520
	CTCTACCTTG	AGGAGGATCT	GGTAGCCCTG	AGAAAGCAAA	CCTACGCTCG	GACAAGATCA	2580
	AAACACCCAA	GCTTGATGTC	AATTAACCTT	GATGATGTGG	AAAAACAGTC	CTGTGACTCA	2640
25	ACTCAAGCTT	TGCTAACCTT	TACCAGCTCC	AGCATCACTT	ATGACCTGCC	TCCAGTTCCT	2700
	GTGCCATCAC	CAGCTTATCC	AGTGACTGAG	AGCTGCCATC	TTTCTCTGCT	GGCATTGTGC	2760
	CCATGTCTCT	AATTAATATG	TGAAGGAAAA	TGTTTTCAAA	GGTTGAGAAC	CTGAAAAATG	2820
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Seq ID NO: C169 DNA Sequence
Nucleic Acid Accession #: NM_003506.1
Coding sequence: 259..2379

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	CTCATTTTCA	GGAAAGCCTG	AAAATGAGTA	AAATAGTGAA	ATGAGGAATT	TGAACATTTT	180
	ATCTTTGGAT	GGGATCTCTC	TGAGGATGCA	AAGAGTGATT	CATCCAAGCC	ATGTGGTAAA	240
40	ATCAGGAATT	TGAAGAAAAAT	GGAGATGTTT	ACATTTTGTG	TGACGTGTAT	TTTTCTACCC	300
	CTCCTAAGAG	GGCAGCTCT	CTTCACCTGT	GAACCAATTA	CTGTCCCGAG	ATGTATGAAA	360
	ATGGCTTACA	ACATGACGTT	TTTCCCTAAT	CTGATGGGTC	ATTATGACCA	GAGTATTGCC	420
	GGGTGGAAAA	TGGAGCATTT	TCTTCTCTCT	GCAAACTCGG	AATGTTCAAC	AAACATTGAA	480
	ACTTTCCTCT	GCAAGCATT	TGTACCAACC	TGCATAGAAC	AAATTCATGT	GGTCCACCT	540
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	ATTTCTAAGA	AAATTTGAAA	ATAGTCTTCT	TTTATACTGT	AAAAAAAGAT	ATACCAAAAA	2940
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Seq ID NO: C170 DNA Sequence
 Nucleic Acid Accession #: NM_000582
 Coding sequence: 88..990

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Seq ID NO: C171 DNA Sequence
 Nucleic Acid Accession #: NM_002821
 Coding sequence: 150..3362

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	ACTACATGGT	GCTGGAATAT	GTGGATCTGG	GAGACCTCAA	GCAGTTCCTG	AGGATTTCOA	2820
10	AGAGCAAGGA	TGAAAAATTG	AAGTCACAGC	CCCTCAGCAC	CAAGCAGAAG	GTGGCCCTAT	2880
	GCACCCAGGT	AGCCCTGGGC	ATGGAGCACC	TGTCCAACAA	CCGCTTTGTG	CATAAGGACT	2940
	TGGCTGCGCG	TAACTGCCCTG	GTCACTGCC	AGAGACAAGT	GAAGGTGTCT	GCCCTGGGCC	3000
	TCAGCAAGGA	TGTGTACAAC	AGTGAGTACT	ACCACTTCOG	CCAGGCCTGG	GTGCCGCTGC	3060
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	CCTTGGGTGT	GCTGATGTGG	GAAGTGTITA	CACATGGAGA	GATGCCCAT	GGTGGGCAGG	3180
15	CAGATGATGA	AGTACTGGCA	GATTTCAGG	CTGGGAAGGC	TAGACTTCCT	CAGCCCGAGG	3240
	CTGCGCCTTC	CAAACTCTAT	CGGCTGATGC	AGCGCTGCTG	GGCCCTCAGC	CCCAAGGACC	3300
	GGCCCTCCTT	CAGTGAGATT	GCCAGCGCCC	TGGGAGACAG	CACCGTGAC	AGCAAGCCGT	3360
	GAGGAGGGAG	CCCGCTCAGG	ATGGCCTGGG	CAGGGGAGGA	CATCTCTAGA	GGGAAGCTCA	3420
20	CAGCATGATG	GGCAAGATCC	CTGTCTCTCT	GGGCCCTGAG	GTGCCCTAGT	GCAACAGGCA	3480
	TTGCTGAGGT	CTGAGCAGGG	CCTGGCCTTT	CCTCCTCTTC	CTCACCTCA	TCCTTTGGGA	3540
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	TTCTCCCTTT	GACCGGGTCC	AACTCTGCCA	CTCATCTGCC	AACTTTGGCT	GGGGAGGGCT	3720
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	CTTTTGACAC	TATATAAAC	GCCCTTTTGG	TATGCACCAC	GGGGGGCTTT	TATATGTAAT	4020
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	GCCATCCTTA	CCCCACACTT	TTATTGTGT	CGTTTGTGT	TTGTTTGTGT	TTTTTGTITT	4140
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Seq ID NO: C172 DNA Sequence

Nucleic Acid Accession #: NM_002309.2

Coding sequence: 65..673

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	ATGTCAACAC	AACCTCATGA	ACCAGATCAG	GAGCCAACTG	GCACAGCTCA	ATGGCAGTGC	240
	CAATGCCCTTC	TTTATTCTCT	ATTACACAGC	CCAGGGGGAG	CCGTTCCCCA	ACAACCTGGA	300
45	CAAGCTATGT	GGCCCCAAAG	TGACGGACTT	CCCGCCCTTC	CACGCCAAAG	GCAACGGAGA	360
	GGCCAAGCTG	GTGGAGCTGT	ACCGCATAGT	OGTGTACCTT	GGCACCTCCC	TGGGCAACAT	420
	CACCCGGGAC	CAGAAGATCC	TCAACCCAG	TGCCCTCAGC	CTCCACAGCA	AGCTCAACGC	480
	CACCGCCGAC	ATCCTGGGAG	GGCTCCTTAG	CAACGTGCTG	TGCCCGCTGT	GCAGCAAGTA	540
	CCACGTGGGC	CATGTGGAGG	TGACCTACGG	CCCTGACACC	TGGGTGAAGG	ATGTCTTGCA	600
50	GAAGAAGAAG	CTGGGCTGTC	AACTCCTGGG	GAAGTATAAG	CAGATCATCG	CCGTGTGGGC	660
	CCAGGCCTTC	TAGCAGGAGG	TCTTGAAGTG	TGCTGTGAAC	CGAGGGATCT	CAGGAGTTGG	720
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	GGGGGCTGTG	GGCAGACCCC	GAGGGTGCCT	GGCCAGTCCA	CTCCACTCTG	GGCTGGGCTG	840
	TGATGAAGCT	GAGCAGAGTG	GAAACTTCCA	TAGGGAGGGG	GCTAGAAGAA	GGTGGCCCTT	900
55	CCTCTGGGAG	ATTGTGAGCT	GGGGAGCGTG	GGCTGGACTT	CTGGCTCTAC	TTGTCCCTTT	960
	GGCCCTCTGC	TCACTTTGTG	CAGTGAACAA	ACTACACAA	TCACTACAA	GAGCCCTGAC	1020
	CACAGGCTGA	GACAGCAGGG	CCCAGGGGAG	TGACACAGCC	CCACAGAAAT	TATCACCATC	1080
	TGTGCTTTTG	CTGCCCTTTA	GGTTGGGACT	TAGGTGGGCC	AGAGGGGCTA	GGATCCCAAA	1140
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60	AGGCTGTCTT	CTTTTGAGGA	TGATCAGAGA	ACTTGGGCAT	AGGAACAATC	TGGCAGAAAT	1260
	TTCCAGAAAG	AGGTCACTTG	GCATTACAGC	TCTTGGGGAG	GCAGAGAAGC	CACCTTCAGG	1320
	CCTGGGAAGG	AAGACACTGG	GAGGAGGAGA	GGCCTGGAAA	GCTTTGTGTG	GTCTTGTGTT	1380
	CTCTTCCCGG	TGATCTTCCC	TGCAGCCTGG	GATGGCCAGG	GTCTGATGGC	TGACACTGCA	1440
	GCAGGGGTTT	GTGGAGGTGG	GTAGGGCAGG	GGCAGGTTGC	TAGTCAAGTT	GCAGAGGTTT	1500
65	TGAGGGACCC	AGGCTCTTCC	TCTGGGTAAA	GGTCTGTAA	AAGGGGCTGG	GGTAGCTCAG	1560
	AGTAGCAGCT	CACATCTGAG	GCCCTGGGAG	GTCTTGTGAG	GTCAACAGAG	GGTACTTGAG	1620
	GGGGAAGTGA	GGCCGTCTCT	GGTCCCCAGG	GCAAGGGAAC	AGCAGAACTT	AGGGTCAGGG	1680
	TCTCAGGGAA	CCCTGAGCTC	CAAGCGTGTG	GTGGGTCTGA	CCTGGCATGA	TTTCTATTTA	1740
	TTATGATATC	CTATTATAT	TAACTTATTT	GTGCTTTCAG	TGGCCAAAGT	AATTCCCTTT	1800
70	TCCTGGTCTC	CTACTCAACA	AAATATGATG	ATGGCTCCCG	ACACAAGCGC	CAGGGCCAGG	1860
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	GCTCCACCCC	CATCCCTTAC	TGTGACTTGC	TTTAGGTGT	CAGGGTCCAG	GCTGCAGGGG	2040
	CTGGGCCAAT	TTGTGGAGAG	GCCGGGTGCC	TTTCTGTCTT	GCTTCCAGGG	GGCTGGTTCA	2100
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	CCCATGCTGC	CTCTGAAATA	GCGCCCTGGA	ACAACCTTGC	CCCTGCACCC	AGCATGCTCC	2280
	GACACAGCAG	GGAAGCTCCT	CCTGTGGCCC	GGACACCCAT	AGACGGTGGG	GGGGGCTCTG	2340
	CTGGGCCAGA	CCCCAGGAAG	GTGGGTGAGA	CTGGGGGGAT	CAGTGCACCA	TTGCTCCCAA	2400
80	GAGGAGGAGA	GGGAGGCTGC	AGACGCGCTGG	GACTCAGACC	AGGAAGCTGT	GGGCCCTCCT	2460
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	AAGGAGGCAG	CAGAGTTGGG	GCAGCTGCTC	AGAGCAGTGT	TCTGGCTCTT	TCTCAAAACC	2640
	TGAGGCGGCT	GCCGCGCTCC	AAGTTCTCTC	GACAAGATGA	TGGTACTAAT	TATGGTACTT	2700
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	CCCTTGTGCA	GGATGCAAGG	ACTGCCTTCT	CCTTCTGTCT	TCATCCGGCT	TAGCTTGGGG	2940
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	GCTGATTCCA	CCCGGGGGGC	CCGGCTGACT	CGCCCATCAC	CTCATCTCCC	TGTGGACTTG	3060
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	TTTTTTTAAA	AAGCACTGCT	AGTTTACTTG	TCTCTCTCCC	CCATCGTCCC	CATCGTCTTC	3420
	CTTGTCCCTG	ACTTGGGGCA	CTTCCACCTT	GACCCAGCCA	GTCACGCTCT	GCCTTGCOCG	3480
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Seq ID NO: C173 DNA Sequence
Nucleic Acid Accession #: XM_097508
Coding sequence: 44..2788

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	CTGATGCTTG	CAGACAATCT	AGCTGGGAGG	AATCCCGCA	GAGGCGCTGT	GGGAGCTGGC	300
	GAGCCTGCAG	TGCTGCGGCC	TAGATGCCAA	CCTCATCTCC	CTGGTCCCGG	AGAGGAGCTT	360
	TGAGGGGCTG	TCTTCCCTCC	GCCACCTCTG	GCTGGACGAC	AATGCACTCA	CGGAGATCCC	420
35	TGTGAGGCC	CTCAGGGCC	TCCCTGCCCC	GCAGGCCATG	ACCCCTGGCCC	TCAACCGCAT	480
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	TAAACAACGC	ATCCAGCATC	TGGGGACCCA	CAGCTTCGAG	GGGCTGCACA	ATCTGGAGAC	600
	ACTAGACCTG	AATTATAACA	AGCTGCAGGA	GTTCCCTGTG	GCCATCCGGA	CCCTGGGCAG	660
	ACTGCAGGAA	CTGGGGTTCC	ATAACRAACA	CATCAAGGCC	ATCCCAAGAA	AGGCCCTTCAT	720
40	GGGGAACCC	TGCTTACAGA	CGATACACTT	TTATGATAAC	CCAATCCAGT	TTGTGGGAAG	780
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	ACTGTCTCAC	AATCAAAATG	AGGAGCTGCC	CAGCCTGCAC	AGGTGTGAGA	AATTGGAGGA	1020
45	AATCGGCTTC	CAACACAACC	GCATCTGGGA	AATTGGAGCT	GACACCTTCA	GCCAGCTGAG	1080
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50	GTGCTGTCTC	TATGGGATGT	GTGCCAGCTT	CTTCAAGGCC	TCTGGGCACT	GGGAGGCTGA	1380
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	AAACTCAGCA	GTGTGATCTA	TAGCAGGATG	GCCAGTCCCT	TGGCTCCACT	GATCACTCTC	2940
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Seq ID NO: C174 DNA Sequence
Nucleic Acid Accession #: NM_130849

Coding sequence: 101..2044

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  GCTGACCTGC TCCTTGACG GGGGGGTGCG CCACTACATC CTGAGAGCTC TCCTGAGCTC 1200
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  CCGGAGGAGC CTGGAGGAGG GGCCTTGGG CCACAGCAGC CATAGCCAGG GGGGCCACAG 1440
  CCACGGTGTG TCCTTGACG TGCCACCCAG CGAGCTCCGG CAGCCCAAGC CCCCCACAGA 1500
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  GAGACTGAGC CCAGGTTTGA GGCTACTGCC CTATATGATC ACTCTGGGCG ACGCGGTGCA 1620
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  GGCCACCTCG CTGGCGGTGT TCTGCCACGA GTTGGCCACG GAGCTGGGGG ACTTCGCCGC 1740
  CTGTCTGACG TCGGGGCTGT CCGTGGGCGA AGCACTGCTG CTGAACCTGG CCTCCGCTG 1800
35 |      |      |      |      |
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  CTGGATCCTG GCAGTGCCCA CGGCGCTGTT CCTCTACGTA GCACCTGCGC ACATGCTCCC 1920
  GGGGATGTTG AAGTACGGG ACCCGGGGCC CTGGCTCCTC TTCTGCTGC ACAACGTGGG 1980
  CCTGTGGGGG GGCTGGACCG TCCTGTGCTG GCTGTCCCTG TAGGAGGATG ACATCACCTT 2040
  CTGATACCTG GCCCTAGTCC CCAACCTTTG ACTTAAGATC CCACACCTCA CAAACCTACA 2100
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Seq ID NO: C175 DNA Sequence

Nucleic Acid Accession #: NM_018971

Coding sequence: 1..1128

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  CTGCTGATCG TGGGGGAGCG CAGCCTGCAC CGCGCCCGGT ACTACCTGCT GCTGAGCTG 180
  TGCTTGGCGG ACGGGCTGCG CGCGCTCGCC TGCCCTCCCG CCGTCACTGCT GGGCGCGCGG 240
  CGTGGCGGGG CCGCGCGGGG GCGCGCGCGG GCGCGGCTGG GCTGCAAGCT GCTGCGCTTC 300
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  TACCTGGCCA TGCGCAGCA CCGCTTCTAT GCAGAGCGCC TGGCGGCTGG GCGCTGCGCC 420
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  TACCTCGGCC TGCTCTTCTT CATCCAAGAC CGCGCAAGA TGGCGCGCGC GCGCTGCTG 660
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  ACCGCTCCG TGTGGCTGAC CTTCGCGCAG GCGCGCATCA ACCCGCTG GTGCTTCTCT 1020
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Seq ID NO: C176 DNA Sequence

Nucleic Acid Accession #: NM_005631

Coding sequence: 290..2653

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  GCGGAGGGGC CGGGCGCGGC GAGCGTCCG GGGGGGCGCG GCGCGGATT CTCTGGGCGC 180
  ACAGTTCGCG TGAGCGCGCT CCGCGGCGCG CGAGGTCTGT CFTGTGGCGG GGGGGCTCCG 240
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  CGGCGGGGCT GCCCCCTGCG AGCGGCTGCG CTACAACGTT TGCTTGGGCT CGGTGCTGCC 540
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	CATCAAGTTC	AACAGTTCAG	GCCAGTGCAG	AGTGCCCTTG	GTTCGGACAG	ACAACCCCAA	900
	GAGCTGGTAC	GAGGACGTGG	AGGGCTGGGG	CATCCAGTGC	CAGAACCOCG	TCTTCACAGA	960
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	CACGCTCTTC	ACCCCTGGCCA	CATTGCTGGC	TGACTGGGGG	AACTCGAATC	GCTACCCCTGC	1080
10	TGTTATTCTC	TTCTACGTCA	ATGCGTGTCT	CTTTGTGGGC	AGCATTTGGCT	GGCTGGCCCA	1140
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	CCTGATGGCT	GGTGTGTGTT	GGTTTGTGGT	CCTCACCTAT	GCCTGGCACA	CTTCCTTCAA	1320
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20	CATTACCTTC	AGCTTGCCTC	TCTACGACTT	CTTCAACGAG	GCTGAGTGGG	AGCGCAGCTT	1740
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35	GGGCTGGGG	CCATTCTACT	CCCGCACCAA	CCTGATGGAC	ACAGAACTCA	TGGATGCAGA	2640
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	CAGGCGAGGT	GAGCTCCAGC	TGCTGCGCAC	GGCGGCTTAC	CTCCACACCA	CAACCACTTT	1680
25	CACCTGAGAT	TGCAGCCCTG	TCTGTGTGAC	CCTGATCACC	CTCTGGGTGT	ACGTGTACGT	1740
	GGACCCAAAC	AATGTGCTGG	ACGCCGAGAA	GGCCTTTGTG	TCTGTGCTCT	TGTTTAATAT	1800
	CTTAAGACTT	CCCTCTCAAC	TGCTGCCCA	GTTAATCAGC	AACCTGACTC	AGGCCAGTGT	1860
	GTCTCTGAAA	CGGATCCAGC	AATTCCTGAG	CCAAGAGGAA	CTTGACCCCC	AGAGTGTGGA	1920
	AAGAAGAGCC	ATCTCCCCAG	GCTATGCCAT	CACCATACAC	AGTGGCACCT	TCACCTGGGC	1980
30	CCAGGACCTG	CGCCCCACTC	TGCACAGCCT	AGACATCCAG	GTCCCGAAAG	GGGCACTGGT	2040
	GGCGGTGGTG	GGGCTGTGGG	GCTGTGGGAA	GTCTCTCCCTG	GTGTCTGCCC	TGCTGGGAGA	2100
	GATGAGAAAG	CTAGAAGGCA	AAGTGACAT	GAAGGGCTCC	GTGGCCTATG	TGCCCCAGCA	2160
	GGCATGGATC	CAGAACTGCA	CTCTTCAGGA	AAAGGTGCTT	TTCGGCAAAG	CCCTGAACCC	2220
	CAAGCGCTAC	CAGCAGACTC	TGGAGGCGCTG	TGCCCTGTCTA	GCTGACCTGG	AGATGCTGCC	2280
35	TGGTGGGAGT	CAGACAGAGA	TGGAGAGAA	GGGCATTAAAC	CTGTCTGGGG	GCCAGCGGCA	2340
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	ACTGTCCGCG	GTGGACTCTC	ATGTGGCCAA	GCACATCTTT	GACCACTCA	TCCGGCCAGA	2460
	AGGCGTGTCTG	CGAGGCAAGA	CGCGAGTGCT	GGTGACGCAC	GGCATTAGCT	TCCTGCCCCA	2520
	GACAGACTTC	ATCATTTGTG	TAGCTGATGG	ACAGGTGTCT	GAGATGGGCC	CGTACCCAGC	2580
40	CCTGTCTGAG	TGCAGACGGCT	CTTTTGCCAA	CTTTCTCTGC	AACTATGCC	CCGATGAGGA	2640
	CCAGAGGCAC	CTGAGGAGCA	GCTGGACCGC	GTGGAAAGGT	GCAGAGGATA	AGGAGGCACT	2700
	GCTGATTGAA	GACACACTCA	GCAACCAAC	GGATCTGACA	GACAATGATC	CAGTCACTTA	2760
	TGTGTGCCAG	AAGCAGTTTA	TGAGACAGCT	GAGTGCCCTG	TCCTCAGATG	GGGAGGGACA	2820
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45	GAAGGCAAGT	GGGCACTGA	CCAGGAGGA	GAAGCAGGCC	ATTGGCACTG	TGGAGCTCAG	2940
	TGTGTCTCTG	GATTATGCCA	AGGCCGTGGG	GCTCTGTACC	ACGCTGGCCA	TCTGTCTCCT	3000
	GTATGTGGGT	CAAAGTGCGG	CTGCCATTGG	AGCCAATGTG	TGGCTCAGTG	CCTGGACAAA	3060
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50	CATCCAGCTG	GCCCGTGTGT	TGCACCAAGG	ACTGCTGCAC	AACAAGATAC	GCTGCCCACT	3240
	GTCTCTCTTT	GACACCAAC	CATCAGGCGG	CATCTGAAC	TGCTTCTCCA	AGGACATCTA	3300
	TGTGTTGAT	GAGGTTCTGG	CCCTGTCTAT	CCTCATGCTG	CTCAATTCTT	TCTTCAAGCC	3360
	CATCTCTCACT	CTGTGTGTCA	TCATGGCCAG	CACGCGCTC	TTCACTGTGG	TGCTCTGCC	3420
	CCTGGCTGTG	CTCTACACCT	TAGTGACAGG	CTTCTATGCA	GCCACATCAC	GGCAACTGAA	3480
55	GGGGCTGGAA	GCTCAGCGCC	GCTCACCTAT	CTACTCCAC	TTTTCCGAGA	CAGTGAAGTG	3540
	TGCCAGTGTG	ATCCGGGCGT	ACACCGCAG	CCGGGATTTT	GAGATCATCA	GTGATACTAA	3600
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	CGAGTGGAG	TTCTGTGGGA	ACTGTGTGGT	GCTCTTGTCT	GCACTATTGT	CCGTCACTGG	3720
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60	ATTTGCTCTG	AAGTGAATGA	TACGAATGAT	GTGAGATTGG	GAATCTAACA	TGCTGGCTGT	3840
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	CCGCCCTCCC	GAAGTTGGC	CCCCACGTGG	GGAGGTGGAG	TTCCGGAATT	ATTCTGTGGG	3960
	CTACCGCGCG	GGCCTAGACC	TGGTGTGAG	AGACCTGAGT	CTGCATGTGC	ACGGTGGCGA	4020
	GAAGGTGGGG	ATCGTGGGCC	GCACTGGGGC	TGGCAAGTCT	TCCATGACCC	TTTGCTCTGT	4080
65	CGGCATCTCT	GAGGCGGCAA	AGGGTGAAAT	CGGCATTGAT	GGCCTCAATG	TGGCAGACAT	4140
	CGGCCTCCAT	GACCTGTGCT	CTCAGCTGAC	CATCATCCCG	CAGGACCCCA	TCTGTCTCTC	4200
	GGGACCCCTG	CGCATGAACC	TGGACCCCTT	CGGCAGCTAC	TCAGAGGAGG	ACATTTGGTG	4260
	GGCTTTGGAG	CTGTCCCAAC	TGCACAAGTT	TGTAGCTGCC	CAGCGCGCAG	CGCTGGACTT	4320
	CCAGTGTCTA	GAGGGCGGGG	AGAACTCTAG	CGTGGGCGAG	AGGCAGCTCG	TGTGCTGTGC	4380
70	CGAGCCCTCT	CTCCGCAAGA	GCCGATCTCT	GGTTTATAGC	GAGGCCACAG	TGCGCATGGA	4440
	CCTGGAGACT	GACAACTCTA	TCCAGGCTAC	CATCCGCACC	CAGTTTGATA	CCTGCACTGT	4500
	CCTGACCATC	GCACACCGGC	TTAAACACTAT	CATGGACTAC	ACCAGGGTCC	TGGTCTCTGA	4560
	CAAAGGAGTA	GTAGCTGAAT	TTGATTCTCC	AGCCAACCTC	ATTGCAGCTA	GAGGCATCTT	4620
	CTACGGGATG	GCCAGAGATG	CTGACTTTCG	CTAAAATATA	TTCCTGAGAT	TTCCTCTCTG	4680
75	CCTTTCTCTG	TTTCTATCAG	GAAGGAAATG	ACACCAATA	TGTCCGAGA	ATGGACTTGA	4740
	TAGCAAAAC	TGGGGGCACC	TTAAGATTTT	GCACCTGTAA	AGTGCCCTTAC	AGGGTAACTG	4800
	TGCTGAATGC	TTTAGATGAG	GAAATGATCC	CCAAGTGGTG	AATGACACGC	CTAAGGTAC	4860
	AGCTAGTTTG	AGCCAGTTAG	ACTAGTCCCC	CGTCTCCCG	ATTCCCAACT	GAGTGTATT	4920
	TGCACACTGC	ACTGTTTCTA	AATAACGATT	TTATGAAATG	ACCTCTGTCC	TCCCTCTGAT	4980
80	TTTTTCATAT	TTCTTAAAGT	TTGTTTCTG	TTTTTAAATA	AAAAGCTTTT	TCTCTCTGGA	5040
	ACAGAAGACA	GCTGCTGGGT	CAGGCCACCC	CTAGGAACCT	AGTCTGTGAC	TCTGGGTGTC	5100
	TGCTGTAATC	CATTAAAAAT	GGGAGTACTG	ATGAATATAA	ACTACATGGT	CAACAGTAAA	5160
	AAAAAAAAAA	AAAAAA					5176

Seq ID NO: C180 DNA Sequence

Nucleic Acid Accession #: NM_004626
Coding sequence: 124..1188

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GGCGTGTGCTATGGCATCAAATGGCTGGCGCTGTCTTCAAGAACCATCGGCCTGGCACTG240
10    AACAGAGCGCAACACTGCAAGCAGCTGGAGCGTCTGTGTGTCTGCACAGGTGCAGCTGTGC300
CGCAGCAACCTGGAGCTCATGCACAGGTGTCACGCGCGCGCGAGGTATGAAGGCC360
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15    TGGCGCCCGCTCCAGGTGAGGCCACCGCGCGCGGAAACCCTGGGAGGATGTGCGGAC600
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25    CCTACACAGACCGCGTGGTGCAGCGGTGCACCTGTAAAGTACCAGTGGTCTGCTACGTC1140
ACCTGCGCGAGGTGTGAGCGTACCGTGGAGCGCTATGTCTGCAAGTGAAGCCCTGCCCTC1200
CGCCCAAGCGAGGAGCGAGGACTCTGCTCAAGGACCCCTCAACACTGGGCGAGGGGCGCT1260
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Seq ID NO: C181 DNA Sequence
Nucleic Acid Accession #: NM_031866
Coding sequence: 6..2090

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50    ACGACACGCAAGACGAGCGCGGGCCCTGGAGGTGCACCAAGTTCTGGCGCGCTGTGGAGATCC240
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60    ACTGCGCGCTGCCCTGCCACAAACCCCTTTTCAGCCAGGAAGAGCGCGCGCTTCAACGCTCT840
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65    GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG1140
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70    TCAGCTCGGTGAGCGCGAGCCCGGTGGCGCGCATCTGCTAATGGGCAACAGAGCCTGG1440
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5 CGCGTTAATT TCTGTTGGCT GAGGAGGGTG GACTCTGCGG CGTTTCCAGA ACCCGAGATT 2400
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 CTCTTTCTG ATCCATGGAT AACCACTCTC ACTTTAGTGG ATGTAAATGG AACTTCTGCA 3120
 15 AGGCAGTAAT TCCCTTAGG CCTTGTATT TATCCTGCAT GGTATCACTA AAGGTTTCAA 3180
 AACCTGAAA AAAA 3195

Seq ID NO: C182 DNA Sequence
 Nucleic Acid Accession #: XM_050625
 Coding sequence: 222..1109

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 GCACCCAGCG AAGAGAGCGG GCCCGGAGCA AGCTCGAAGT CCGGCGCCCT GCGCTTCTCC 180
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 AGCTGTGTAT CACCTCGGTG AAGCGGTGGG AGAAGGGGCA GAGAGAGTTC AAGCGCATCT 1080
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 45 TCCTAGCTGC TCCAGTCTCA GCCTGGGCGG CTTCGCCCTG CCTTTTGCAC GTTTGCAATC 1260
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 TT 1382

Seq ID NO: C183 DNA Sequence
 Nucleic Acid Accession #: NM_001306.1
 Coding sequence: 199..861

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 75 ACCACCCCGT CGAGCCCAT CCGGCCGCTG CCCCCATGTC GCGCTGGGCA GGGACCGGCA 1200
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Seq ID NO: C184 DNA Sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

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 GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180

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AAAGACCTGT GCTTTTGCAT TTGCACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
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CTATTATAGC ATCTCTGACT TTTCTTTACA CTCCTCTGAG GGAAGTAATT CACCCTTAG 360
CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTATCAAC AAAGTCTTGC 420
CAATGGTTTC CATCACTCTC TTGGCATTGG TTACCTGCC AGGTGTGATA GCAGCAATTG 480
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AGATTAGACA TGGTTGGGAA GACGTACCCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
TGTAAGATTA CTGTTTACAC ACAATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
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20 Seq ID NO: C185 DNA Sequence
Nucleic Acid Accession #: NM_001775.1
Coding sequence: 70..972

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GTGCTCGCGG TGGTCTGCCC GAGGTGGCGC CAGACGTGGA GCGGTCCGGG CACCAACCAAG 240
CGCTTTCCCG AGACCCGCTCT GCGCGATGTC GTCAAGTACA CTGAAATTC TCTCGAGATG 300
AGACATGTAG ACTGCCAAGG TGTATGGGAT GCTTTCAAGG GTGCATTTAT TTCAAACAT 360
CCTTGCAACA TTACTGAAGA AGACTATCAG CCACTAATGA AGTTGGGAAC TCAGACCGTA 420
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50 Seq ID NO: C186 DNA Sequence
Nucleic Acid Accession #: XM_120513.2
Coding sequence: 1..2208

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Seq ID NO: C187 DNA Sequence
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Seq ID NO: C188 DNA Sequence

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Coding sequence: 89..1237

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Coding sequence: 1..1401

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Seq ID NO: C190 DNA Sequence
 Nucleic Acid Accession #: XM_054869.2
 Coding sequence: 26..2902

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 Nucleic Acid Accession #: NM_000793.2
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35	TGCTTGTGTT	GGCTCTGGCC	TGGCCTGGTG	GCTGGCCAG	GGGGCAGCAG	TGCTTAGAGC	4560
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	GGAACTCTCC	ATCTAAGATT	TCTTCCAGGG	AATGCCAGCA	ATCAGGCAGC	ACCCAGCTGT	4680
	GGGGGCAGTG	GGTGGGGGA	GACCCACATT	GATGACTTTT	TTTTTTTCTT	TTAATGAAGA	4740
	AACACCAAG	AAAGCTGTGG	AAAGGACCTG	CCCCACATGA	AAAGGATAAG	CCAAGATGGC	4800
40	TGTAACACCA	GAGCAATTTGA	GCTGCCACTC	TTGGAGCACA	TTGATTTTTC	AAAAGCCAGC	4860
	TCGTGCAGGA	AAGGAGGTGC	TGTTATGACA	GCTCTTCCAG	TGGGCAAGA	GGAGGCCCAT	4920
	AATTTCTTCC	ATTGCTAGCT	CATCTGTGGG	ACCAATTGTC	TGTAAGCAAC	CTGTGGCCTG	4980
	CACTTGTGGC	CTCGAAGGAA	GCACAAACCC	TCCATCCACT	TCCCATTTTC	TCTGCCCTTT	5040
	TCCACCTCCC	CCTTCCATCC	CACCACTGTC	CAGTGGCTCC	CAGAAAGCCT	TATTGAGCCC	5100
45	CTTGTGAGCA	CTTGGGGCTG	CGGAGGCCCT	TCCCTACTGG	TCTGGCCCTT	CCTGAGAGGC	5160
	AGGTCTTCCG	TCCTCAGAGC	CTTCTGGAA	CAAGGAGAAT	GCCTGTGCAG	GTGGACACAC	5220
	AGGCCCTGGC	TGTGCTCTTC	ACTTGTCTTC	CAGGGGGAG	CTTCAOGTTG	CCGAGTGGAA	5280
	GAACCATGAC	CTCCACTTGC	TTCCAAAGTG	CTAGGGAAAT	TTACGGGTAC	GCTGGTTCCC	5340
	CTCTCCAGCT	GGAGGCCGAG	TTTCTGGGGA	CTGCAGATT	TTCTACTCTG	TGATCGATTG	5400
50	AATGCCCGAT	GCTTCTGTTT	CATTCCCAGC	CCTTTCTACT	ATGCATTTTC	CTTTTATCAC	5460
	GTGTATTAAG	TTAAATACTG	TGTTATTATC	ACTAAAAAGT	ACATGAACCT	AAGAGACAAC	5520
	TAAGCCCTTC	GTGTTTTTCC	ACAGGTGTTT	AAGCTTCTCT	GTACAGTTGA	AATAAACAGA	5580
	CAGCAAAATG	GTAAAAAAA	AAAAAAAATA	A			5611

Seq ID NO: C193 DNA Sequence
Nucleic Acid Accession #: NM_018646
Coding sequence: 217..2394

	1	11	21	31	41	51	
60	GCTCTGCCAA	GTGTAACAAA	CTCACAGCCC	TCTCCAAACT	GGCTGGGGCT	GCTGGGAGAC	60
	TCCCAAGGAA	CTCGTCAGGA	AGGCAGGAGA	CAGGAGACGG	GACCTCTACA	GGGAGACGGT	120
	GGGCGGGCCC	TTGGGGGGGC	TGATGTGGCC	CCAAGGCTGA	GTCCCGTCAG	GGTCTGGCCT	180
	CGGCTCAGG	CCCCAAGGA	GCCGGCCCTA	CACCCCATGG	GTTTGTCACT	GCCCAAGBAG	240
65	AAAGGGCTAA	TTCTCTGCCT	ATGGAGCAAG	TTCTGCAGAT	GGTTCAGAG	ACGGGAGTCC	300
	TGGGCCAGCA	GCCGAGATGA	GCAGAACCTG	CTGCAGCAGA	AGAGGATCTG	GGAGTCTCCT	360
	CTCTTCTAG	CTGCCAAAGA	TAATGATGTC	CAGGCCCTGA	ACAAGTTGCT	CAAGTATGAG	420
	GATTGCAAGG	TGCACAGAG	AGGAGCCATG	GGGAAACAG	CGCTACACAT	AGCAGCCCTC	480
	TATGACAACC	TGGAGGCCGC	CATGGTGTCT	ATGGAGGCTG	CCCCGAGCTG	GGTCTTTGAG	540
70	CCCATGACAT	CTGAGCTCTA	TGAGGGTCAG	ACTGCACTGC	ACATGCTGTG	TGTGAACAG	600
	AACATGAACT	TGTTGCGAGC	CCTGCTTGCC	CGCAGGGCCA	GTGCTCTGTC	CAGAGCCACA	660
	GGCACTGCCT	TCCGCGTAG	TCCCTGCAAC	CTCATCTACT	TTGGGGAGCA	CCCTTTGTCC	720
	TTTGCTGCCT	GTGTGAACAG	TGAGGAGATC	GTGCGGCTGC	TCAATTGAGCA	TGGAGCTGAC	780
	ATCCGGGGCC	AGGACTCCCT	GGGAAACACA	GTGTTACACA	TCTCATCTCT	CCAGCCCAAC	840
75	AAAACCTTTG	CCTGCCAGAT	GTACAACTGT	TTGCTGTGCT	ACGACAGACA	TGGGGACCAAC	900
	CTGCAGCCCC	TGGAGCTCGT	GCCTAATCAC	CAGGGTCTCA	CCCTTTTCAA	GCTGGCTGGA	960
	GTGAGGGGTA	ACACTGTGAT	GTTCAGCAC	CTGATGCAGA	AGCGGAAGCA	CACCCAGTGG	1020
	ACGTATGGAC	CACGTGACCTC	GACTCTCTAT	GACCTCACAG	AGATCGACTC	CTCAGGGGAT	1080
	GAGCAGTCCC	TGCTGGAATC	TATCATCACC	ACCAAGAAGC	GGGAGGCTCG	CCAGATCTCTG	1140
80	GACCAAGCGC	CGGTGAAGGA	GCTGGTGAGC	CTCAAGTGGA	AGCGGTACGG	GCGGCGGTAC	1200
	TTCTGCATGC	TGGGTGCCAT	ATATCTGCTG	TACATCATCT	GCTTCACCAT	GTGCTGCATC	1260
	TACGCCCCGC	TCAAGCCGAG	GACCAATAAC	CGCACAGGCC	CCCGGACAA	CACCTCTTAA	1320
	CAGCAGAAGC	TACTTCAGGA	AGCCTACATG	ACCCCTAAGG	ACGATATCCG	GCTGGTGGGG	1380
	GAGCTGGTGA	CTGTCAATTG	GGCTATCATC	ATCCTGCTGG	TAGAGGTGCC	AGACATCTTC	1440
	AGAATGGGGG	TCATCGCTTT	CTTTGGACAG	ACCATCCTTG	GGGGCCCATT	CCATGTCTCT	1500

5 ATCATCACCT ATGCGCTTCAT GGTGCTGGTG ACCATGGTGA TGGCGCTCAT CAGTGCCAGC 1560
 GGGGAGGTGG TACCCATGTC CTTTGCACTC GTGCTGGGCT GGTGCAAGCT CATGTACTTC 1620
 GCCCGAGGAT TCCAGATGCT AGGCCCCCTC ACCATCATGA TTCAGAAGAT GATTTTTGGC 1680
 GACCTGATGC GATTCGTGCT GTGATGGCT GTGGTCATCC TGGGCTTGGC TTCAGCCTTC 1740
 TATATCATCT TCCAGACAGA GGACCCCGAG GAGCTAGGCC ACTTCTAGA CTACCCCATG 1800
 GCCCTGTTCG GCACCTTCGA GCTGTTCTT ACCATCATCG ATGCGCCAGC CAACTACAAC 1860
 GTGGACCTGC CCTTCATGTA CAGCATCACC TATGCTGCTT TGGCATCAT OGCCACACTG 1920
 CTCATGCTCA ACCTCCTCAT TGCCATGATG GCGGACACTC ACTGGCGAGT GGCCCATGAG 1980
 CGGGATGAGC TGTGGAGGGC CCAGATTGTG GCCACCAOGG TGATGCTGGA GCGGAAGCTG 2040
 CCTCGCTGCC TGTGGCTCTG CTCGGGGATC TGGCGAOGGG AGTATGGGCT GGGAGACCGC 2100
 TGGTTCTGCG GGGTGGAGA CAGGCAAGAT CTCACCGGC AGCGGATCCA ACGCTACGCA 2160
 CAGGCTTCC ACACCCGGGG CTCTGAGGAT TTGGACAAAG ACTCAGTGA AAAACTAGAG 2220
 CTGGGCTGTC CCTTCAGCCC CCACCTGTCC CTTCTATGTC CCTCAGTGTG TCGAAGTACC 2280
 TCCCGCAGCA GTGCCAATTG GAAAAGGCTT CGGCAAGGGA CCTGAGGAG AGACCTGCGT 2340
 15 GGGATAATCA ACAGGGGTCT GGAGGACGGG GAGAGCTGGG AATATCAGAT CTGACTGCGT 2400
 GTTCTCAGCT CGCTTCTGG AACCTGCTCT CATTTCCTG GGTGCATCA ACAAACAA 2460
 AACCAACAC CCAGAGGTCT CATCTCCAG GCCCCAGGGG AGAAGAGGA GTAGCATGAA 2520
 CGCCAGGAA TGTAGTTGA GAATCACTGC TCCAGGCTG CATTACTCT TCAGCTCTGG 2580
 20 GGCAGAGGAA GCGCCAGCCA AGCAGGGG TGGCAGGGG TGAGGAAGTC TCCTGTGGCC 2640
 TGCTCATCAG CCTTCGACA GGAGCACTGC ATGTGAGAGC ACTTAAAAA CAGGCCAGCC 2700
 TGCTTGGCG CTCGCTCTCC ACCCAGGGT CATAAGTGGG GAGAGAGCCC TTCCAGGGC 2760
 ACCCAGGCA GTGCAAGGAA GTGCAGAGCT TGTGGAAGC GTGTGAGTA GGGAGACAGG 2820
 AACGGCTCTG GGGGTGGGAA GTGGGGCTAG GTCTTGCCA CTCATCTTC AATAAAGTCG 2880
 25 TTTTGGATC CTGAAAAA AAAAAA 2918

Seq ID NO: C194 DNA Sequence
 Nucleic Acid Accession #: NM_021910.1
 Coding sequence: 260..601

30 1 11 21 31 41 51
 GTTCTCCACA ACTGCCAGCA ATCCTTCCAC CAGGCAAAAC ACATCATCTA AGGAAAAGAA 60
 GTGAGGTTTG CTTAGGGCGT GGCAGCTTGG GATAAAGCA GGAATCCGCC TGGCAGCCCG 120
 35 ATTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACA GGCCCGAGTT TCACCCAGTC 180
 CCCACTCCAC GGTGACGCTG CGGCTTATCT CTCAGCCAG CGAGATGCCA GCCTTCTCTG 240
 CCGGGGCGAG CGCTCTGACA TGCAAGAGGT GACCTTGGGC CTGCTTGTGT TCCTGGCAGG 300
 CTTTCTCTGC CTGGACGCA ATGACCTAGA AGATAAAAC AGTCTTCTCT ACTATGACTG 360
 GCACAGCTTC CAGGTTGGCG GGTCTCATCT CGCTGGGTT CTGTGCGCCA TGGGCATCAT 420
 40 CATGCTCATG AGTGAGTGA GAGGCTCGGG GGAGCAGGGG GGCCGGGGCT GGGGCTCCCC 480
 TCCCTGACC ACTCAGCTCT CCCCACAGG TGCAAAATGC AAATGCAAGT TTGGCCAGAA 540
 GTCCGCTCAC CATCCAGGGG AGACTCCACC TCTCATCACC CCGGCTCAG CCCAAGCTG 600
 ATGAGGACAG ACCAGCTGAA ATTGGTGGGA GACCCGTTCT CTGTCCCGAG GTCCGTCTCT 660
 TGCAAGAAA CTTGAAGTCC AGGATGGAAT TCTTCTCTCT CTGCTGGGAC TCCTTTGCT 720
 45 GGCAGGGCTT CATCTCAGCT CTCGCAAGAG GGTCTCTTTG TTCAATTTTT TTTAATCTAA 780
 AATGATTGTG CCTCTGCCA AGCAGCTGG AGACTTCTTA TGTGTGCAAT GGGGTGGGGC 840
 TTGGGCGACC ATGAGAAGGT TGGCGTGGCC TGGAGGCTGA CACAGAGGCT GGCAGTGGC 900
 CTGCTTGTG TGAAAAGCCC ACAGGCTCTG TCCCTTGTGG CTTGGACAT GGCACAGGCC 960
 CGCCCTCTGC CTCTCAGCC ATGGGACCTC ATATGCAATT TGGGATTATC TAGTAGCCAA 1020
 50 AAGGAATGAA AGAGAGCTCT AACCAGATGG AACACTGGAA CATTCCAGTG GACCTGGAC 1080
 CATTCCAGAA AACCTGGGAG ATAGGATCGT CCGGCTATGA TGGAAAGTGT CAGACAGTTT 1140
 ATAATAGTAA GCCCTGTGA CCCTCTCACT TACCCGAGA CCTCACTTA TTACAAGATC 1200
 TTTCCAAATA CCCAAATATC CCTGCAAGCC CGTTAAATAA TTCCCTATGC TACCTTTAAT 1260
 AACATACAT GACCATATAG TGTGAGAACT TCCAAACAGC CTCAAAGTCC CTGAGACTC 1320
 55 CCCAATACCT AATAAGGCA CTGAAATGTT CTCATGAACT ACCCCACAAC ACGCCTAAAA 1380
 CTCAAACAC CCAAAATAT CTCCTCCAAT GTCCTGAGAC ATGAACCCAA AAAGAGACCC 1440
 ACAATAAACT CGTGACTTGT CCCCCTC 1466

Seq ID NO: C195 DNA Sequence
 Nucleic Acid Accession #: NM_005971.2
 Coding sequence: 176..439

60 1 11 21 31 41 51
 GTTCTCCACA ACTGCCAGCA ATCCTTCCAC CAGGCAAAAC ACATCATCTA AGGAAAAGAA 60
 GTGAGGTTTG CTTAGGGCGT GGCAGCTTGG GATAAAGCA GGAATCCGCC TGGCAGCCCG 120
 65 ATTCTCCCG GAACCTCTGC TCAGCCTGGT GAACCAACA GGCCCGAGTT TCACCCAGTC 180
 GAAGGTGACC CTGGGCTCTG TTGTGTTCTT GGCAGGCTTT CTGTCTCTGG ACGCCAAATGA 240
 CCTAGAAGAT AAAAACAGTC CTTTCTACTA TGACTGGCAC AGCTCCAGG TTGGGGGGCT 300
 70 CATCTGCGCT GGGGTTCTGT GGGCCATGGG CATCATCATC GTCATGAGTG CAAAATGCAA 360
 ATGCAAGTTT GGGGTTCTGT CCGGTACCCA TCAGGGGAG ACTCCACCTC TCATCACCCC 420
 AGGCTCAGCC CAAAGCTGAT GAGGACAGAC CAGCTGAAAT TGGTGGAGG ACGCTTCTCT 480
 GTCCCGAGGT CCTGTCTCTG CACAGAAACT TGAATCCAG GATGGAATTC TTCCTCTCT 540
 GCTGGGACTC CTTTGCAATG CAGGCGCTCA TCTCACTCT CGCAAGAGGG TCTCTTTGTT 600
 75 CAATTTTTT TAATCTAAAA TGATGTGGC TCTGCCCCAG CAGCCTGGAG ACTTCTATG 660
 TGTGCAATTG GGTGGGCTT GGGGACCAT GAGAAGGTTG GGTGCCCCG GAGGCTGACA 720
 CAGAGGCTGG CACTGAGCCT GCTTGTGGG AAAAGCCAC AGGCTGTTC CTTGTGGCT 780
 TGGGACATGG CACAGGCCCG CCTCTGCTCT CTTGAGCAT GGGACCTCAT ATGCAATTG 840
 GGATTTACTA GTAGCCAAAA GGAATGAAAG AGAGCTCTAA CCAGATGGAA CACTGGAACA 900
 80 TTCCAGTGA TCCAGGACCA TTCCAGGAAA ACTGGGACAT AGGATCGTCC CGCTATGATG 960
 GAGGTGTTCA GACAGTTTAT AATAGTAAGC CCCTGTGACC CTCTCACTTA CCGGAGAGCC 1020
 TCACTTTATT ACAGATCTTT TCCAAATACC CAAATATCCC TGCAAGCCCG TTAATAATT 1080
 CCTATGCTA CCTTAATAA CATACAATGA CCACATAGTG TGAGAACTTC CAACAAGCCT 1140
 CAAAGTCCCT TGAGACTCCC CAATACCTAA TAAGGCTATG GAAATGTTCT CATGAAGTAC 1200
 CCCACAACAC GCCTAAAACT CAAAACACC AAAAAATCT CTCCAATGT CTGAGACAT 1260

GAACCCAAAA AGAGACCCAC AATAAACTCG TGACTTGTCC CCTC

1304

Seq ID NO: C196 DNA Sequence
Nucleic Acid Accession #: NM_004961.2
Coding sequence: 55..1575

5

1	11	21	31	41	51	
GCCAGAGCGT	GAGCCGCGAC	CTCCGCGCAG	GTGGTGGCGC	CGGTCTCCGC	GGAAATGTTG	60
TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	GGTCGAGGGA	120
CCTCAGACTG	AATCAAAGAA	TGAAGCCTCT	TCCCGTGATG	TTGTCTATGG	CCCCAGCCCC	180
CAGCCTCTGG	AAATCAGCTC	CCTCTCTGAG	GAAACAAAGT	CAACTGAGAC	TGAGACTGGG	240
AGCAGAGTTG	GCAAACTGCC	AGAAGCCTCT	CGCATCCTGA	ACACTATCCT	GAGTAATTAT	300
GACCAACAAC	TGCGCCCTGG	CATTGGAGAG	AAGCCCACTG	TGGTCACTGT	TGAGATCGCC	360
GTCAACAGCC	TTGGTCTCTT	CTCTATCCTA	GACATGGAAT	ACACCATTGA	CATCATCTTC	420
TCCAGACTCT	AGTGGGAGAA	AOCCTCTGTG	TACAACGACA	CCTTTGAGTC	TCCTGTCTCG	480
AATGGCAATG	TGGTGAGCCA	GCTATGGATC	CCGGACACCT	TTTTTAGGAA	TTCTAAGAGG	540
ACCCACGAGC	ATGAGATCAC	CATGCCCAAC	CAGATGGTCC	GCACTACAA	GGATGGCAAG	600
GTGTTGTACA	CAATTAGGAT	GACCATTGAT	GCCTGATGCT	CACCTCCACT	GCTCAGATTT	660
CCAATGGATT	CTCCTCTTTG	CCCTCTATCT	TTCTCTAGCT	TTTCTTATCC	TGAGAATGAG	720
ATGATCTACA	AGTGGGAGAA	TTTCAAGCTT	GAAATCAATG	AGAAGAACTC	CTGGAAGCTC	780
TTCCAGTTTG	ATTTTACAGG	AGTGAGCAAC	AAACTGAAA	TAATCACAAC	CCCAGTTGGT	840
GACTTCATGG	TCAATGACAT	TTTCTTCAAT	GTGAGCAGGC	GGTTTGGCTA	TGTTGCCCTT	900
CAAAACTATG	TCCCTTCTTC	CGTGACCAAG	ATGCTCTCCT	GGGTTTCTCT	TTGGATCAAG	960
ACAGAGTCTG	CTCCAGCCCG	GACCTCTCTA	GGGATCACCT	CTGTTCTGAC	CATGACCAAG	1020
TTGGGCACTT	TTTCTGTGTA	GAATTTCCCG	CGTGTCTCCT	ATATCACAGC	CTTGGATTTC	1080
TATATGCCCA	TCGTCTCTGT	CTTCTGCTTC	TGCGCTCTGT	TGGAGTTTGC	TGTGCTCAAC	1140
TTCTGTATCT	ACAAACAGAG	AAAAGCCCAT	GCTTCTCTTA	AACTCCGCCA	TCCTCGTATC	1200
AATAGCCCTG	CCCATGCCCG	TACCCGTGCA	CGTTCCCGAG	CCTGTGCCCG	CCAACATCAG	1260
GAAGCTTTTG	TGTGCCAGAT	TGTCAACACT	GAGGGAAGTG	ATGAGAGGGA	CGCCCCGTCT	1320
TGCTCAGCCC	AGCAGCCCCC	TAGCCAGGTT	AGCCCTGAGG	GTCCCGCAGC	CCTCTGCTCC	1380
AAGCTGGCCT	CGTGTGAGTG	GTGCAAGOGT	TTTAAGAAGT	ACTTCTGCAT	GGTCCCGGAT	1440
TGTGAGGGCA	GTACCTGGCA	GCAGGGCCGC	CTCTGCATCC	ATGCTTACCG	CCTGGATAAC	1500
TACTCGAGAG	TTGTTTCCCG	AGTGACTTTC	TTCTTCTTCA	ATGTCCTCTA	CTGGCTTGTT	1560
TGCCCTTAAT	TGTAGGTACC	AGCTGGTACC	CTGTGGGGCA	ACCTCTCCAG	TTCCCCAGGA	1620
GGTCCAGGCC	CCTTGCCAAAG	GGAGTTGGGG	GAAAGCAGCA	GCAGCAGCAG	GAGCGACTAG	1680
AGTTTTTCTC	GCCCCATTCC	CCAAACAGAA	GCTTGCAGAG	GGTTTGTCTT	TGTCGCCCTT	1740
CTCCCTTACC	TGGCCCATTC	ACTGAGTCTT	CTCAGCAGAC	CATTTCAAAT	TATTAATAAA	1800
TGGGCCAOCCT	CCCTCTTCTT	CAAGGAGCAT	COGTGATGCT	CAGTGTTCAA	AACCACAGCC	1860
ACTTAGTGAT	CAGCTCCCTA	AAACCATGCC	TAAGTACAGG	CGGATTAGCT	ATCTTCCAAC	1920
AATGCTGATC	ACCAGACAAT	TACTGCATTT	TTCCAGAAGC	CCACTATTGC	CTTTGTAGTG	1980
CTTTGGGCCC	AGTTCTGGCC	TCAGCCTCAA	AGTGCAACCA	CTAGTTGCTT	GCCTATACCT	2040
GGCACCCTAT	TAAGATGCTG	GGCAGCAGTA	TAACAGGAGG	AAGAGATCCC	TCTCCTTTGG	2100
TCAGATTATT	ATGTTCTCTG	TTCTCTCTCC	CTGCTACCCC	TTTCTCTGCA	GATAGATAGA	2160
CACCTGGCAT	ATCCCTTTAG	GAAGAGGGGG	GGGCAGCAAG	AGAGCCTATT	TGGGACAGCA	2220
TTCTCTCTCT	TCCTGCTCTG	TGACATCTCC	CTCTCCTTGC	TGGCTCCATC	TTTGTCTGTC	2280
ACTACCAATT	CAATGCCCTT	CATCCAATGG	GTATCTATTT	TTGTGTGTGA	TTATAGTAAC	2340
TACTCCCTGC	TTTATATGCC	ACCCCTCTTC	TTCTCTTTGA	CCCCGTGAC	TCCTTCTGTA	2400
ACTTTCCAGT	TGACTTCCCC	TAGCCCTGAC	CCAGGCACCTA	GGCCTTGGTG	ACTTCTCGGG	2460
GCCAGAGAAC	TAAGGAAACT	CGGCTTTGCA	ACAGGCATTA	CTGCCCATTG	ATTGGTGGCC	2520
ACCCAGGGCA	AACTGTGGGA	GTCTATCAC	TTGCTTGACC	CCTGGACCCA	TAAACCAAGT	2580
CACGTGTATA	CCCGGGGCAC	TCTAACCATC	ACAATCAATC	AATCAAATTC	CCTTAAATTT	2640
GTATGGCAGT	GGAACTTTGG	CAAGACACTT	TTGACAAGTT	GTGTCTGATT	GGAGCTTCAT	2700
GATAGCCTTG	TGACATCTTT	AGGGCAGGAT	TCCTTATCCC	ATTTTGACAG	TGAAACCCCT	2760
GAGTCAAGAA	TTTCTGTGGG	ACTGTGGATC	TCACTGGAAG	CTATCCAAGA	GCCCACTGTC	2820
ACCTTCTAGA	CCACATGATA	GGGCTAGACA	GCTCAGTTCA	CCATGATTCT	CTTCTGTCTC	2880
CTCTGCTGGC	ACACCAAGTG	CAAGGCCCAAG	AATGGGCAAC	TCTCTTTAGC	TCAATTTCTG	2940
GGCCTGAGGT	GCTCAGACTG	CCCCCAAGAT	CAATCTCTCT	CTGGCTGTAG	TAACCCAGTG	3000
GAATGAATTT	GGACATGCCC	CAATGCTTCT	ATATGCTAAG	TGAAATCTGT	GCTGTGAATT	3060
TGTTGGGGGG	TGGATAGGGT	GGGGTCTCCA	TCTACTTTTT	GTCAACATCA	TCTGAAATGG	3120
GGAAATATGT	AAATAATAT	ATCAGCAAGG	CAAAAAGAAA	AAAAAAA		3168

Seq ID NO: C197 DNA Sequence
Nucleic Acid Accession #: NM_021984.1
Coding sequence: 572..1753

65

1	11	21	31	41	51	
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TCCAAAGTTC	TTCCAGTCCT	CCTAGGCATC	TTATTGATCC	TCCAGTCGAG	AACATGTATA	120
CAGAGAAGTG	CTCAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAT	GACCAAGCGG	180
GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAA	CCOCTTTGTT	240
CAGTGCCTCC	CAGCAAAAGG	AGCACTATCC	GGACTTCTAA	CACCATCGGG	TGGAGGGACC	300
TCAGACTGAA	TCAAGAAATG	AAGCCTCTTC	CCGTGATGTT	GTCTATGGCC	CCCAAGCCCA	360
GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AAACAAGTCA	ACTGAGACTG	AGACTGGGAG	420
CAGAGTTGGC	AAACTGGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCTTGA	GTAATTATGA	480
CCACAAACTG	CGCCCTGGCA	TTGGAGAGAA	GCCCACTGTG	GTCACTGTGG	AGATCTCCGT	540
CAACAGCCTT	GGTCTCTCTT	CTATCTCTAGA	CATGGAATAC	ACCATGTACA	TCATCTTCTC	600
CCAGACCTGG	TACGACGAA	GCCTCTGTTA	CAACGACACC	TTTGAGTCTC	TTGTCTGTAA	660
TGGCAATGTG	GTGAGCCAGC	TATGGATCCC	GGACACCTTT	TTTAGGAATT	CTAAGAGGAC	720
CCAAGAGCAT	GAGATCAACA	TGCCCAACCA	GATGGTCCGC	ATCTACAAGG	ATGGCAAGGT	780
GTTGTACACA	ATTAGGATGA	CCATTGATGC	CGGATGCTCA	CTCCACATGC	TCAGATTTCC	840
AATGGATTCT	CACCTCTGCC	CTCTATCTTT	CTCTAGCTTT	TCTATCTCTG	AGAATGAGAT	900
GATCTACAAG	TGGGAAAATT	TCAAGCTTGA	AATCAATGAG	AAGAAGCTCT	GGAGCTCTT	960

	CCAGTTGGAT	TTTACAGGAG	TGAGCAACAA	AACGTAAATA	ATCACAACCC	CAGTTGGTGA	1020
	CTTCATGTC	ATGACGATT	TCTTCAATGT	GAGCAGGCG	TTTGGCTATG	TTGCCTTTCA	1080
	AAACTATGTC	CCTTCTCCG	TGACCAAGAT	GCTCTCTGG	GTTCCTTTT	GGATCAAGAC	1140
5	AGAGTCTGCT	CCAGCCCGGA	CCTCTCTAGG	GATCACTCT	GTCTGACCA	TGACCAAGTT	1200
	GGGACCTTT	TCTGTAAGA	ATTCCCGCG	TGCTCTCTAT	ATCAGAGCCT	TGGATTCTTA	1260
	TATCGCCATC	TGCTTGTCT	TCTGCTTCTG	CGCTCTGTTG	GAGTTTGGCTG	TGCTCAACTT	1320
	CCTGATCTAC	AACCAAGCAA	AAGCCCATGC	TTCTCTTAAA	CTCCGCCATC	CTGATATCAA	1380
	TAGCCGTGCC	CATGCCCGTA	CCCGTGCAAG	TTCCCGAGCC	TGTGCCCGCC	AACATCAGGA	1440
10	AGCTTTTGTG	TGCCAGATTG	TCACCACTGA	GGGAAGTGAT	GGAGAGGAGC	GCCCGTCTTG	1500
	CTCAGCCGAC	CAGCCCCCTA	CCCCAGGTAG	CCCTGAGGGT	CCCCGAGCC	TCTGCTCCAA	1560
	GCTGGCCTGC	TGTGAGTGGT	GCAAGCGTTT	TAAGAAGTAC	TTCTGCAATG	TCCCGAGTTG	1620
	TGAGGGCAGT	ACCTGGCAGC	AGGCCCGCCT	CTGCATCCAT	GTCTACCGCC	TGGATAACTA	1680
	CTCGAGAGTT	GTTCCTCCAG	TGACTTCTCT	CTTCTTCAAT	GTGCTCTACT	GGCTTGTGTT	1740
15	CCTTAACTTG	TAGGTACCCG	CTGCTACCC	GTGGGGCAAC	CTCTCCAGTT	CCCCAGGAGG	1800
	TCCAAAGCCC	TTGCCAAGGG	AGTTGGGGGA	AAGCAGCAGC	AGCAGCAGGA	GCGACTAGAG	1860
	TTTTTCTGTC	CCCATCTCCC	AAACAGAAAG	TTGCAGAGGG	TTTGTCTTTG	CTGCCCTCTT	1920
	CCCTTACCTG	GCCCATTCAC	TGAGTTTCT	CAGCAGACCA	TTTCAAATTA	TTAATAAATG	1980
	GGCCACCTCC	CTCTTCTTCA	AGGAGCATCC	GTGATGCTCA	GTGTTCAAAA	CCACAGCCAC	2040
20	TTAGTGATTA	GCTCCCTAAA	ACCATGCCCTA	AGTACAGGCG	GATTAGCTAT	CTTCCAACAA	2100
	TGCTGACCA	CAGACAATTA	CTGCATTTT	CCAGAAGCCC	ACTATTGCC	TTGCAAGTGT	2160
	TTGGGCCAG	TGTGGCCTC	AGCCTCAAAG	TGCACCGACT	AGTTGCTTGC	CTATACTGCT	2220
	CACCTCATTA	AGATGCTGGG	CAGCAGTATA	ACAGGAGGAA	GAGATCCCTC	TCCTTTGGTC	2280
	AGATTATTAT	GTCTCAGTT	CTCTCTCCCT	GCTACCCCTT	TCTCTGCGA	TAGATAGACA	2340
25	CTGGCAATTAT	CCCTTTAGGA	AGAGGGGGGG	GCAGCAAGAG	AGCCTATTG	GGACAGCATT	2400
	CTCTCTCTC	TGCTGCTGTG	ACATCTCCCT	CTCCTTGCTG	GCTCCATCTT	TGCTCTGCAC	2460
	TACCAATTCA	ATGCCCTTCA	TCCAATGGGT	ATCTATTTT	TGTGTGATT	ATAGTAACCTA	2520
	CTCCCTGCTT	TATATGCCAC	CCTCTTCCCT	CTCTTTGACC	CCTGTGACTC	TTTCTGTAA	2580
	TTTCCCAAGT	ACTTCCCTTA	GCCCTGACCC	AGGCACTAGG	CCTTGGTGAC	TTCTTGGGGC	2640
30	CAAGAACTA	AGGAACTCG	GCTTTGCAAC	AGGCATTACT	CGCCATTGAT	TGGTGGCCAC	2700
	CCAGGGCACA	CTGTCCGAGT	TCTATCACTT	GCTTGACCCC	TGGACCCATA	AACCAAGTCA	2760
	CTGTTATACC	CGGGGCACTC	TAACCATCAC	AATCAATCAA	TCAAATTCCC	TTAATTGTGT	2820
	ATGGCACTGG	AACTTTGCCA	AAGCACTTTT	GACAAATGTT	GTCTGATTGG	AGCTTCATGA	2880
	TAGCCTTTGT	ACATCTTTAG	GGCAGGATTC	TTATCCCAT	TTTGCAAGT	AAAACCTTGA	2940
35	GTACAGATT	TCTGTGGGAC	TGTGGATCTC	ACTGGAAGCT	ATCCAAGAGC	CCACTGTGAC	3000
	CTTCTAGACC	ACATGATAGG	GCTAGACAGC	TCAATTACCC	ATGATTCTCT	TCTGTCACTT	3060
	CTGCTGGCAC	ACCAAGTGGCA	AGGCCAGGAA	TGGCGACCTC	TCTTTAGCTC	AATTTCTGGG	3120
	CCTGAGGTGC	TCAGACTGCC	CCCAAGATCA	AATCTCTCCT	GGCTGTAGTA	ACCAAGTGGG	3180
	ATGAATTTGG	ACATGCCCTCA	ATGCTTCTAT	ATGCTAAGTG	AAATCTGTGT	CTGTAATTTG	3240
40	TTGGGGGGTG	GATAGGGTGG	GGTCTCCATC	TACTTTTGT	CACCATCATC	TGAAATGGGG	3300
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Seq ID NO: C198 DNA Sequence
Nucleic Acid Accession #: NM_021987.1
Coding sequence: 572..1657

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50	CAGAGAAGTG	CTCAATCAT	AGTGTACAG	CTGATGAGTT	GTCAAAATAT	GACCAAGCGG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAA	CCCCCTTTGT	240
	CACGTGCTCC	CAGCAAGGCG	AGCACTATCC	GGACTTCTAA	CACCATCCGG	TGAGGGGACC	300
	TCAGACTGAA	TCAAGAAATG	AAGCCCTCTC	CGGTGATGTT	GTCTATGGCC	CCCCAGCCCA	360
	GCCTCTGGAA	AATCAGCTCC	TCTCTGAGGA	AACAAAGTCA	ACTGAGACTG	AGACTGGGAG	420
55	CAGAGTTGGC	AAACTGCCAG	AAGCCTCTCG	CATCCTGAAC	ACTATCCTGA	GTAATTATGA	480
	CCACAACTG	CGCCCTGGCA	TTGGAGAGAA	GCACCTGTG	GTCACTGTG	AGATCTCCGT	540
	CAACAGCCCT	GGTCTCTCT	CTATCCTAGA	CATGGAATAC	ACCATGTACA	TCATCTTCTC	600
	CCAGACCTGG	AATTCATAGA	GGACCCAGCA	GCATGAGATC	ACCATGCCCA	ACCAGATGGT	660
60	CCGACCTTAC	AAGGATGGCA	AGGTGTTGTA	CACAAATTAG	ATGAACATTT	ATGCCGATG	720
	CTCACTCCAC	ATGCTCAGAT	TTCCAAATGA	TTCTCACTCT	TGCCCTCTAT	CTTCTCTAG	780
	CTTTTCTTAT	CCTGAGAAAT	AGATGATCTA	CAAGTGGGAA	AATTTCAAGC	TTGAAATCAA	840
	TGAGAGAGAC	TCTTGGAAAG	TCTTCCAGTT	TGATTTTACA	GGAGTGAGCA	ACAAATCTGA	900
	AATAATCACA	ACCCCAAGTT	GTGACTTCAT	GGTCATGAGC	ATTTTCTTCA	ATGTGAGCAG	960
65	GCGGTTTGGC	CGCCTTGGCT	TTCAAAACTA	TGTCCCTTCT	TCCGTGACCA	CGATGCTCTC	1020
	CTGGGTTTCC	TTTGGATCA	AGACAGAGTC	TGCTCCAGCC	CGGACCTCTC	TAGGGATCAC	1080
	CTCTGTTCTG	ACCATGACCA	CGTTGGGCAC	CTTTTCTOGT	AAGAATTTCC	CGGTGTCTC	1140
	CTATATCACA	GCTTGGGATT	TCTATATCGC	CATCTGCTTC	GTCTTCTGCT	TCTGCGCTCT	1200
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70	TAAACTCCGC	GCCTCTCGTA	TCAATAGCCG	TGCCCATGCC	CGTACCCGTC	CAGGTTCCCG	1320
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75	CCATGTCTAC	CGCCTGGGTA	ACTACTCGAG	AGTTGTTTTC	CCAGTGACTT	TCTTCTTCTT	1620
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	GGAAGAGATC	CCTCTCCTTT	GGTCAGATTA	TTATGTTCTC	AGTTCTCTCT	CCCTGCTACC	2220

	CCTTTCTCTG	CAGATAGATA	GACACTGGCA	TTATCCCTTT	AGGAAGAGGG	GGGGGCGACA	2280
	AGAGAGCCTA	TTTGGGACAG	CAITCCTCTC	TCTCTGCTGC	TGTGACATCT	CCCTCTCCTT	2340
	GCTGGCTCCA	TCCTTGTCTC	GCACATACAA	TTCAATGCCC	TTCAATCCAAT	GGGTATCTAT	2400
5	TTTTGTGTGT	GATTATAGTA	ACTACTCCCT	GCTTTATATG	CCACCTCTCT	CCTTCTCTTT	2460
	GACCCCTGTG	ACTCTTCTGT	TAACCTTCCC	AGTGACTTCC	CCTAGCCCTG	ACCAGGCATC	2520
	AGGCCTTGGT	GACTTCTCTG	GGCCAGAAAG	CTAAGGAAAC	TGGCTTTTGC	AACAGGCATT	2580
	ACTGCGCAAT	GATTGGTGCC	CACCCAGGGC	ACACTGTCCG	AGTTCTATCA	CTTGCTTGAC	2640
	CCCTGGACCC	ATAAACCGAT	CCACTGTAT	ACCCGGGGCA	CTCTAAOCAT	CACAATCAAT	2700
10	CAATCAAATT	CCCTTAAATT	TGTATGGCAC	TGGAACCTTG	GCAAAGCACT	TTTGACAAAT	2760
	TGTGTCTGAT	TGGAGCTTCA	TGATAGCCTT	GTGACATCTT	TAGGGCAGGA	TTCTTATCCC	2820
	CAITTTGTCAG	ATGAAACCCC	TGAGTCACAG	ATTTCTGTGG	GACTGTGGAT	CTCACTGGAA	2880
	GCTATCCAAG	AGCCCACTGT	CACCTTCTAG	ACCACATGAT	AGGGCTAGAC	AGCTCAGTTC	2940
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15	CTCTCTTTAG	CTCAATTCTT	GGGCTTGAGG	TGCTCAGACT	GCCCCCAAGA	TCAATCTCT	3060
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20	Seq ID NO: C199 DNA Sequence Nucleic Acid Accession #: NM_021990.1 Coding sequence: 1309..2490						
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	CAGAGAAGTG	CTCAAAATCAT	AAGTGTACAG	CTGATGAGTT	GTCAAAAAT	GACCACAGCG	180
	GTGTAAAGAA	AGCCAAATCA	AGGACCCGAA	TGTGAGCAGG	ACCTCAGAG	CCCCCTTGT	240
30	CACCTGCCTCC	GACCAAAAGC	AGCACTATCC	GGACTTCTAA	CACCATCGGT	GAGTTTCATA	300
	CCTTGGCAGA	TGGCCTTTAA	CAITTTTGT	TAATTCAATT	ATCTTACTA	ATCTTCTTCT	360
	TTTTCTTGGC	TGTGTGTGAG	GGCTGTGGAG	CTCAGGGTGG	ACTCCTGTG	GGCAGCCAGT	420
	TCTGGATGG	CTGTCTGTGG	GTGGAGGACT	CCTGCCCTTC	CTGTTTAGAC	ACCCACAAAG	480
	GCTGCTCTTT	AGCCTCCTTC	CCTTCATCCC	CTTCCCCTGC	CCCCAGTGCA	ACGAGTATTA	540
35	CACAACCAAC	AAAACCGCAA	AATATTCCCA	CAATTTTCTG	GTCTCTCTCG	GGAGAGGCCG	600
	CTCTGGCTTT	TCTCTCTCAG	CCTGGCCCTC	TGCTGTCTCC	TCACCTCTGG	TTGGTGTCTG	660
	TCAGGCTGAC	TAGAGGCCAA	GGCGACCAAC	ACTAGGCAAA	CGCGGCCAGC	GCTCAGACAT	720
	AAATGCCCTC	TTCAITTCAC	GTGTAACATT	CTTTTAAAT	CTAGGTCTTG	GTITTTGTGA	780
	TTTTTTCTTA	AATAAAGAG	TGATCATAAA	AGAGGGACAG	CATAGAAAGT	CCCCAAGAG	840
40	CAGCAAGGTT	TTAAAGAAAT	TCACAAGCCT	AATCTGTAC	TGCTTTATAA	TTTGCTATTA	900
	CCAGTCACAA	TTTAACTAGG	TTTTGTGTGG	AAAACCTGTT	TTGGTTTGCT	TCTGTCCCAA	960
	GAGGCACTAG	CTGGGGCCCC	TACAGAGTGC	AGGGCAGAGC	TTCAITTTTC	GTITGAAATG	1020
	TCTAGGGTCG	AGGGACCTCA	GACTGAATCA	AAGAATGAAG	CCTCTCCCG	TGATGTTGTC	1080
	TATGGCCCCC	AGCCCCAGCC	TCTGGAAAAT	CAGCTCCTCT	CTGAGGAAAC	AAAGTCAACT	1140
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	ACTGTTGAGC	TCTCCGTCAA	CAGCCTTGGT	CCTCTCTCTA	TCCTAGACAT	GGAAATACAC	1320
	ATTGACATCA	TCTTCTCCCA	GACCTGGTAC	GACGAACGCC	TCTGTTACAA	CGACACCTTT	1380
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	TACAAGGATG	GCAAGGTGTT	GTACACAATT	AGGATGACCA	TTGATGCCGG	ATGCTCACTC	1560
	CACATGCTCA	GATTTCCAAT	GGATTCTCAC	TCTTGGCCTC	TATCTTTTCT	TAGCTTTTCC	1620
	TATCCTGAGA	ATGAGATGAT	CTACAAGTGG	GAAAATTCTA	AGCTTGAAT	CAATGAGAAG	1680
	AACCTCTGGA	AGCTCTTCCA	GTTTGATTTT	ACAGGAGTGA	GCAACAAAAC	TGAATAATC	1740
55	ACAAACCCAG	TTGGTGACTT	CATGTTCTAT	ACGATTTTCT	TCAATGTGAG	CAGGCGGTTT	1800
	GGCTATGTGG	CCCTTCAAAA	CTATGTCCCT	TCTTCCGTGA	CCACGATGCT	CTCCTGGGTT	1860
	TCCTTTTGA	TCAAGACAGA	GTCTGCTCCA	GCCCGGACCT	CTCTAGGGAT	CACCTCTGTT	1920
	CTGACCATGA	CCAGTGTGGG	CACCTTTTCT	CGTAAGAATT	TCCCCTGTGT	CTCCTATATC	1980
	ACAGCCTTGG	ATTTCTATAT	CGCCATCTGC	TTGCTCTTCT	GCTTCTGCGC	TCTGTTGGAG	2040
60	TTTGTGTGTC	TCAACTTCCCT	GATCTACAAC	CAGACAAAAG	CCCATGCTTC	TCCTAAACTC	2100
	GGCCATCCTC	GTATCAATAG	CCGTGCCCAT	GCCCGTACCC	GTGCACTGTC	CCGAGCCTGT	2160
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65	TACCGCTCTG	ATAACTACTC	GAGAGTTGTT	TTCCAGTGA	CTTCTCTCT	CTTCAATGTG	2460
	CTCTACTGGC	TGTTTGGCTT	TAACTGTAG	GTACCACTG	GTACCTGTG	GGGCAACCTC	2520
	TCCAGTTCCT	CAGGAGGTCC	AAGCCCTTGG	CCAAGGAGT	TGGGGGAAAG	CAGCAGCAGC	2580
	AGCAGGAGCG	ACTAGAGTTT	TTCTGCCCCC	ATTCCCCCAA	CAGAAGCTTG	CAGAGGGTTT	2640
70	GTCTTTGCTG	CCCCCTCCTC	CTAOCCTGCC	CATTCACTGA	GTITTTCTCAG	CAGACCATTT	2700
	CAAAATATTA	ATAAATGGGC	CACCTCCCTC	TTCTTCAAGG	AGCATCCGTG	ATGCTCAGTG	2760
	TTCAAAACCA	CAGCCACTTA	GTGATCAGCT	CCCTAAAACC	ATGCCTAAGT	ACAGGCGGAT	2820
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	ATTGCCTTTG	CAGTGTCTTC	GGCCAGTTC	TGGCCTCAGC	CTCAAGATGC	ACCACTAGT	2940
75	TGCTTGCTTA	TACCTGGCAC	CTCATTAAAG	TGCTGGGCAG	CAGTATAACA	GGAGGAAGAG	3000
	ATCCCTCTCC	TTTGGTCAGA	TTAATTATGT	CTCAGTCTCT	TCTCCCTGCT	ACCCCTTTCT	3060
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80	TGTGATTATA	GTAACACTCT	CCTGCTTTAT	ATGCCACCTT	CTTCCCTCTC	TTTGAACCTC	3300
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Seq ID NO: C200 DNA Sequence
Nucleic Acid Accession #: NM_021819.1
Coding sequence: 39..1619

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Seq ID NO: C201 DNA Sequence
Nucleic Acid Accession #: XM_117036.1
Coding sequence: 25..495

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Seq ID NO: C202 DNA Sequence
Nucleic Acid Accession #: XM_167803.2
Coding sequence: 1162..1488

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5 GAGCCTTGCC ACCATCCAG GACTTTGGGC AAGTCACCG CACTCCCTGG GCCTCGGTTT 780
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Seq ID NO: C203 DNA Sequence

Nucleic Acid Accession #: NM_024780.1

Coding sequence: 31..1023

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Seq ID NO: C204 Protein Sequence

Protein Accession #: Eos sequence

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 70 TGGAGAGAAA AAGGAACCTT AGGAAATAG TTGACAAAGA AAAAGCAAA CAGACCCATC 660
 GTATCCTTCA GCTCAATTGC TGTATTCACT GTCTGAACTC CATTTCCCGG GCTTATCGGA 720
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 75 TTACCGTGGC CAAAAGAAC ACCCTCCAGT TCACTGGGCT GAGGTTTTTC ACTGGGGTGG 960
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	TCCTTCTGAT	GGATTCTGTG	TTCTCTTTAG	TCAATTCTCT	CCTGGGGGAG	TTTCTGAGGA	1740
	GAATCATTGG	GATGCAACTG	ATCACAAGTC	TTGGCCTTCA	GGAGTTTGAC	ATTGCCAGGA	1800
	ACGTTCTAGA	ACTGATCTAT	GCACAACTC	TGGTGTGGAT	TGGCATCTTC	TTCTGCCCC	1860
	TGCTGCCCTT	TATCCAAATG	ATTATGCTTT	TCATCATGTT	CTACTCCAAA	AATATCAGCC	1920
	TGATGATGAA	TTTCAGCCCT	COGAGCAAAG	CCTGGCGGGC	CTCAGAGATG	ATGACTTTCT	1980
	TCATCTTCTT	GCTCTTTTTC	CCATCCTTCA	CCGGGCTCTT	GTGCACCCCTG	GCCATCACCA	2040
10	TCTGGAGATT	GAAGCCTTCA	GCTGACTGTG	GCCCTTTTCG	AGGTCTGCCT	CTCTTCATTC	2100
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15	TGGAGCAACA	AGGCTTTTTC	CATTTGGGGG	AACATGATGG	CAGTCTTGAC	TTGCGATCTA	2460
	GAAGATCAGT	TCAGGAAGGT	AATCCAAGGG	CCTGATGACT	CTTTTGGTAA	CCAGACACCA	2520
	ATCAAATAAG	GGGAGGAGAY	GAAATGGAA	TGATTTCTTC	CATGCCACCT	GTGCCCTTAG	2580
	GAACGTGCCC	GAAGAAATCT	CAAGGCTTTA	GCCAGGAGCG	GAAACTGACT	ACCATGTAAT	2640
	TATCAAAGTA	AAATTGGGCA	TTCCATGCTA	TTTTAATAC	CTGGATTGCT	GATTTTTCAA	2700
20	GACAAATATC	TTGGGGTTTT	CCAATAAAGA	TTGTGTGAAT	ATTGAAANRA	RMMWAMAAA	2760
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	GATTGGTTCT	TAGAAATCTC	TCCTGCCAGA	CTTCCAGAGC	CTGGCAAAGG	TTTAGAAACT	2880
	GTGTCTAAGA	AAAGTGGTCC	ATCCTGAATA	AACATGTAAT	ACTCCAGCAG	GGATATGAAG	2940
	CCTCTGAATT	GTAGAACCCTG	CATTTATTTC	TGACTTTGAA	CTAAAGACAT	CCCCCATGTC	3000
25	CCAAAGGTGG	ARTACAACCA	GAGGTCTCAT	CTCTGAACCT	TCTTGGGTAC	TGATTACATG	3060
	AGTCTTTTGA	GTCCGGGATG	GAGGAGGTTT	TGCCCTGTG	AGGTGTTATA	CATGACCATC	3120
	AAAGTCTTAC	GTCAAGCTAG	CTTTGCAGTG	GCAATACCGT	AGCCAATGAG	ATTATCCGCA	3180
	GACGCGATTA	TGCTTAATTC	GAAATTTTCC	CAATACCCCA	CCGTGATGAC	TTGAAATATA	3240
30	ATCAGCGCTG	GCAATTTTTG	ACAGTCTCTA	CGGAGACTGA	ATAAG		3285

Seq ID NO: C205 DNA Sequence
Nucleic Acid Accession #: NM_002250.1
Coding sequence: 397..1680

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40	CTTGCTCTGC	CCCAAGACAC	ACCCTAGCCC	CTCCTTATTC	TCAAAAGGGG	GAGCTGGGGA	180
	GCCTCCCTCT	ACCCTGGGGC	CTCCCTGCCC	CCTCCCGGCC	CTGCCTGGCC	GTCAACCACTC	240
	CCCAAGAGGG	ACAGGGCTCT	GCTGTGCCCT	AGAGCAAAGG	TCCCAAGACC	AGCAGAGCAG	300
	CTGTAGCAGC	TGCAAGCCAC	AGTGGCTGCC	CTGTGCGTGC	TGCGAGGTGG	GGGACCCCTG	360
	GCAGGAAGCT	GGCTGAGCCC	CAAGACCCCG	GGGGCCATGG	GCGGGGATCT	GGTGCTTGGC	420
45	CTGGGGGCTT	TGAGACGCCG	AAAGCGCTTG	CTGGAGCAGG	AGAAGTCTCT	GGCGGCTGCG	480
	GCACTGGTGC	TGGCAGGAAC	TGGCATTTGA	CTCATGTGTC	TGCATGCAGA	GATGCTGTGG	540
	TTGGGGGGGT	GCTCGTGGGC	GCTCTACCTG	TTCTGCTTAA	AATGCACGAT	CAGCAATTTCC	600
	ACCTTCTTAC	TCCTCTGCCT	CATCGTGGCC	TTTCATGCCA	AAGAGGTCCA	GCTGTTTCAT	660
	ACCGACAACG	GGCTGCGGGA	CTGGCGCGTG	GCGCTGACCG	GCGCGCAGGC	GCGCGCAGATC	720
50	GTGTGGAGC	TGTTGTGTGT	TGGGCTGCAC	CCGGGGCCCG	TGCGGGGGCC	GCCGTGCGTG	780
	CAGGATTTAG	GGGCGCGCGT	GACCTCCCGG	CAGCCCTGGC	CGGGATTCTC	GGGCCAAGGG	840
	GAAGCGCTGC	TGTCCCTGGC	CATGCTGCTG	CGTCTCTACC	TGGTGCCCGG	GCGCGTGCTC	900
	CTGGCGAGCG	GCGTCTGTCT	CAACGCTTCC	TACCGCAGCA	TGGCGCTCTC	CAATCAAGTC	960
	CGCTTCCGCC	ACTGGTTCGT	GGCCAGCTTT	TACATGAACA	CGCACCCCTG	CGCCTGCTTG	1020
55	CTGGGCTTCA	CGCTTGGCCT	CTGGCTGACC	ACCGCCTGGG	TGCTGTCCGT	GGCCGAGAGG	1080
	CAGGCTGTTA	ATGCCACTGG	GCACCTTTCA	GACACACTTT	GGCTGATCCC	CATCACATTC	1140
	CTGACCATCG	GCTATGGTGA	CGTGGTGGCG	GGCACCATGT	GGGGCAAGAT	CGTCTGCGTG	1200
	TGCACTGGAG	TCAATGGGTG	CTGCTGCACA	GCCCTGTCTG	TGGCGGTGGT	GGCCCGGAAG	1260
	CTGGAGTTTA	ACAAGGCAGA	GAAGCACTG	CACAACTTCA	TGATGGATAT	CCAGTATACC	1320
60	AAAGAGATGA	AGGAGTCCCG	TGCCCGAGTG	CTACAAGAA	CCTGGATGTT	CTACAAACAT	1380
	ACTCGCAGGA	AGGAGTCTCA	TGCTGGCCCG	AGGCATCAGC	GCAAGCTGCT	GGCCGCCATC	1440
	AACGCGTTCC	GCCAGGTGCG	GCTGAAACAC	CGGAAGCTCC	GGGAACAAGT	GAACTCCATG	1500
	GTGGACATCT	CCAAGATGCA	CATGATCTGT	TATGACCTGC	AGCAGAATCT	GAGCAGCTCA	1560
	CACCGGGCCC	TGGAGAAACA	GATTGACACG	CTGGCGGGGA	AGCTGATGTC	CCTGACTGAG	1620
65	CTGCTTAGCA	CTGCCCTGGG	GCCGAGGCAG	CTTCCAGAAC	CCAGCCAGCA	GTCCAAGTAG	1680
	CTGGACCCAC	GAGGAGGAAC	CAGGCTACTT	TCCCCAGTAC	TGAGGTGGTG	GACATCGTCT	1740
	CTGCCACTCC	TGACCCAGCC	CTGAACAAAG	CACCTCAAGT	GCAAGGACCA	AAGGGGGCCC	1800
	TGGCTTGGAG	TGGGTGGGCT	TGCTGATGGC	TGCTGGAGGG	GACGCTGGCT	AAAGTGGGTA	1860
	GGCTTTGGCC	CACCTGAGGC	CCCAGGTGGG	AACATGGTCA	CCCCACTCT	GCATACCCCT	1920
70	ATCAAAAACA	CTCTCACTAT	GCTGCTATGG	ACGACCTCCA	GCTCTCAGTT	ACAAGTGCAG	1980
	GCGACTGGAG	GCAGGACTCC	TGGGTCCCTG	GGAAAGAGGG	TACTAGGGGC	CCGGATCCAG	2040
	GATTCTGGGA	GGCTTCAGTT	ACCGCTGGCC	GAGCTGAAGA	ACTGGGTATG	AGGCTGGGGC	2100
	GGGCTGGGAG	GTGGCGCCCC	CTGGTGGGAC	AACAAAGAGG	ACACCATTTT	TCCAGAGCTG	2160
	CAGAGAGCAC	CTGGTGGGGA	GGAAAGAGTG	TAACTCACCA	GCCTCTGCTC	TTATCTTTGT	2220
75	AATAATGTT	AAAGCCAG					2238

Seq ID NO: C206 DNA Sequence
Nucleic Acid Accession #: NM_025257.1
Coding sequence: 1..2139

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	TTCTCTGCTC	TCATCTAGG	TTACATCGTG	GTGGGGATTG	TGGCCTGGTT	GTATGGAGAC	180

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 CCGGAGGACC CATGGACTGT GGGAAAAAAC GAGTTCTCAC AGACTGTTGG GGAAGTCTTC 420
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Seq ID NO: C207 DNA Sequence
 Nucleic Acid Accession #: NM_016180.1
 Coding sequence: 26..1618

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Seq ID NO: C208 DNA Sequence
 Nucleic Acid Accession #: NM_003273.1
 Coding sequence: 255..2024

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Seq ID NO: C209 DNA Sequence
 Nucleic Acid Accession #: NM_015720.1
 Coding sequence: 21..1838

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 CTCCTAGTGG GCGCGAGCAC CCAGATGAAG ATCCCTTGG CTCTAGAACC TCAGCTCTTT 1020
 CCGCACTGCG CCTTGAGAC ATGGAATGA CACCTTCTC TGCTACCTTG GACACAGAAG 1080
 ATCTCAACCA GCAGCTCTTA GAAGGCGAGC CAGCTGAAGC TCAATCCAGG ATACCTTGG 1140
 ATTCTACGCA GTGATCTGC AAGGACTGGA GCAATCTGGC TGGGAAAAAC TACATCATTC 1200
 TGAACATGAC AGAAGACATA GACTGTGAGG TGTTCGGGCA GCACCGGGGG CCACAGCTCC 1260
 TGGCCCTGGT GGAAGAGGTG CTGCCCGGCC ATGGCAGTGG CCACCATGGG GCGTGGCACA 1320
 TCTCTCTGAG CAAGCCGAGC GAGAAGGAGC AGCACCTTCT CATGACACTG GTGGGCGAGC 1380
 AGGGGTTGGT GCCCACTCAA GATGTCCTTT CCATGCTGGG TGACATCCG AGGAGCCTGG 1440
 AGGAGATTGG CATCCAGAAC TATTCACAA CCAGCAGCTG CCAGGCGCGG GCGAGCCAGG 1500
 TGCGCAGCGA CTCAGGCAAG CTCTTCTGTT TGCTGGTGGT CATTGGGGCC ATCTGCATCA 1560
 TCATCATTGC GCTTGGCCTG CTCTACAACT GCTGGCAGCG CCGGCTGCCC AAGCTCAAGC 1620
 ACGTGTGCGA CCGGAGGAG CTGCGCTTG TGGAAGACGG CTGCCAGAC AACCCCAAGC 1680
 TGGACGTGCG CAGCGACAGC CAGTCGAGGA TGCAAGAGAA GCACCCAGC CTGAACGGCG 1740
 GCGGGGCGCT CAACGCGCGG GGGAGCTGGG GGGCGCTCAT GGGGGGCAAG CCGGACCCCG 1800
 AGGACTCGGA CGTGTTCGAG GAGGACAGCG ACTGTGAGC GCAGCGAGGC GCAGGCGGAG 1860
 TGGGCGGCGA GGAACCAAGC AGGTGAGACC CGAAACGGAC GGGCCGAGGC CCGCACCCAG 1920
 CCGGCGCTTA CCGGCGCGCC CCGGCGCTG GCGCTCGGCG CCGGCTCCTT CCGCTTCCC 1980
 CCGACTTCC ACGGGGGCTT CGGACCAACT CCTCCTTCC CCGCCGAGGC GCAGGCGCTC 2040
 AAGCCGCTCT TGGCCCGCTT TTCCCGCCCC TGAACCCCG CCGCGCGGG GCGGGCGCGG 2100
 CTTCTGCGC CCGGGGACTC AATTAACCC GCGCGGAGAC CACGCGGGCC CAGCGAAAAA 2160
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2220
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2269

Seq ID NO: C210 DNA Sequence
 Nucleic Acid Accession #: NM_001197.3
 Coding sequence: 61..543

80
 1 11 21 31 41 51
 | | | | |
 GACACGAAGC CTCCCGGGTG GCTTACAGAC GCTGCCAGCA TCGCCGCGCG CAGAGGAGAA 60
 ATGTCGAAG TAAGACCCCT CTCCAGAGAC ATCTTGATGG AGACCTCCT GTATGAGCAG 120

CTCTGGAAC CCCGACCAT GGAGGTTCTT GGCATGACTG ACTCTGAAGA GGACCTGGAC 180
 CCTATGGAGG ACTTCGATTTC TTGGAATGTC ATGGAGGGCA GTGACGCATT GGCCCTGCGG 240
 CTGGCTGCA TCGGGGAOCA GATGGAOGTG AGCCTCAGGG CCGCGGCCT GGCCAGCTC 300
 TCCGAGGTGG CCATGCACAG CCTGGGTCTG GCTTTCATCT ACGACCAGAC TGAGGACATC 360
 AGGGATGTTT TTAGAAGTTT CATGGACGGT TTCACCACAC TTAAGGAGAA CATAATGAGG 420
 TTCTGGAGAT CCCGAAACCC CGGGTCCCTGG GTGTCTGTGG AACAGGTGCT GCTGGCGCTG 480
 CTGTCTGTGC TGGCGCTGCT GCTGCGCGTG CTCACGGGGG GCGTGCACCT GCTGCTCAAG 540
 TGAGGCCCGG GCGGCTCAGG GCGGGGCTGG CCCCACCCC ATGACCACTG CCTGGAGGT 600
 GGCGGCTGCG TGCTGTATTAT TTTTAACTG TTTTCTCATG ATGCTTTTTT ATATTAAAC 660
 CCGAGATAG TGCTGGAACA CTGCTGAGGT TTTATATCA GGTTTTTTGT TTTTTTTTAA 720
 TTCCAGTTTT CGTTTTTTCT AAAAGATGAA TTCTATGGC TCTGCAATTG TCACCGGTTA 780
 ACTGTGGCCT GTGCCAGGA AGAGCCATTC ACTCTGCCC CTGCCACAC GGCAGGTAGC 840
 AGGGGAGTG CTGTGCACAC CCCTGTGTGA TATGTGATGC CCTGGCAAA GAATCTACTG 900
 GAATAGATTC CGAGGAGCAG GAGTGCTCAA TAAATGTGT GTTTCAGCA AAAAAAAAAA 960
 AAA 963

Seq ID NO: C211 DNA Sequence
 Nucleic Acid Accession #: AF272357
 Coding sequence: 83..1060

1 11 21 31 41 51
 GCTGCTCCCG ACGCGGAGCC CGGAGCCCGC GCGGAGCCCC TGGCCTCGCG GTGCCATGCT 60
 GCGCGGCGCG GCGGCGCTGAA GGATGGCGAC GCGCTGCGCT CGCCCTCCCG CGCGGCACCT 120
 GCGGCTGCTG CGGCTGCTGC TCTCGGCGCT CGTCCCTGGC GCGCGCTCGC GTGGAGCGCG 180
 CGCGGCGCAC CGGAGGTAG CGGCTGTGCC CGGAGCCCTG GACTGTGCCG TGAAGAGGGG 240
 GGCAAGGTGT CTTCTGTGTG CACATGCCCT TGGGCCCTGC CTTCAGCCCT TCCAGGAGGA 300
 CCAGCAAGGG CTCTGTGTGC CCAGGATGCG CCGGCTCCCA GCGGGGGGCG GCGCCAGCC 360
 CAGACTGGAA GATGAGATTG ACTTCTGGC CAGGAGCTT GCGCGGAAGG AGTCTGGACA 420
 ATCAACTCGG CCGCTACCCA AGGACCGACA GCGGCTCCCG GAGCCTGCCA CCCTGGGCTT 480
 CTGGCAGCG GCGCAGGGCG TGGAGCTGGG CTCCCTCC ACTCCAGGAA CCGCCAGCGC 540
 CACGCCCCAC ACGTCCCTGG GCTCCCTGTG GTCATCCGAC CCGGTGCACA TGTGCGCCCT 600
 GGAGCCCCGG GGAGGGCAGG GCGACGGCCT CGCCCTTTGT CTGATCCTGG CGTCTGTGT 660
 GCGCGGTGCA GCGGCGCTCT CGGTAGCCTC CCGTGTCTGG TGCGAGCTGC AGCGTGAGAT 720
 CGGCTGACT CAGAGGGCGG ACTACGCCAC TCGGAGGGCC CCGGTCTCAC CTGCAGCTCC 780
 CGGATCTCG CCGTGGGACC AGCGGCTGGC ACAGAGCGCG GAGATGTACC ACTACGACA 840
 CCAACGGCAA CAGATGTCTGT GCCTGGAGCG GCATAAAGAG CCACCCAAGG AGCTGACAC 900
 GCGCTCTCG GATGAGGAGA ATGAGGACGG AGACTTCAAG GTGTACGAGT GCCCGGGCCT 960
 GCGCGCGACC GGGGAAATGG AGGTGCGCAA CCGTCTGTTC GACCAAGCGG CACTGTCCG 1020
 GCGCGTCCCG GCGCCGAGCT CACCGCTGCG ACTGCCATGA CCTGGAGGCA GACAGACGCC 1080
 CACCTGCTCC CGGACTCGA GCGCCCGGG GAGGGGCAGG GCCTGGAGCT TCCCACTAAA 1140
 AACATGTTTT GATGCTGTGT GCTTTTGGCT GGGCCTCGGG CTCACGGCCC TGGGACCCCT 1200
 TGCCAGGGAG ACCCCGGAAC CTTTGTGCCA GGACACCTCC TGGTCCCGCT CACCTCTCCT 1260
 GTTCGGTTTA GACCCCAAA CTGAGGGGG CATGAGAAC CGTAGAGCG AGGAACGGGT 1320
 GGGTAATCT AGAGACAAA GCCAATTAAA GTCCATTCA GAAAAAAAAA A 1371

Seq ID NO: C212 DNA Sequence
 Nucleic Acid Accession #: NM_004445.1
 Coding sequence: 799..3819

1 11 21 31 41 51
 CGGAGGGGGG GGGCCGGGCT GCGTTGCTC CAGCGCGGCG TCTACAGCAG CGGGCGCGCG 60
 GACCGGGGAC CCGAGCTTGG GACCGCGATT CTCGACGCGG GCGCCAGGA TTCTCCCGCG 120
 GCGCCACCTC TGGAGCAGCG CCTGCCGCCA GCGTCAGGTC CACCGCGGAA TCCAGGGAG 180
 TCTCGCGCGG GAAAGGACCC GGGCCGGTGC AACGGGTGCC CCGGACTGGA GAAGACGCGG 240
 GTGGCACCCT GCGAGCTCCA GAGCCCCCGG GTCCACTGCG AGGCTCGGG GGGCGCAGAC 300
 CTGCAGAGAC TGGCGGCAAC GGAAGAAAT AAAGGGATTA TAGTCCACCC AATTACAGA 360
 CTTCTGAGAC TCGAGACAGA GGAGAGATAG AGAACCGCCA ATCTCTAGAT CAACAAGCAA 420
 AGGAGGTGCC AAGCCTGTTT GTCTTCAATG TGACACTGGA GTCTAGATGC TGGGAAGTCC 480
 AAGATCAGGG TGGCGGCATG GTCAGTTCCCT GGGAAGCCT CTCTTCTAGG TTTCAGACTG 540
 CCTCTTCTT TGTGTGTGCC TCGAATGGCA GAAAAGGGG TGGCTGTGG AGGAAGGGAG 600
 GAGAGTAAT GAAGAGAAAG AACTGGAATA ACCCTTGCA GAAAAAAGG AAAAGGGAG 660
 CTTAGCTGTA CACCTGAGT CTTGCAAAAG CTGCAGCCCC ACCCAGGAGC AGGCTGTGG 720
 CTGGGGCGAT GGTGGAGCGC CTGAAGATGT CCGATGGCTA CTGAAGGGGC TGCCCACTTA 780
 GGGAACAGAG TGGCGGCAT GGTGTGTAGC CTATGGGTGC TGCTCCTGGT GTCTTCAGTT 840
 CTGGCTCTGG AAGAGGTATT GCTGGACACC ACCGAGAGAG CATCTGAGAT TGGCTGCTC 900
 ACCTACCCAC CAGGGGGGTG GGAAGAGGTG AGTGTCTGCG ACGACGAGCG ACGCTGACT 960
 CGGACCTTTG AGGCATGTCA TGTGGCAGGG GCGCCTCCAG GCAACGGGCA GGACAAATTG 1020
 TTGCAGACAC ACTTTGTGGA GCGGCGCGGG GCGCAGAGGG GCGACATTGG ACTCCACTTC 1080
 TCTGTGCGGG CATGCTCCAG CCTGGGTGTG AGCGGCGGCA CCGCGCGGA GACCTTCACC 1140
 CTTTACTACC GTGAGGCTGA GGAGCCCCGAC AGCCTTGACA GCGTTTCTCT CTGGCACCTC 1200
 AAACGCTGGA CCAAGGTGGA CACAATTGCA GCAGACGAGA GCTTTCCCTC CTCTCTCTCC 1260
 TCCTCTCTCT CTTCTTCCCT TGCAAGGTGG GCTGTGGGAC CCGACGGGCG TGGGACGCGG 1320
 GCTGGACTGC AACTGAACGT CAAAGAGCGG AGCTTTGGGC CTCTCAACCA ACGCGGCTTC 1380
 TACGTGGCCT TCCAGACAC GGGGGCCTGC CTGGCCTGG TCGCTGTGAG GCTCTTCTCC 1440
 TACACCTGCC CTGCGGTGCT CGATCTCTTT GCTTCTTTTC CAGAGACGCA GGCCAGTGGG 1500
 GCTGGGGGAG CTTCCCTGGT GGCAGCTGTG GGCACCTGTG TGGCTCATGC AGAGCCAGAG 1560
 GAGGATGGAG TAGGGGGCCA GGCAGGAGGC AGCCCCCCA GGCTGCACCT CAACGGGGAG 1620
 GGCAAGTGA TGGTAGCTGT CCGGGGCTGC CGCTGCCAGC CTGGATACCA ACCAGACGGA 1680
 GGAGACAGG CCGCCAAAGC CTGCCACGG GGGCTCTATA AGTCTTCTGC TGGGAATGCT 1740
 CCTGTCTAC CATGCCCTGC CCGCAGTCCG GCTCCCAACC CAGCAGCCCC CGTTTGGCCC 1800
 TGCTTGAGG GCTTCTACCG GGCAGATTCC GACCCACAG AGGCCCCCTG CACTGTCTCT 1860
 CCATCGGCTC CCCAGGAGCT TTGGTTTGAG GTGCAAGGCT CAGCACTCAT GTCACACTGG 1920

	CGCCTGCCCTC	GGGAGCTGGG	GGGTGAGGG	GACCTGCTCT	TCAATGTGCT	GTGCAAGGAG	1980
	TGTGAAGGCC	GCCAGGAACC	TGCGAGCGGT	GGTGGGGCCA	CTTGTACCG	CTGCAGGGAT	2040
	GAGGTCCACT	TCGACCTCG	CCAGAGAGGC	CTGACTGAGA	GCCGAGTGT	AGTGGGGGA	2100
5	CTCCGGGCAC	ACGTACCTTA	CATCTTAGAG	GTGCAGGCTG	TTAATGGGGT	GTCTGAGCTC	2160
	AGCCCTGACC	CTCTCAGGC	TGCAGCCATC	AATGTACGCA	CCAGCCATGA	AGTGCCCTCT	2220
	GCTGTCCCTG	TGGTGACCA	GGTGAGCCGG	GCAATCCAAC	GCAATCACGG	GTCTTGGCCG	2280
	CAGCCCGACC	AGACCAATGG	GAACATCCTG	GACTATCAGC	TCCGCTACTA	TGACCAAGCA	2340
	GAAGACGAAT	CCCACCTCTT	CACCTGACC	AGCGAGACCA	ACACTGCCAC	CGTGACACAG	2400
10	CTGAGCCCTG	GCCACATCTA	TGGTTTCCAG	GTGCGGGCCC	GGACTGCTGC	CGGCCACGGC	2460
	CCCTAGCGGG	GCAAAGTCTA	TTTCCAGACA	CTTCTCAAG	GGGAGCTGTC	TTCCAGCTTT	2520
	CCGGAAGAGC	TCTCTTGGT	GATCGGCTCC	ATCCTGGGGG	CTTTGGCCTT	CCTCTGCTG	2580
	GCAGCCATCA	CCGTGCTGGC	GGTCGTCTTC	CAGCGGAAGC	GGCGTGGGAC	TGGCTACACG	2640
	GAGCAGCTGC	AGCAATACAG	CAGCCACGGA	CTCGGGGTGA	AGTATTACAT	CGACCCCTCC	2700
15	ACCTAGGAGG	ACCCCTGTCA	GGCCATCCGA	GAACCTGCCC	GGGAAGTCGA	TCCTGCTTAT	2760
	ATCAAGATTG	AGGAGGTCA	TGGACAGGCG	TCTTTTGGAG	AAGTGCGCCA	GGGCGCGCTG	2820
	CAGCCACGGT	GCAGAGTGGG	GCAGACTGTG	GCCATCCAGG	CCCTGTGGGC	CGGGGGCGCC	2880
	GAAAGCCTGC	AGATGACCTT	CCTGGGCGCG	GCCGAGTGC	TGGGTCAAGT	CCAGCACCCC	2940
	AACATCTTGC	GGCTGGAGGG	CGTGTCAAC	AAGAGCCGAC	CCCTCATGGT	GCTGACGGAG	3000
20	TTCATGGAGC	TTGGCCCCCT	GGACAGCTTC	CTCAGGCAGC	GGGAGGGCCA	GTTCAGCAGC	3060
	CTGCAGCTGG	TGGCCATGCA	GCGGGGAGTG	GCTGCTGCCA	TGCAGTACCT	GTCCAGCTTT	3120
	GCCTTGGTCC	ATCCTCTGCT	GTCTGCCAC	AGCGTGTGG	TGAATAGCCA	CTTGGTGTGC	3180
	AAGGTGGCCC	GTCTTGGCCA	CAGTCTCAG	GGCCCAAGTT	GTTCCTTCCG	CTGGGCAGCC	3240
	CCAGAGGTCA	TTGCACATGG	AAAGCATACA	ACATCCAGTG	ATGCTCGAG	CTTTGGGATA	3300
25	CTCATGTGGG	AAGTGTGAG	TTATGGAGAA	CGGCTTACT	GGGACATGAG	TGAGCAGGAG	3360
	GTACTAAATG	CAATAGAGCA	GGAGTTCGCG	CTGCCCCGCG	CTCCAGGCTG	TCCTCTGGA	3420
	TTACATCTAC	TTATGTTGGA	CACITGGCAG	AAGGACCGTG	CCCGCGCGCC	TCATTTTGAC	3480
	CAGCTGTGGG	CTGCATTGGA	CAAGATGATC	CGCAAGCCAG	ATACCTTGCA	GGCTGGCGGG	3540
	GACCCAGGGG	AAAGGCCCTT	CCAGGCCCTT	CTGACCCCTG	TGGCCCTGGA	CTTCTCTTGT	3600
30	CTGGACTCAC	CCCAAGGCTG	GCTTTCAGCC	ATTGAGCTGG	AGTGCTACCA	GGACAACTTC	3660
	TCCAAGTTTG	GGCTCTGTAC	CTTCAGTGAT	GTGGCTCAGC	TCAGCCTAGA	AGACCTGCCT	3720
	GCCCTGGGCA	TGACCTTGGC	TGGCCACAG	AAGAAGCTGC	TGCAACACAT	CCAGCTCCTT	3780
	CAGCAACACC	TGAGGCAGCA	GGGCTCAGTG	GAGGTCTGAG	AATGACGATA	CCCGTGACTC	3840
	AGCCCTGGAC	ACTGGTCCGA	GAAGGGACAT	GTGGGACGTC	AGCCGGGCTC	CAACAGCCTC	3900
35	TGTGAGAGAT	GCCCAACACC	AAACCAACCC	CTCCGATGAG	CTGCATTCCC	TGGTCTCTCG	3960
	CCTCTCCACC	AGCCCCCTCC	TCATTAAAGG	GAAAGAAGGG	AATTTGCAAA		4010

Seq ID NO: C213 DNA Sequence

Nucleic Acid Accession #: XM_043340.4

Coding sequence: 195..1067

40	1	11	21	31	41	51	
	GGGCGGCGCC	CAATGGGCTG	CGCGGAGCGT	CACCTCCCGG	CAGCGGGAGG	CGAGTGGCGA	60
45	GTGGCGAGTG	GGGAGTGTCA	GGGGGGCGGC	CGGCGGGGCG	GGGCGGCGCC	GAGGAGGCGT	120
	TGGCAGCGGG	CTCGGACCCA	CGCGGCGCGG	CGGCGCGCCT	GGCCTGCAGC	GCTCCCAACC	180
	CGGCGGCGGG	CAGAGTGGCC	TTTGACTTCA	GGAGGTTTGA	CATCTACAGG	AAGTGGCCCA	240
	AGGACCTTAC	GCAGCCAAAG	TACACCGGGG	CCATTATCTC	CATCTGCTGC	TGCCTCTTCA	300
	TCTCTTCTCT	CTTCTCTCTG	GAGCTCACCG	GATTATTAAC	GACAGAAAGT	GTGAACGAGC	360
50	TCATATGTGA	TGACCCAGAG	AAGGACAGCG	GTGGCAAGAT	CGACGTCAGT	CTGAACATCA	420
	GTTTTACCCAA	CTGCACTGTC	GAGTGGTGTG	GGCTTGACAT	TCAGGATGAG	ATGGGCAGGC	480
	ACGAAGTGGG	CCACATCGAG	AACCTCATGA	AGATCCCGCT	GAACAATGGG	GCAGGCTGCC	540
	GCTTCGAGGG	GCAGTTCAGC	ATCAACAAGG	TCCCGGCAAA	CTTCCAGCTG	TCCACACACA	600
	GTGCCACAGC	CCAGCCACAG	AAACCCAGACA	TGACGCATGT	CATCCACAAG	CTCTCCTTTG	660
55	GGGACACGCT	ACAGGTCCAG	AACATCCACG	GAGCTTTCAA	TGCTCTCGGG	GGAGCAGACA	720
	GACTCACCTC	CAACCCCTCG	GCCTCCACAG	ACTACATCCT	GAAGATTGTG	CCCAAGGTTT	780
	ATGAGGACAA	GAGTGGCAAG	CAGCGGTACT	CCTACCACTA	CACGCTGGCC	AACAAGGAAT	840
	ACGTGCGCTA	CAGCCACACG	GGCGGCATCA	TCCCTGCAAT	CTGCTTCCGC	TACGACCTCA	900
	GCCCCATCAC	GGTCAAGTAC	ACAGAGAGAC	GGCAGCGGCT	GTACAGATTG	ATCACCAACG	960
60	TCTGTGCCAT	CATTGGCGGG	ACCTTCAACG	TGCGCGGCAT	CCTGGACTCA	TGCATCTTCA	1020
	CAGCCTCTGA	GGCCTGGAAG	AAGATCCAGC	TGGGCAAGAT	GCATTGACGC	CACACCCAGC	1080
	CTAATGGCGG	AGGACCTTGG	GCATCGCCAG	CCTTGCCCTCC	AGTGCCCTGT	CTCCTTTGGC	1140
	CCTCAATCTG	GTCCCAATTC	TGGCTGTGTC	CCAAAGGGTG	TGTGGGAAGT	GGGGGGAAAG	1200
	TAGAGGATGG	CTGATGTTT	TGCAGCTACC	TCCTTTCCCC	GTGTTTCTTT	TTAGACAAAT	1260
65	TACACTGCTC	GAAAGTTGAG	TTCCCTTTTC	CCTGGGGAGC	CCCAAGAAAC	GAGTCAGGCA	1320
	AGGGGTGGGG	AGTCCAGGGG	AACATCCAG	AATGCATATC	GATCAGCTCT	CAGCCAGGCT	1380
	TCGACAACTC	CGCAGCCCCC	ACTAGGTGGA	CACATTAATG	ATTTGGTTTC	TCCCTGGGC	1440
	AGCCAACTCG	CCCCAGAGGC	ACCAGACCTG	GGCTTTTACG	TTTGGGACCA	GGCTGCCCAA	1500
	AGGTACTCCT	TTATACACCC	GGCACCTTCC	ACGAAAGATG	GTACTTCCCA	AGCAAGCCCC	1560
70	TATGATTGTT	CACATAGAT	GGAAATGTGT	GGCATGCACA	TGAGTTGAAA	TTCTTTTATG	1620
	CATTTTITTT	AAGAAAAAAA	AAAAACAAC	TCTGAGGACA	TAGGGGATGT	CAGTTTCTTA	1680
	TGGAAGAGAC	ACCTCTGACC	CGTTATTCTT	ATAATCAAAA	TCTGAAGGGA	AAAAAATGTT	1740
	TTAGTTCTTT	CCCCACTCGT	TGGGTTCAAC	TAGATTAAAA	GGCTGATTTT	CAG	1793

Seq ID NO: C214 DNA Sequence

Nucleic Acid Accession #: NM_002151.1

Coding sequence: 246..1499

80	1	11	21	31	41	51	
	TGAGGCCCGC	TTTCCAGGGA	CCCTACCTGA	GGGCCACAG	GTGAGGCAGC	CTGGCCTAGC	60
	AGGCCCCACG	CCACGCGCTC	TGCTTCCAGG	CGGCGCGCTG	CTGCGGGGCC	ACCATGCTCC	120
	TGCCCCAGGC	TGGAGACTGA	CCCGACCCCG	GCACTACCTC	GAGGCTCCGC	CCCCACCTGC	180
	TGGACCCACG	GGTCCACACC	TGGCCACGGA	GGTCAGCCAG	GGAATCATT	ACAAGAGGCA	240
	GTGACATGGC	GCAGAAAGGAG	GGTGGCCGGA	CTGTGCCATG	CTGCTCCAGA	CCCAAGGTGG	300

5	CAGCTCTCAC	TGCGGGGACC	CTGCTACTTC	TGACAGCCAT	CGGGGCGGCA	TCCTGGGCCA	360
	TTGTGGCTGT	TCTCTCTCAGG	AGTGACCAGG	AGCGCTGTGA	CCCAAGTGCAG	GTCAAGCTCTG	420
	CGGACGCTCG	GGCTCATGGTC	TTTGACAAGA	CGGAAGGGAC	GTGGGCGCTG	CTGTGCTCCT	480
	CGCGCTCCAA	CGCCAGGGTA	GCGGACTCA	GCTGCGAGGA	GATGGGCTTC	CTCAGGGCAC	540
	TGACCCACTC	CGAGCTGGAC	GTGCGAACGG	CGGGCGCCAA	TGGCACTGCG	GGCTTCTTCT	600
	GTGTGACGA	GGGGAGGCTG	CCCCACACCC	AGAGGCTGCT	GGAGGTCATC	TCCGTGTGTG	660
	ATTGCCCCAG	AGGCCGTTTC	TTGGCCGCCA	TCTGCCAAGA	CTGTGGCCGC	AGGAAGCTGC	720
	CGGTGGACCG	CATCGTGGGA	GGCCGGGACA	CCAGCTTGGG	CCGGTGGCCG	TGGCAAGTCA	780
10	GCCTTGGCTA	TGATGGAGCA	CACCTCTGTG	GGGATCCCT	GCTCTCCGGG	GACTGGGTGC	840
	TGACAGCCGC	CCACTGCTTC	CCGAGCGGA	ACCGGTCTCT	GTCCCGATGG	CGAGTGTTTG	900
	CCGGTGGCTT	GGCCAGGCCC	TCTCCCAAG	GTCTGCAGCT	GGGGTGCAG	GCTGTGGTCT	960
	ACCACGGGGG	CTATCTTCCC	TTTGGGAGCC	CCAACAGCGA	GGAGAACAGC	AACGATATTG	1020
	CCCTGGTCCA	CCTCTCCAGT	CCCTGCCCC	TCACAGAATA	CATCCAGCCT	GTGTGCTCC	1080
15	CAGCTGCCGG	CCAGGCCCTG	GTGGATGGCA	AGATCTGTAC	CGTGACGGGC	TGGGGCAACA	1140
	CGCAGTACTA	TGGCCAACAG	GCCGGGTAC	TCCAGAGGCG	TGGAGTCCCC	ATAATCAGCA	1200
	ATGATGTCTG	CAATGGCGCT	GACTTCTATG	GAAACAGAT	CAAGCCCAAG	ATGTTCTGTG	1260
	CTGGCTACCC	CGAGGGTGGC	ATTGATGCCT	GCCAGGGCGA	CAGCGTGGT	CCCTTTGTGT	1320
	GTGAGGACAG	CATCTCTGGG	ACGCCACGTT	GGCGCTGTG	TGGCATTGTG	AGTTGGGGCA	1380
20	CTGGCTGTGC	CCTGCCCCAG	AAGCCAGGCG	TCTACACCAA	AGTCAGTGAC	TTCCGGAGT	1440
	GGATCTTCCA	GGCCATAAAG	ACTCACTCCG	AAGCCAGCGG	CATGGTGACC	CAGCTCTGAC	1500
	CGGTGGCTTC	TGCTGTGCGA	GCCTCCAGGG	CCGAGGTGA	TCCCGTGGT	GGGATCCAGC	1560
	CTGGGCGGAG	GATGGGACGT	TTTTCTTCTT	GGGCCCGGTC	CACAGTCCA	AGGACACCTT	1620
	CCCTCCAGGG	TCTCTCTTTC	CACAGTGGCG	GGCCCACTCA	GCCCCAGAGC	CACCCAACTT	1680
25	CACCTCTCTG	ACCCCACTGT	AAATATTGTT	CTGCTGTCTG	GGACTCTGT	CTAGGTGCCC	1740
	CTGATGATGG	GATGCTCTTT	AAATAATAAA	GATGGTTTGG	ATT		1783

Seq ID NO: C215 DNA Sequence
Nucleic Acid Accession #: AB037745.1
Coding sequence: 26..1744

30	1	11	21	31	41	51	
	ATGGTGGAAC	ACGCTGCCCA	CAAAACATGGA	AACGACCGTT	CTCAGTGGGA	TCAACTTCGA	60
35	GTACAGGGGC	ATGACAGGCT	GGGAGGTGGC	TGGTGATCAC	ATTACACAG	CTGCTGGAGC	120
	CTCAGACAAT	GACTTCAATG	TTCTCACTCT	GGTTGTGCCA	GGATTTAGAC	CTCCGAGTGC	180
	GTGATGGGCA	GACACAGAGA	ATAAAGAGGT	GGCCAGAATC	ACATTTGTCT	TTGAGACCTC	240
	CTGTTCTGTG	AACCTGTGAGC	TCTACTTCAT	GGTGGGTGTG	AAATTCTAGGA	CCAACACTCC	300
	TGTGGAGACG	TGGAAAGGTT	CCAAAGGCAA	ACAGTCTAT	ACCTACATCA	TTGAGGAGAA	360
40	CATACCAACG	AGCTTCACTT	GGGCTTCCCA	GAGGACCACT	TTTCATGAGG	CAAGCAGGAA	420
	GTACACCAAT	GACGTGTGCA	AGATCTACTC	CATCAATGTC	ACCAATGTGA	TGAATGGCGT	480
	GGCTTCTTAC	TGCGTCTCCG	GTGCCCTAGA	AGCCTCTGAT	GTGGGCTCCT	CCTGCACCTC	540
	TTGTCTCTCT	GGTTACTATA	TTGACCGAGA	TTCAGGAACC	TGCCACTCCT	GGCCCCCTAA	600
	CACAATCTCG	AAAGCCCAAC	AGCCTTATGG	TGTCCAGGCC	TGTGTGCCCT	GTGTTCCAGG	660
45	GACCAAGAAC	AACAGATCC	ACTCTCTGTG	CTACAATGAT	TGCACCTTCT	CACGCAACAC	720
	TCCAACCAAG	ACTTTCAACT	ACAACCTTCT	CGCTTTGGCA	AACACCGTCA	CTCTTGTCTG	780
	AGGGCCCAAG	TTCACTTCCA	AAGGGTTGAA	ATACTTCCAT	CACITTAACC	TCAGTCTCTG	840
	TGGAAACACG	GGTAGGAAAA	TGTTCTGTGT	CACCGACAAT	GTCAGTGACC	TCCGGATTCC	900
50	TGAGGGTAGG	TCAAGGTTCT	CCAAATCTAT	CACAGCCTAC	GTCTGCCAGG	CAGTCATCAT	960
	CCCCCCAGAG	GTGACAGGCT	ACAAGGCCGG	GGTTTCTCTA	CAGCGTGCA	GCCTTGTCTG	1020
	TCGACTTATT	GGGGTGACAA	CAGATATGAC	TCTGGATGGA	ATCACTTCCC	CAGCTGAAGT	1080
	TTTCCACCTG	GGCTCTTGGG	GAATACCGGA	CGTGATCTTC	TTTTATAGGT	CCAATGATGT	1140
	GACCCAGTCC	TGCAGTCTTG	GGAGATCAAC	CACCATCCGC	GTCAGGTGCA	GTCCACAGAA	1200
	AACGTCTCTG	AAAGGTTTGC	TGCTGCCAGG	AACTGTCTCA	GATGGGACCT	GTGATGGCTG	1260
55	CAACTTCCAC	TTCTGTGTGG	AGAGGCGCGC	TGCTTGCCCG	CTCTGTCTAG	TGGCTGACTA	1320
	CCATGCTATC	GTGACAGCTG	GTGTGCTGTG	GATCCAGAGG	ACTACTTACG	TGTGGCGAGA	1380
	ACCCAGCTTC	TGCTCTGGTG	GCATTTCTCT	GCCTGAGCAG	AGAGTCAACC	CTGCAAAAC	1440
	CATAGATTTC	TGGCTGAAAG	TGGGCATCTC	TGCAGGCACC	TGTACTGCCA	TCCTGTCTAC	1500
	CGTCTTGACC	TGCTACTTTT	GGAAAAAGAA	TCAAAAACCTA	GAGTACAAGT	ACTCCAAGCT	1560
60	GGTGATGAAT	GCTACTCTCA	AGGACTGTGA	CCTGCCAGCA	GCTGACAGCT	GGGCCATCAT	1620
	GGAGGGCGAG	GATGTAGAGG	ACGACCTCAT	CTTTACCAAG	AAGAAGTAC	TCCTTGGGAA	1680
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	GTTCCTCCAA	ATGGCCCATC	CGCCAGAGCC	ATAGCTTCGT	CTGCTCATAA	TTCTTATAGC	2100
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	TCAAGCTCTG	AATCCAGCA	CTTTGGGAGG	CCGAGGCGGG	CAGATCATGA	GGTCCGGAGA	2460
75	TTGAGACCAT	CCTGGCTAAC	ACGGTGAAGC	CCGCTCTCTA	CTGGAATATC	AAAAAATTAG	2520
	CCGGGCGTGG	TGGCGGGTGC	CTGTGTTCCC	AGCTACTCGG	GAGGCTGAGG	CGGGAGAAAT	2580
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	CCATCTCAGC	CTCTCAAGTA	GCTGGGACTA	CGAGTGTGCA	CCACAGGCTT	CACATAATTT	2880
	TGTGTTTTTC	GTAGACAAGG	GGTTTCAACG	TGTTGCCAGG	GCTGGTCTCC	AACCTCTGGG	2940
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	CACCTCAGCT	TTTATTTGTT	TTTTAAACCA	CGTAGCTCAT	TGCTTCTCT	TAAGTAAATG	3060
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 Nucleic Acid Accession #: NM_004864.1
 Coding sequence: 26-952

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Seq ID NO: C432 DNA Sequence
 Nucleic Acid Accession #: NM_052858.1
 Coding sequence: 54..1259

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	CAGGGGGCTA CAGGGGCATC ACCAGCTTGG GGGGCATTTA CTACTATCAG TTCCGAGGGG 780
	CTTACAGTGG CTTTGTATGG TCTGACGGG AGAAGGCCCA GCAACTGAT GTCCAGTTCT 840
	ACCAGCTAAA CTGCCCCATG GTCACTGTGG CAATGGCCTG TAGTGGAGCC CTCACAGCCC 900
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	TCTACTTCCA CTACCTCTCT GCTGCCTATG GCTCTCTGT GTGTAAAGAG AGGCAGGCGC 1080
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	CTTCTGAGT CTTCTGTGAG TGAGGGACCA ATCAAAATTA TTTTTCAAAA AGCAAAAAAA 1500
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Seq ID NO: C434 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 261..2861

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Protein Accession #: NP_005805.1

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 35 LNQEQLAQP ASGQPVSLKN ISTDTSYYI CTSSNEEGTQ FCNITVAVRS PSMNVALYVG 240
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Protein Accession #: Eos sequence

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 IAESYYPEYL INLVQQLQT QAASSIYDSS YLGYSVAVGE FSGDDTDEFV AGVPKGNLTY 300
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Seq ID NO: C219 Protein Sequence
Protein Accession #: NP_002412.1

65 1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSP PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGFV 60
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLYRIEN 120
 70 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSLHST DIGALMYPYSY 240
 TFSGDVQLAQ DDIDGIAIY GRSQNPVQPI GPOTPKACDS KLTFDAITTI RGEVMFPKDR 300
 PYMRTNPFYP EVELNFIISV WPQLPNGLEA AVEFADRDEV RPFKGNKYWA VQGNVNLHG 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWRV DEYKRSMDPG YPKMIAHDFP 420
 75 GIGHKVDVAF MKDGFYFYPH QTRQYKFDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C220 Protein Sequence
Protein Accession #: Eos sequence

80 1 11 21 31 41 51
 MHSFPPLLLL LFWGVVSHSP PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGFV 60
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLYRIEN 120
 YTPDLPRADV DHAIEKAFQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFQPGPG IGGDAHFDED ERWTNNFREY NLHRVAHAEL GHSGLSLHST DIGALMYPYSY 240

TFSGDVQLAQ DDIDGIAIY GRSQNFVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
 FYMRTNPFYP EVELNFISVF WPQLPNGLEA AYEAFADRDEV RFPKGNKYWA VQGQNVLHGY 360
 PKDIYSSPGF PRTVKEIDAA LSEENTGKTY FVANKYWRV DEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDVAF MKDGPFFYFFH GTRQYKDPK TKRILTLQKA NSWFNCRKN 469

Seq ID NO: C221 Protein Sequence
 Protein Accession #: NP_055146.1

1 11 21 31 41 51
 MVRKPVVSTI SKGGYLGQNV NGRLPSLGNK EPPGQEKVQL KRKVTLLRGV SIIIGTIIGA 60
 GIFISPKGVL QNTGSVGMSL TIMTVCGVLS LFGALSYAEL GTTIKKSGGH YTYILEVFGP 120
 LPAFVRVWVE LLIRPAATA VISLAFGRYI LEPPFIQCEI PELAIAKLTA VGITVVMVLN 180
 SMSVNSARI QIFLTCKLT AILIIIVPGV MQLIKGQTQN PKDAFSGRDS SITRLPLAFY 240
 YGMAYAGWF YLNFVTEVEE NPEKTIPLAI CISMATIGV YVLINVAFTY TINAEELLS 300
 NAVAVTFSEI LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFTVASREGH LPEILSMIHV 360
 RKHTPLPAVI VLHPLTMINL FSGDLDSLLN FLSPARWLF GLAVAGLIYL RYKCPDMERP 420
 FKVPLPAPAL PSFTCLFMVA LSLYSDPFST GIGFVITLTG VPAYVLPFIW DKKPRWPRIM 480
 SEKITRTLQI ILEVVEEDK L 501

Seq ID NO: C222 Protein Sequence
 Protein Accession #: NP_003237.1

1 11 21 31 41 51
 MGLAWLGLVL FLHVCVGTNR IPESGGDINSV FDIPELTGAA RKGSGRRLVK GPDPSSPAFR 60
 IEDANLTPPV PDDKPDQLVD AVRAEKGLL LASLRQMKKT RGTLLALERK DHSQGVFSVV 120
 SNKRAGTLDL SLTVQKQHV VSVSEALLAT GQWKSITLFV QEDRAQLYID CEKMEAELO 180
 VPIQSVFTRD LASIARLRIA KGVNDNFQGG VLQNVRFVFG TTPEDILRNK GCSSSTSVLL 240
 TLDNNVNGS SPAIRTNYYG ETKDQLAIC GISCELSM VLRLGLRTI VTTIQDSIRK 300
 VTEENKRCN ELRRPPLCYH NGVQYRNNEE WTVDSCTECH CONSVTICKK VSCPIMPSCN 360
 ATVPDGGCCP RCNPSDSADD GWSPSENTS CSTSCGNGIQ QRGRSCDNLN NRCBGSVQT 420
 RTCHIQCCKD RFKQDGGWSH WSPWSSCSVT CGDGVITRIR LCNPSPPQMN GKPCGEARE 480
 TKACKDACP INGGMGFWSP WDICSVTGGG GVQKRSRLCN NPAPQFGGKD CVGDVTENQI 540
 CNKQDCPIDG CLSNPCFAGV KCTSYPDGWS KCGACPPGYS GNGIQCTDVD ECKEVPDACP 600
 NHNGEHRCEI TDPGYNCLPC PPRFTGSQPF GQGVHATAN KQVCKPRNFC TDGTHDCNKN 660
 AKCNLYGHYS DPMYRCCKP GYAGNGIICG EDTDLDGWPN ENLVCVANAT YHCKKNCNPN 720
 LFNSSQEDYD KDGIQDACCDD DDDNDKIPDD RDNCPFHYNP AQYDYDRDDV GDRCDNCPYN 780
 HNPDAQDTN NGEEDACAAD IDGDGILNER DNCQYVYNVD QRDMDMDGVG DQCDNCPLEH 840
 NPDQLSDSD RIGDTCNNQ DIEDDGHQNN LDNCPYVFNQ NQADHDKDGK GDACDHDDDN 900
 DGIFPDKDCN ELVNPDPQKD SDGDGRGDAC KDDFDHDSVP DIDDICPENY DISETDFRRF 960
 QMIPLDPKGT SQNDPNWVVR HQGKELVQTV NCDPGLAVGY DEFNAVDPSG TFPINTERDD 1020
 DYAGFVFGYQ SSSRFYVVMV KQVTQSYWDT NPTRAQGYSG LSVKVVNSTT GPGEHLRNAL 1080
 WHTGNTTPQV RTHMDPRHI GWKDPYAYRW RLSHRPKTGF IRVVMYEGKK IMADSGPIYD 1140
 KTYAGGRGLG FVFSQEMVFF SOLKYECDP 1170

Seq ID NO: C223 Protein Sequence
 Protein Accession #: NP_002183.1

1 11 21 31 41 51
 MPLLNLGRFL LASCNIIIVRS SPTPGSEHGS AAPDCPSCAL AALPKDVPNS QPEMVEAVKK 60
 HILNMLHKK RPDVTPFVK AALLNAIRKL HVGKVGNGY VEIEDDIGRR AEMNEMEQT 120
 SEIITPAESG TARKTLHFBI SKEGSDLSV EBAEVWLFK VPKANRTRK VTIRLFQQQK 180
 HPQGSOLDGE EAEVGLKGE RSELLSEKV VDARKSTWHV FVSSSIQRL LDQKSSLDV 240
 RIACEQCQES GASLVLLGKK KKKSEEGEGK KGGGEGGAG ADEEKEQSHR PFLMLQARQS 300
 EDHPHRRRRR GLECDGKVIN CCKKQFFVGF KDIGWNDWII APSGYHANYC EGECPSHLAG 360
 TSGSSLSFHS TVINHYMRG HSPFANLKSC CVPTKLRPMS MLYYDDGQNI IKXDIQNMIV 420
 EECGCS 426

Seq ID NO: C224 Protein Sequence
 Protein Accession #: NP_000086.1

1 11 21 31 41 51
 MVFDTACVLL LTLAALGASG QGQSPLGSDL GPQMLRELQE TNAALQDVVD WLRQQVREIT 60
 FLQNTVMCD ACQMQQSVRT GLPSVRPLLH CAPGFCPPGV ACIQTESGGR CGPCPAGFTG 120
 NGSHCTDVNE CNAHPCPPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETGQHN CVPNVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240
 ADCVLERDGS RSCVCRVWGA GNGILCGRDT DLDGFPDEKL RCPHFQCRKD NCVTVFNSGQ 300
 EDVDRDIGD ACDFDADGDG VPNEKDNCPV VRNPQQRNTD EDKWDACDN CRSQKNDDQK 360
 DTDQDGRGDA CDDIDIGDRI RNQADNCPRV PMSDQKDSG DGIGDADINC PQKSNPDQAD 420
 VDHFVGDAC DSDQDQDGDG HQDSRDNCPT VFNSAQEDSD HDGQGDACDD DDDNDGVFDS 480
 RDNCRIVPFP QGEDADRGV GDVCQDDFDA DKVVDKIDVC PENAEVTLTD FRAPQTVVLD 540
 PEGDAQIDFN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DFEGTFHVNT VTDDDYAGFI 600
 FGVDSSSYF VVMKQMEQT YMQANPFRV AEPGIQLKAV KSSTGPGEOL RNALNHTGDT 660
 ESQVRLMTD PRNVGWKDKK SYRNWPLQHRP QVGYIRVRFY EGPELVADSN VVLDTTMRGG 720
 RLGVFCFSQE NIIMANLRYR CNDTIPEDYE THQLRQA 757

Seq ID NO: C225 Protein Sequence
 Protein Accession #: NP_612464

1 11 21 31 41 51

MRPQGPAASP QRLRGLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSFG ANIGPOTPGI PGRDGFKEK GECLRESFEE SMTPNYKQCS WSSLNYGIDL 120
 GKIAECTPTK MRNSALRVL FSGSLRLKCR NACCQWYFT FNGABCSGPL PIEAIIVLDQ 180
 GSPENSTIN IHTSSVSEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRITIEE 240
 LPK 243

Seq ID NO: C226 Protein Sequence
 Protein Accession #: NP_003216.1

1 11 21 31 41 51
 MATMENKVIC ALVLVSMAL GTLAEATET CTVAFRERQN CGFPGVTPSQ CANKGCCFDD 60
 TVRGVPCFY PNTIDVPPEE ECEF 84

Seq ID NO: C227 Protein Sequence
 Protein Accession #: NP_056234.1

1 11 21 31 41 51
 MPKRAHWGAL SVVLILWGH PRVALACPHP CACYVPSEVH CTFRSLASVP AGIARHVERI 60
 NLGPNISIAL SETSPAGLTK LELLMIHNE IPSIPDGLR DLSSIQVFKF SYNKLRVITG 120
 QTLQGLSNLM RLHIDENKIE FIHPQAFNGL TSLRLHLLEG NLLHQLHPST FSTFTFLDYF 180
 RLSTIRHLYL AENMVRTLPA SMLRNMPLLE NLYLQGNFWT CCEMRWFLE WDAKSRGILK 240
 CKKDKAYEGG QLCAMCFSPK KLYKHEIHKL KDMTCLKPSI ESPLRQNRSR SIEEQEQEE 300
 DGGSQLILEK PQLPQWSISL NMTDEHGNMV NLVCDIKKPM DVYKIHNAQT DPPDIDINAT 360
 VALDFECPMT RENYEKLWKL IAYYSEVPVK LHRELMLSKD PRVSYQYRQD ADEEALYYTG 420
 VRAQILAEPE WVMQPSIDIQ LNRQSTAKK VLLSYTQYS QTISTKDTRO ARGRSWVMIE 480
 PSGAVQRDQT VLEGGPQLQS CNVKASESPS IFWVLEPGSI LKAPMDPDPS KFSILSGWL 540
 RIKSMESPSDS GLYQCIQVR DEMDRMVYRV LVQSPSTQPA EKDTVTIGKN PGESVTLPCN 600
 ALAIPEAHLS WILPNRIIN DLANTSHVYM LPNGTSLIPK VQVSDSGYYR CVAVNOQCAD 660
 HFTVGITVTY KSGSLPSKRG RRPQAKALSR VREDIVEDEG GSGMGDEENT SRLLHFKDQ 720
 EVFLKTKDDA INGDKAKKGG RRKLKLWKS EKEPETNVAE GRRVPESRRR INMANKQINP 780
 ERWADILAKV RGNLPLKGTB VPPLIKTTSP PSLSLEVTPP FPAVSPSPAS PVQTVTSAGE 840
 SSADVPLIGE ESHVLTISSE ASMGLEHNNH GVILVEPEVT STPLBEVVD LSEKTEEITS 900
 TEGDLKGTA PTLISEPYEP SPTLHTLDTV YEKPTHEETA TEGWSAADVG SSPEPTSSEY 960
 EPFLDAVSLA ESEPMQYFDP DLETQSQDPE DKMKEDTFAH LTPPTIMVN DSSTSGLFED 1020
 STIGEPQVPG QSHLQGLTDN IHLVKSLSST QDTLLIKKGM KEMSQTLCQG NMLESDPHTS 1080
 RSSESEQGS KSITLFDSTL GIMSGMSPVK KPAETTVGTL LDKDTTIVTT TPRQKVPASS 1140
 TMSTHPSRRR PNRRRLRPN KFRHRHKQTP PTFAPSETP STQPTQAPDI KISSQVESSL 1200
 VPTAWDNTV NTPKQLEMEK NAEPTSKGTP RRGHGKRPNK HRYTPSTVSS RASGSKPSPS 1260
 PENKRHNIVT PSSETILLPR TVSLKTEGTY DSDLYMTTTR KIYSSPVKQV ETLFVTKPT 1320
 SDGKEIKDDV ATNVDKHKSD ILVTGESITN AIPTSRSLVS TMGEFKBESS PVGPGTPTM 1380
 NPSRTAQPR LQTDIPVTS GENLTDPLL KELEDVDFTS EFLSSLTVST PPHQEEAGSS 1440
 TTLSSIKVEV ASSQAETTTL DQDHLETTVA ILLSETRPQN HTPTAARKE PASSSPSTIL 1500
 MSLGQTITTK PALPSPRISQ ASRDSKENVF LNYVGNPETE ATPVNNEGTQ HMSGPNELST 1560
 PSSDRDAENL STKLELEKQV FGSRLPRGP DSQRQDGRVH ASHQLTRVPA KPILPTATVR 1620
 LPEMSTQAS RYFVTSQSPR HWINKPEITT YPSGALFENK QFTTFLRLST TIPLPLHMSK 1680
 PSIPSKPTDR RTDQPNYISK VFCNNNIPRA RNPVGKPPSP RHPHYSNGL PFTNTKLSF 1740
 PQLGVTRRPQ IPTSPAPVMR ERKVIPGSYN RIHSHSTFHL DFGPPAPPFL HTPQTGSPS 1800
 TNLQINPMVS STQSSISFIT SSVQSSGSPH QSSSKFPAGG PPASKFWSLG EKPQILTKSP 1860
 QTVSVTAETD TVFPCEATKG PKPFVTWTKV STGALMTPT RIQRFVILKN GTLVIRKQV 1920
 QDRGQYMCTA SNLHGLDRMV VLLSVTVQOP QILASHYQDV TVYLGDTIAM ECLAKGTAP 1980
 QISWIPDDR VQWTVSPVES RITLHENRTL SIKEASFSDR GVYKCVASNA AGADSLAIRL 2040
 HVAALPPVIH QEKLENIPL PGLSIHIHCT AKAAPLPSVR WVLGDGTQIR PSQFLHGNLF 2100
 VFPNGTLYIR NLAPDQSGRY ECVAAANLVGS ARRTVQLNVQ RAAANARITG TSPRRITVRY 2160
 GGTLKLDCA SGPFWRLH RLPKSRMIDA LPSFDSRIKV FANGTLVKS VTDKADGDLV 2220
 CVARNKVDD YVVLKVDDVM KPAKIEHKEE NDHKVPYGGD LKVDCAVATL PNPEISWSL 2280
 DGSLVNSPMQ SDDSGGRTRK YVVFNGTLY FNEVGMREGE DYTCFAENQV GKDEMVRVK 2340
 VVTAPATRN KTYLAVQVPY GDVVTACEA KGEPMKVTW LSPTNKVIPT SSEKYQIYQD 2400
 GTLLIQKQAR SDSGNYTCLV RNSAGEDRKT VHIHNVQPP KINGNPNPIT TVREIAAGGS 2460
 RKLIDCKAEG IPTFVRLHAF PEGVVLPAFY YGNRITVHGN GSLDIRSLRK SDSVQLVMA 2520
 RNEGGEARLI VQLTVLEPME KPIFHDPISE KITAMAGHTI SLNCSAAGTP TFSLVWVLPN 2580
 GTDLQSGQQL QRPYHKADGM LHISGLSSVD AGAYRCVARN AAGHTERLVS LKVLKPEAN 2640
 QYHNLVSI NGETLKLPT PPGAGQGRFS WTLPNGMHLE GPQTLGRVSL LDNGTLTVRE 2700
 ASVFDRTYV CRMETEYGPS VTSIPVIVIA YPPRITSEPT PVIYTRPGNT VKLNCMAGI 2760
 PKADITWELP DKSHLAKGVQ ARLYGNRFLH PQGSLTIQHA TQRDAGPYK MAKNILGSDS 2820
 KTTYIHVF 2828

Seq ID NO: C228 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MPGTLKTRTG APADYRVILK TSQEDBLDVP DDISVRVMS QSVLVSVDVP VLEKQKKVVA 60
 SRQYTVRYRE KGLARWDYK QIANRRVLIE NLIPDTVYEF AVRIISQGERD GKWSTSVFQR 120
 TPESAPTTAP ENLNVWPNVG KPTVVAASWD ALPETEGKVK VCLDGLTGLFS VSSFPQSAKS 180
 PONTFPHTRP LSNHLQSPS PILETLLLPW WMVCSLGNAI FSKSGPQTGE ANDLTPKPSL 240
 SLCOQECSCST QKDFSCLAYL IDIQTKQVKN DPQLEGSVPG PCFLFYFLTP MLDIGGFSFI 300
 MCYEDPVS8 LTGNSLKSVA ASKADVQNT EDNGKPEKPE PSSPSRAPA SSQHPSPVAP 360
 PQGNNAKILL LDLNKLILAN GGAPRKPQLR AKKAEELDLQ STEITGEEL GSREDSMSP 420
 SDTQDQRTIL RPPSRHGHV VAPGRTAVRA RMPALPRREG VDKPGFSLAT QPRPGAPPSA 480
 SASPAIHAST QGTSHRPSLF ASLNDNDLVD SDEDERAVGS LHPKGAFAQ RPALSFSRQS 540
 PSSVLDRSS VHPGAKPAS ARRTPHSGAA EEDSSASAPP SRLSPFHGGS SRLLPTQPHL 600
 SSPLSKGGRD GEDAPATNSN APSRSTMS8 VSHLSSRTQ VSEGAESDG ESHGDGDRD 660

5 GGRQAEATAQ TLRARPASGH PHLLRHKPPA ANGRSPSRPS IGRGPRLQPS SSPQSTVPSR 720
 AHPRVPSHSD SHPKLSSGIH GDEDEKPLP ATVVNDHVPS SSRQFISRGW EDLRRSPQRG 780
 ASLHRKPIIP ENPKSTGADT HPQGYSSLA SKAQDVQOST DADTEGHSFK AQPSTDRHA 840
 SPARPPAARS QQHPSVPRRM TPGRAPEQQP PPPVATSQHH PGQSRDAGR SPSQRLSLT 900
 QAGRPRPTSQ GRSHSSSDPY TASSRGMFLT ALQNQDEDAQ GSYDDSDTEV BAQDVRAFAH 960
 AARAKEAAS LPKHQVESP TGAGAGGDRH SQRGHAASPA RPSRPGGPQS RARVPSRAAP 1020
 GKSEPPSKRP LSSKSQSVS AEDEEEDAG FFKGGKEDLL SSSVPKWPS STPRGGKAD 1080
 GSLAKEEREP AIALAPRGGS LAPVKRPLPP PPGSSPRASH VPSRPPPSA ATVSPVAGTH 1140
 10 FWPRTTTRAP PGHFTTTPML SLRQRMHAR FRNPLSRQPA RPSYRQGYNG RPNVEGKVLP 1200
 GSNKPGNGQR IINGPGQTKM VVDLDRGLVL NAEGRYLQDS HGNPLRIKLG GDGRTIVDL 1260
 GTPVVSQDGL PLFGQGRHGT PLANAQDKPI LSLGGKPLVG LEVIKCTTHP PTTTMTPTT 1320
 TTPLTPTTTP RPTTATTMQP TTTTTPLTTP TPRPTTATTR RTTTRRTTTP VRTTTRTTT 1380
 TTPKPTTPIP TCPPTGLERH DDDGNLIMSS NGIPECYABE DEFSGLETDV AVFTEAYVI 1440
 15 YDEDEYFETS RPTTTEPST TATTPRVIPE EGAISSPPEE EPDLAGRKRK VAPYVTYLNK 1500
 DPSAPCSLTD ALDHPQVDSL DEIIPNDLKK SDLPQPHAPR NITVVAVEGC HSPFIVDWK 1560
 ATPGDLVTGL LVYSASYEDF IRNKFSTQAS SVTHLPIENL KENTRYVFKV QAQNPFGYGP 1620
 ISPSVSFVTE SDNPLLVVRP PGELSGSHS LSNMIPATRT AMDGNM 1666

20 Seq ID NO: C229 Protein Sequence
 Protein Accession #: NP_003005.1

25 1 11 21 31 41 51
 MFLSILVALC LNLHLALGVR GAPCEAVRIP MCRHMPWNIT RMPNHLHHST QENAILAIEQ 60
 YEELVDVNCV AVLRFFFCAM YAPICTLEFL HDPIKPKCSV CQRARDDCRP LMKMYNHSWP 120
 ESLACDELVP YDRGVCIISP AIVTDLPEDV KWIDITPDMM VQERPLDVDC KRLSPDRCKC 180
 KKVKPTLATY LSKNYSVVIH AKIKAVQRSG CNEVTTVVDV KEIFKSSSPI PRTOVPLITN 240
 SSCQCCHILP HQDVLIMCYE WSRMMLLEN CLVEKWRDQL SKRSIQWEER LQEQRRTVQD 300
 30 KKTAGRTSR SNPPKPKGKP PAKPKPASPKK NIKTRSAQKR TNPKRV 346

35 Seq ID NO: C230 Protein Sequence
 Protein Accession #: NP_005931.1

35 1 11 21 31 41 51
 MAPAAMLRSA AARALLPFML LLLQLPPPLL ARALPPDVHH LHAERRGPQP WHAALPSSPA 60
 PAPATQEAER PASSLRPPRC GVDPDSGLS ARNRQKRFVL SGGREKTDL TYRILRFPWQ 120
 40 LVQEQVRQTH AEALKVWSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DGPGLLAHA 180
 PPFKTHREGD VHFQDYDETWT IGDDQGTDLQ QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
 YPLSLSPDDC RGVQHLVGQP WPTVTSRTPA LGPOAGIDTN EIAPLEPDAP PDACEASFDA 300
 VSTIRGELFP FKAGPVWRRL GGQLQPGYPA LASRHWQGLP SFVDAAFEDA QGHIWFFQGA 360
 QYVVDGKPK VLGPAPLTLEL GUVRFVHAA LVWGPEKNKI YPFRGRDYWR FHPSTRRVD 420
 45 PVPRRATDWR GVPSIDAAP QDADGYAYFL RGRLYWKFPD VKVKALEGFP RLVGPDFFGC 480
 AEPANTFL 488

50 Seq ID NO: C231 Protein Sequence
 Protein Accession #: NP_076927

50 1 11 21 31 41 51
 MGENDPPAVE APFSFSLFPG LDDLKISPA PDADAVAAQI LSLPLKFFP IIVIGIALI 60
 LALATGLGIH FDCSGKYRCR SSFKCIELIA RCGVSDCKD GEDEYRCVRV GQGNVILQVF 120
 55 TAASNKTMCS DWAQKHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEPV SIDHLPLDDK 180
 VTALHHSYVY REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWFW QASLQPGGYH 240
 LCGSGVITPL WIIIAHCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGKVCWT SGWGATEDGG DASFVLNHA 360
 VPLISNRIEN HRDVGGLIIS PMLCAGYLT GGVDSQCGDS GGGLVQCERR LWKLVGATSF 420
 60 GIGCAEVNKP GYVTRVTSPL DWIHEQMERD LKT 453

65 Seq ID NO: C232 Protein Sequence
 Protein Accession #: NP_003211

65 1 11 21 31 41 51
 MLWKLTDNIK YEDCEDRHG TSNGTARLPQ LGTVGQSPYT SAPPLSHTPN ADFQPFYFPP 60
 FYQFIYPQSQ DFXSHVNDPY SLNPLHAQPP PQHPGWPGQR QSQESGLLHT HRGLPHQLSG 120
 LDPRRDYRRH EDLLHGPHAL SSGLDLSIH SLPHAI BEVP HVEDPGINIP DQTVIKGPFV 180
 70 SLKSNSENAV SAIPINKDNL PGGVVNPNFV FCSVPGRSL SLSTSKYKVT VAEVQRRLSP 240
 PECLNASLLQ QVLRRAKSN GGRSLREKLD KIGLNLPAQR KAANVTLLT SLVEGEAVHL 300
 ARDFGVVCTE EPPAKAVAEF LNRQHSDFNE QVTRKNMLLA TKQICKFTD LLAQDRSPLG 360
 NSRPNPILFP GIQSCLTHTN LISHGPGSPA VCAAVTALQN YLTELKAMD KMYLNNPNS 420
 75 HTDNNAKSSD KEEKHRK 437

80 Seq ID NO: C233 Protein Sequence
 Protein Accession #: NP_002979.1

80 1 11 21 31 41 51
 MKGLAAALLV LVCTMALCSC AQVGTNKELC CLVYTSWQIP QKFIVDYSET SPQCPKPGVI 60
 LLTRGRGQIC ADPNKKWVQK YISDLKINA 89

Seq ID NO: C234 Protein Sequence
 Protein Accession #: NP_004054.1

	1	11	21	31	41	51	
5	MILQAHLHSL	CLMLLYLATG	YGQEGKFSGP	LKPMTFSIYE	QGEPSQIIPQ	FKANPPAVTF	60
	ELTGSTDNIF	VIEREGLLYY	NRALDRETRS	THNLQVAALD	ANGIIVEGPV	PITIEVKDIN	120
	DNRPTFLQSK	YEGSVRQNSR	PGKFLYVNA	TDLDDPATPN	GQLYYQIVIQ	LFMINNVMYF	180
	QINNKTGAIS	LTREGSQZLN	PAKNPSYNLV	ISVKDMGGQS	ENSFSDTTSV	DIIVTENIWK	240
	APKPVEMVEN	STDHPHIKIT	QVRWNDPGAQ	YSLVDKEKLP	RFPFSIDQEG	DIYVTQPLDR	300
10	EEKDAYVFYA	VAKDEYKPL	SYPLBIHVKV	KDINDNPPTC	PSPVTVFEVQ	ENERLGNSIG	360
	TLTAHRDEE	NTANSFLNYR	IVEQTPKLFM	DGLFLIQTYA	GMLQARQSL	KKQDTPQYNL	420
	TIEVSKDKFK	TLCEYQINVI	DINDQIPIFE	KSDYGNLTLA	EDTNIGSTIL	TIQATDADEP	480
	FTGSSKILYH	IYKGDSEGR	GVDTPHTNT	GYVVIKPLD	PETAAVSNIV	FKAENPEPLV	540
	PGVKYNASSP	AKPTLIVTDV	NEAPQFSQHV	FQAKVSEDA	IGTKVGNVTA	KDPEGLDISY	600
15	SLRGDTRGWL	KIDHVTGEIP	SVAPLDREAG	SPYRVQVVAT	EVGGSSLSV	SEPHLILMDV	660
	NDNPPRLAKD	YTGFFCHPL	SAPGSLIFEA	TDDQHLFRG	PHFTFSLGSG	SLQNDWEVSK	720
	INGTHARLST	RHTEFSEREY	VVLIRINDGG	RPPLEGIVSL	PVTFPCSVEG	SCFRPAGEQT	780
	GIPTVGMVAG	ILLTLLLVIG	IILAVVFIRI	KKDKGKDNVE	SAQASEVKPL	RS	832

Seq ID NO: C235 Protein Sequence
Protein Accession #: NP_004434.1

	1	11	21	31	41	51	
25	MARARPPPPP	SPPPGLPLLL	PPLLLPLLL	LPAGCRALEE	TIMDTKWVTS	ELAWTSHPES	60
	GMEVSVGYDE	AMNPIRTYQV	CNVRESSQMN	WLRTGFIWRR	DVQRVYVELK	FTVRDCNSIP	120
	NIPGSCKETP	NLFYFEADSD	VASASSPFWM	ENFYVKVDTI	AFDESPSRLD	AGRVNTKVR	180
	FGPLSKAGFY	LAFQDQGACM	SLISVRAPYK	KCASTAGTAG	LFPETLTQAE	PTSLVIAPGT	240
	CIPNAVEVS	PLKLYCNGDG	EMMVPGACT	CATGHEPAAK	ESQCRPCPPG	SYKAKQGGGP	300
	CLPCPPNSRT	TSPAASICTC	HNNFYRADSD	SADSACTTVP	SPPRGVISNV	NETSLILEWS	360
30	EPRLDGGRDD	LLYNVICKKC	HGAGGASACS	RCDNVEFPV	RQLGLTERRV	HISHLAHTR	420
	YTFEVQAVNG	VSGKSPLEPR	YAAVNITTNQ	AAPSEVPTLR	LHSSGSSSLT	LSNAPPERFN	480
	GVILDYEMKY	FEKSEGLAST	VTSQMNVSQV	DGLRPDARYV	VQVRARTVAG	YQYSRPAEF	540
	ETTSESGSA	QQQLQQLPLI	VGSATAGLVF	VVAVVVIAIV	CLRKQRHGS	SEYTEKLQY	600
	IAPGMKYIID	PFTYEDPNEA	VREPAKEIDV	SCVKIEEVIG	AGEPGEVCRG	RLKQPGRRV	660
35	FVAIKTKLVG	YTERQRDFL	SEASIMQFQD	HPNIIRLEGV	VTKSRVPMIL	TEFMENCALD	720
	SPLRLNDGQF	TVIQLVGMRL	GIAAGMKYLS	EMNYVHRLA	ARNILVNSML	VCKVSDPGLS	780
	REFLEDDPSD	TYTSSLGSKI	PIRWTAPEAI	AYRKFTASD	VMSYGIWMWE	VMSYGERPYW	840
	DMSNQDVINA	VEQDYLPPP	MDCPTALHQL	MLDCWVRDNR	LRPKFSQIVN	TLDKLRNAA	900
40	SLKVIASAGS	GMSQPLDRT	VPDYTTFTTV	GDWLDIAKMG	RYKESFVSAG	PASFDLVAMQ	960
	TAEDLLRIGV	TLAGHQKKIL	SSIQDMRLQM	NQTLFPVQV			998

Seq ID NO: C236 Protein Sequence
Protein Accession #: NP_001795.1

	1	11	21	31	41	51	
45	MYVGYVLDDK	SPVYGPAPRP	ASLGLGPANY	GPPAPPPAPP	QYPDFSSYSH	VEPAPAPPTA	60
	WGAPFPAPKD	DMAAAYGGPG	AAAPASPASL	AFGPPPDPSF	VPAPPGPGPG	LLAQPLGGPG	120
	TPSSPGAQR	TPYEWRRSV	AAGGGGSGSK	TRTKDKYRVV	YTDHQLRLEK	KBPYYSRYIT	180
50	IRRKSELAAN	LGLTERQVKI	WFQNRRAKER	KVNKKKQQQQ	QQPQPPMARD	ITATPAGPSL	240
	GGLCPNNTSL	LATSSPMFVK	EEFLP				265

Seq ID NO: C237 Protein Sequence
Protein Accession #: NP_068813.1

	1	11	21	31	41	51	
55	MGSDRARKGG	GGPKDFGAGL	KYNSRHEKVN	GLEEGVEFLP	VNNVKVKEKH	GPGRWVVLAA	60
	VLIGLLVLLQ	GIGFLVWHLQ	YRDVRVQKVF	NGYMRITNEN	FVDAYENSNS	TEFVSLASKV	120
60	KDALKLLYSQ	VPLPGPYHKE	SAVTAPESEGS	VIAYYWEFS	IPQHLVEEAE	RVMAEERVVM	180
	LPFRARSLKS	FVTVSVVAFP	TDSKTVQRTQ	DNSCSPGLHA	RGVELMRFTT	PGFPDSPYPA	240
	HARCOVALRG	DADSVLSLTP	RSPDLASCD	RGSDLVTVYN	TLSPMEPHAL	VQLGTYPPS	300
	YNLTFFHSQN	VLLITLITNT	ERRHPGFAT	FFQLPRMSSC	GGRLRKAQGT	FNSFYYPGHY	360
	FPNIDCTWNI	EVPNNQHVKV	RFKFFYLLEP	GVPAGTCPKD	YVEINGEKYC	GERSQPVVTS	420
65	NSNKITVRFH	SDQSYTDTGF	LAEYLSYDSS	DPCPGQPTCR	TGRCIRKELR	CDGWADCTDH	480
	SDELNCSCDA	GHQFTCKNKP	CKPLFWWCDS	VNDGDNDSDE	QCCSCPAQTF	RCSNGKCLSK	540
	SQCCNGKDDC	GDGSEASCP	KVNVTCTKH	TYRCLNGLCL	SKGNPECDGK	EDCSDGSGDEK	600
	DCDCGLRSTP	RQARVVGGTD	ADEGEWPMQV	SLHALGQGH	CGASLISPNW	LVSAACYID	660
	DRGFYSYDPT	QWTAFLGLHD	QSORSAPGVQ	ERRLKRISH	PPFNDPTFDY	DIALLELEKP	720
70	AEYSSMVRPI	CLPDASHVFP	AGKAIMVTGW	GHTQYGGTGA	LILQKGBIRV	INQTTCEMLL	780
	PQQITPRMMC	VGPLSGGVDS	CQGDSSGGPLS	SVEADGRIFQ	AGVVSNGDGC	AQRNKPQVYT	840
	RLPLFRDWIK	ENTGV					855

Seq ID NO: C238 Protein Sequence
Protein Accession #: Bos sequence

	1	11	21	31	41	51	
80	MPPFLLEAV	CVPLFSRVFP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
	SVKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QGEVKARIKR	120
	MVFKGGRRET	ELALKYLLHR	GLPGGRNASV	PQILITVTDG	KSQGDVALPS	KQLKRGVTV	180
	FAVGVRPFR	RELHALASEP	RGQHVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
	PCEHRTLEMV	REFAGNAPCW	RQSRRTLAVL	AAHCFFYSWK	RVFLTHPATC	YRTTCPGPCD	300
	SQPQNGGTC	VFEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360

5 RAKVFVKRFV RAVLESDSRA RVGVATYSRE LLVAVFVGEY QDVPLDVNSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVS 480
 EAVRAELEBI TGSFKHVMVY SDPQDLFNQI PELQKLCSE QPGRCTQAL DLVFMLD TSA 540
 SVGPENFAQM QSVFRSCALQ FEVNPQVTV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVGS A GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLNNNGI 660
 SVLVVGVGVFV LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK QPVNLCCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR FLRRP 755

10 Seq ID NO: C239 Protein Sequence
 Protein Accession #: Eos sequence

15 1 11 21 31 41 51
 MPPFLLEAV CVPLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMPLDGSN 60
 SVGKGSFERS KHPAIVTCDG LDISPFRVVR GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
 MFPKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
 FAVGVRFPRM ELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCM RGSRRTLAVL AAHCFYFSWK RVFLTHPATC YRTTCFPGCD 300
 SQPCQNGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
 20 RAKVFVKRFV RAVLESDSRA RVGVATYSRE LLVAVFVGEY QDVPLDVNSL DGIPFRGGPT 420
 LTGSALRQAA ERGFGSATRT QDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVS 480
 EAVRAELEBI TGSFKHVMVY SDPQDLFNQI PELQKLCSE QPGRCTQAL DLVFMLD TSA 540
 SVGPENFAQM QSVFRSCALQ FEVNPQVTV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 25 APYLGGVGS A GTALLHIYDK VMTVQRGARP GVPKAVVLT GGRGAEDAAV PAQKLNNNGI 660
 SVLVVGVGVFV LSEGLRRLAG PRDSLHVAA YADLRYHQDV LIEWLCEGAK QPVNLCCKPSP 720
 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAPGP 807

30 Seq ID NO: C240 Protein Sequence
 Protein Accession #: XP_097386.1

35 1 11 21 31 41 51
 MPKSEPLGCL SPASRAPGSA AATGANLPAA SGGPGPLGPP CTCPPRSLGR GRAGSRAGSS 60
 PSGCVCVSGI LRVSVDGPA SRRWVDLDSN SEDLSLLTTP MIVGTGGVGG GWARGWVPAQ 120
 EKEVAEGSGH AGRGNGRRLLQ RVYGARSWIL GRKPCLQRL PASGGFVQFQ PCPSPATACR 180
 WGFKFGVAFW GAAQHPPLCR LGGGRVPSA TRTLDGF 217

40 Seq ID NO: C241 Protein Sequence
 Protein Accession #: CAC03433

45 1 11 21 31 41 51
 MLSSTDTFCA SWELVVRVDH PNEEQQKQVT LRVSGLDHVG GVMLKLVEQI NISQDWSDF 60
 LWWEQKHCWL LKTHWTLDKY GVQADAKLLP TPQHKMLRLR LPNLKMLRLR VSFSAVVFKA 120
 VSDICKILNI RRSEELSLK PSGDYFKKCK KDKNNKEPI IEDILNLESS PTASGSSVSP 180
 GLYSKTMFPI YDPIINGTAS STMTWFSDF LTRQNCSTLA PSQPPQSPEA LADMYQPRSL 240
 VDKAKLNAGW LDSSRSLEME GIQEDELILL RFKYYSFFDL NPKYDAVRIN QLYEQARWAI 300
 50 LLEEDICTEE EMLIPAAQY HSKLSLSAE TQDFAGESEV DEISAALSNI ETVLEGGKAD 360
 SLEEDITDIP KLADNLKLFK PKLLPKAFK QYWFIFKDS IAYFKNKELE QGEPLKLANL 420
 RGCEVVPDVN VAGRKFGIKL LIPVADGMNE MYLRCDHENQ YAQWMAACML ASKQKTMADS 480
 SYQPEVLNII SLFRKKNRNS ASQVASSLEN MDMNPECFVS PRCAKHKHSK QLAARILEAH 540
 QNVAQMPLVE AKLRPIQAW SLPEFGLTYY LVRPFKSKKD DILGVSYNRL IKIDAATGIP 600
 55 VTTWRFTNIK QMNVNWTRO VVIEFDQNVF TAFCTLADSC KIVHEYIGGY IFLSTRSKDQ 660
 NETLDEDLFH KLTGGQD 677

60 Seq ID NO: C242 DNA Sequence
 Nucleic Acid Accession #: NM_005170
 Coding sequence: 337..918

65 1 11 21 31 41 51
 GGGCGTGAGA AAGCGACGCG CGGCGGCGCG GAGGAGGGTT ATCTATACAT TTA AAAACCA 60
 GCGCGCTGCG CCGCGCTGCG GGAGACCTGG GAGAGTCCGG CCGCACGCGC GGGACACGAG 120
 CGTCCCAAGC TCCTGGGCGG GTACGGCCTG CCACCACTAG GCCTCCTATC CCGGGCTCC 180
 AGACGACCTA GACGCGTGC CCGGGGAGT TGCCTGGCGG CGCGGTGCCA GAAGCCCTCT 240
 TGGGGGCGCA CAGTTTTCCT CGTGCCTCC GGTTCCTCTG CCTGCACCTT CCTGCGGCGC 300
 GCGGGGACCT GGAGCGGGCG GGTGGATGCA GGCGGATG ACGGCGGCAC ACTGCCCAGG 360
 70 TCGCGCCCC CTGCGCCCC CGTCCCTGTC GGCTGCGCTG CCGGGCGGAG ACCCGCGTCC 420
 CCGGAACCTG TGCGCTGCAG CCGCGGCGCG CGACCGGCCA CCGCAGAGAC CGGAGCGGCG 480
 GCAGCGGCGG TAGCGCGGCG CAATGAGGCG GAGCGCAACC GCGTGAAGCT GGTGAACCTG 540
 GGCTTCCAGG CGCTGCGGCG GCACGTGCGG CACGCGCGCG CCAGCAAGAA GCTGAGCAAG 600
 GTGGAGACGC TGCGCTCAGC CGTGGAGTAC ATCGCGCGCG TGCGAGCGCT GCTGGCCGAG 660
 75 CACGAGCGCG TGCGCAACGC GCTGGCGGGA GGGCTGAGGC CGCAGGCGGT GCGGCGGTCT 720
 GCGCGCGCGG GCGCGCCAGG GACCAACCGG GTGCGCGCT GCGCTCCCGG CGCTTCTTGG 780
 TCCCGGGGCC GCGGGGCGAG CTCGGAGCCC GGCTCCCGCG GTTCGCGCTA CTCGTCCGAC 840
 GACAGCGGCT GCGAAGGCG GCTGAGTCTT GCGGAGCGCG AGCTACTCGA CTCTCTCCAGC 900
 80 TGGTAGGGG GCTACTGAGC GCCCTCGACC TA 932

Seq ID NO: C243 Protein Sequence
 Protein Accession #: NP_060233.1

1 11 21 31 41 51

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MSGGHQLQLA	ALNFWLLMAT	LQAGFGRTGL	VLAADVSESR	SAEQKAVIRV	IPLKMDPTGK	60
LNLTLEGVFA	GVAEITPAEG	KLMQSHPLYL	CNASDDDNLE	PGFISIVKLE	SPRRAPRPCL	120
SLASKARMAG	ERGASAVLFD	ITEDRAAAEQ	LQQLPLGLTWP	VVLINGNDAB	KLMEFVYKNO	180
KAHVRIELKE	PPANPDYDVW	ILMTVVGTIF	VILASVLRI	RCRPRHSRPD	PLQORTAWAI	240
SQLATRRYQA	SCRQARGSWP	DSGSSCSSAP	VCAICLEEPS	BQELRLVISC	LHEFHRCVD	300
PWLHQHRTCP	LCVFNITEGD	SFSQSLGFSR	SYQEPGRRLH	LIRQHPGHAH	YHLPAAYLLG	360
PSRSVARPP	RPGPFLPSQE	PGMGRHHRF	PRAAHPRAPG	EQQLLAGAQH	PYAQGWGMHS	420
LQSTSHQPA	CPVPLRRARP	PDSGSGGESY	CTERSGYLAD	GPASDSSSGP	CHGSSSDSVV	480
NCTDISLQGV	HGSSSTFCSS	LSSDFDPLVY	CSPKGDQPRV	DMQPSVTSRP	RSLSDSVPTG	540
ETQVSSHVHY	HRHRHHYK	RFQWHGRKPG	PETGVPPQSRP	PIPRTPQPE	PPSPDQQVTG	600
SNSAAPSGRL	SNPOCPRALP	EPAPGPDVAS	SICPSTSSLF	NLQKSSLSAR	HPQRKRGGP	660
SEPTPGSRPQ	DATVHPACQI	PFHYTPSVAY	PWSPEAHPLI	CGPPLDKRL	LPETPGPCYS	720
NSQPVNLCIT	PRQPLEPHFP	GEGPSEWSSD	TAEGRPCPYP	HQVLSAQPG	SBEELBELCE	780
QAV						783

Seq ID NO: C244 DNA Sequence
Nucleic Acid Accession #: NM_004289
Coding sequence: 493..1695

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1	11	21	31	41	51	
GCCGCCGCCCT	CGTCCACCGG	AGGAGCCGGC	GCCAGCGTGG	ACGGGGGCAG	CCAGGCTGTG	60
CAGGGGGGCG	CGCGGGACCC	COGAGCGGCT	CGGAGTGGCC	CCTTGGACGC	CGGGGAAGAG	120
GAGAAGGCAC	CCGCGGAACC	GACGGCTCAG	GTGCCGGAAG	CTGGCGGATG	TGCGAGGAG	180
GAGAATGGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTTCCCA	GCATGAGGAA	240
AATGAAGAAA	GGGTGTGAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAATGA	TGATGATGAA	300
AACAAATAG	CAGAGAAACG	TGACTGGGAG	GCAGAAAAGA	CACTGAATC	TAGAAATGAG	360
AGACATCTGA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAAG	ACTTATTCCA	GTGTCTTTCA	420
TCACAGCCTG	AAAATCACT	GGAGGGCAGC	TCATTGGGAG	ATATTCTCT	TCCAGGCGAGT	480
ATCAGTGATG	GCATGAATTC	TTGAGCAGAT	TATCATGTAA	ACTTCAGCCA	GGCTATAAGT	540
CAGGATGTGA	ATCTTCATGA	GGCCATCTTG	CTTTGTCCCA	ACAATACATT	TAGAAGAGAT	600
CCAACAGCAA	GGACTTCACA	GTCAAGAA	CCATTCTGTC	AGTTAAATTC	TCATACCACC	660
AATCTGAGC	AAACCTTTCC	TGGAACATA	TTGACAGGAT	TTCTTTTACC	GGTTGACAA	720
CATATGAGGA	ATCTAACCA	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGAT	780
GAGATAAACT	TAATGTCTAT	GGCCACAGAA	GACAACTTTG	ATCCAATCGA	TGTTTCTCAG	840
CTTTTGTGAT	AACCAAGATC	TGATTCTGGC	CTTTCTTTAG	ATTCAAGTCA	CAATAATACC	900
TCTGTCTATCA	AGTCTAATTC	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
ACTGACCATG	AATCTAGTTC	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
GAACCCAGTA	AGCTTTGTCA	CTTGGAATCAA	AGTGATTCTG	ATTTCCATGG	AGATCTTACA	1080
TTTCAACAGC	TATTTCAATA	CCACACTTAC	CACCTACAGC	CAACTGCACC	AGAATCTACT	1140
TCTGAACCTT	TTCCGTGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CCTTGAAGAC	1200
ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTCT	1260
GTAGATGAAA	TTGTGCGCAT	GCCTGTTGAT	CTTTTCAATA	GCATGTTAAG	TAGATATTAT	1320
CTGACAGACC	TACAACTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
GCTGCGCAGA	ACTGTCTGTA	ACGCAAAATT	GACATAATTT	TGAATTTAGA	AGATGATGTA	1440
TGTAACCTGC	AAGCAAGAAA	GGAACTCTCT	AAGAGAGAGC	AAGCACAATG	TAACAAGCT	1500
ATTAACATAA	TGAACAGAAA	ACTGCATGAC	CTTTATCATG	ATATTTTATG	TAGATTAAGA	1560
GATGACCAAG	GTAGCCAGAT	CAATCCCAAC	CACATATGCT	TCCAGTGTAC	CCATGATGGA	1620
AGTATCTTGA	TAGTACCCAA	AGAACTGGTG	GCCTCAGGCC	ACAAAAGGA	AACCCAAAAG	1680
GGAAAGAGAA	AGTGAAGAAA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTCTA	1740
GAAACTGATT	ATTTGATCA	GAAACCATTG	AAACTGCTTC	AAGAATTTGA	TCTTTAAGTA	1800
CTGCTACTTG	AATAACTCAG	TTAAGCGTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
CTTCAAGATC	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCATTGT	1920
ATACAAAATT	CATAGTTATG	TCCAAAGAAT	AGGTTAACAT	GAAAACCCAG	TAAAGACTTT	1980
CATCTGTGCA	GCCATCCTTT	TAAAGAGTAA	GTTGGTTACT	TCAAAAAGAG	CAAAACTGCG	2040
GGATCAAATT	ATTTTAAGAG	GTATTTCACT	TTTAAATGCA	AAATAGCCCT	ATTTTCATTT	2100
AGTTTGTAG	CACATATAGT	AGCTTTTCAA	ACACTATTTT	AATCTTTATA	TTTAACTTAT	2160
AAATTTTGTCT	TTCT					2174

Seq ID NO: C245 Protein Sequence
Protein Accession #: NP_004433

65
70
75
80

1	11	21	31	41	51	
MLRLRLGAAL	LLLPLLAAVE	ETLMDSTTAT	AELGWMVHPP	SGWBEVSGYD	ENMNTIRTYQ	60
VGNVFBSSQN	NWLRTKPIRR	RGARHRIHVM	KFSVRDCSSI	PSVPGSCKET	FNLYYYEADF	120
DSATKTFPNW	MENPFWKVDI	IAADESPSQV	DLGGRVMKIN	TEVRSFPGVS	RSGPYLAFQD	180
YGGGMSLIAV	RVFYRKCPRI	IQNGAIFQET	LSGAESTSLV	AARGSCIANA	BEVDVPIKLY	240
CNGDCWNGYV	IGRCMCKAGP	BAVNGTVCR	GCPSTGTFKAN	QGDSEACTHCP	INSRTTSEGA	300
TNCVCWNGYV	RADLDPLDMP	CTTIPSAPOA	VISSVNETSL	MLEWTPPRDS	GGREDLVYNI	360
ICKSCGSGRG	ACTROGDNVQ	YAPRQLGLTE	PRIYISDLLA	HTQYTFBIQA	VNGVTDQSPF	420
SPQFASVNI	TNQAPSAVS	IMHGVSRIVD	SITLSWSQPD	QPNQVILDYE	LQYKEKELSE	480
YNATAIKSGT	NTVTVQGLKA	GAIYVQVRA	RTVAGYGRYS	GRMYQMTMB	AEYQTSIQEK	540
LPLIIGSSAA	GLFVLIAVVV	IAIVCNRRRG	FERADSEYTD	KLQHYTSGHM	TPGMKIYIDP	600
PTYEDFNEAV	REFADPIDIS	CVKIEQVIGA	GEFGEVCSGH	LKLPGKREIF	VAIKTLKSGY	660
TEKQRDRFLS	EASIMQPDFH	PNVIHLEGVV	TKSTFVMIIT	SPMENGSLDS	FLRQNDGQFT	720
VIQLVGLMRG	IAAGMKYLAD	MNYVHRDLAA	RNILVNSMLV	CKVSDFLGSR	FLEDDTSDPT	780
YTSALGGKIP	IRWTAPEAIQ	YRKPTSASDV	WSYGIVMMEV	MSYGERPYMD	MTNQDVINAI	840
BQDYRLPPPM	DCPSALHQLM	LDCWQKDRNH	RPKFGQIVNT	LDMIRNPNS	LKAMAPLSSG	900
INLPLLDRTI	PDYTSFNTVD	ENLEAIKMGQ	YKESFANAGF	TSFDVVSQMM	MEDILRVGLT	960
LAGHQKKILN	SIQVMRAQMN	QIQSVEV				987

Seq ID NO: C246 Protein Sequence

Protein Accession #: NP_114148.1

	1	11	21	31	41	51	
5							
	MDARRVPQKD	LRVKKNLKKF	RYVKLISMET	SSSSDDSCDS	FASDNFANTR	LQSVREGCRT	60
	RSQCRHSGLP	RVAMKPPARS	TRGATNKKAE	SRQPSNSVT	DSNSDSEDES	GMNFLEKRAL	120
	NIKQNKAMLA	KLMSLESEFP	GSFGRHRPLP	GSDSQSRRPR	RRTFPGVASR	RNPERRARPL	180
	TRSRSRILGS	LDALPMEEBE	EEDKYMLVRK	RKTVDGYMNE	DDLPRSRRSR	SSVTLPHIIR	240
10	PVEEITGGV	GERLQQFSKR	RYITVHWALL	VINAVRRLLI	PKQTAETQTA	GAPEASSVAP	300
	AFETVMVKRS	GMLCWTGTI	ARLVEESATA	VSAGSEMDGV	RLGSLCI		347

Seq ID NO: C247 Protein Sequence
Protein Accession #: NP_036577.1

	1	11	21	31	41	51	
15							
	MENPSAAL	GKALCALLLA	TLGAAGQPLG	GESICSARAP	AKYSITPTGK	WSQTAFPKQY	60
	PLFRPPAQWS	SLIGAHHSSD	YSMWRKNQYV	SNGLRDFAER	GEAWALMKEI	EAAGALQSV	120
	HAVPSAPAVP	SGTQQTSAEL	EVQRRHSLVS	FVVRIVPSPD	WFGVDSLDL	CDGDRWREQA	180
20	ALDLYPYDAG	TDSGFTFSFP	NFATIPQDTV	TEITSSSPSH	PANSFYYPRL	KALPPIARVT	240
	LVRLRQSPRA	FIPPAFVLPS	RDNEIVDSAS	VPETPLDCEV	SLWSSWGLCG	GHCGRIGTKS	300
	RTRYVRVQPA	NNGSPCEPEL	EEAECVPDNC	V			331

Seq ID NO: C248 Protein Sequence
Protein Accession #: NP_063947.1

	1	11	21	31	41	51	
25							
	MLQDPDSQDP	LNSLDVKPLR	KPRIPMETFR	KVGIPIIIAL	LSLASIIIVV	VLIKVILDKY	60
30	YFLCGQPLHF	IPRQLCDGE	LDCPLGEDEE	HCVKSFPPEP	AVAVRLSKDR	STLQVLDSAT	120
	GNWFSACPDN	PTALAEATAC	RQMGYSKPT	FRAVEIGPDQ	DLDDVEITEN	SQELMRNNS	180
	GPCLSGSLVS	LHCLACGKSL	KTPRVVGEE	ASVDSWPHQV	SIQYDKQHC	GGSIIDPHWV	240
	LTAARCFRKH	TDVFNWVRA	GSDKLGSFPP	LAVAKIIIE	FNPMYPKDN	IAMLKLQFP	300
	TFSGTVRPIC	LPFFDEBLTP	ATPLMIIGWG	FTKQNGGKMS	DILLQASQV	IDSTRCNADD	360
35	AYQGEVTEKM	MCAGIPEGGV	DTCQGDSSGP	LMYQSDQNHV	VGIVSWGYGC	GGPSTPGVYT	420
	KVSAYLNMWY	NVWKAE					437

Seq ID NO: C249 Protein Sequence
Protein Accession #: NP_003036.1

	1	11	21	31	41	51	
40							
	MGCKVLNLIG	QOMLRRKVVD	CSREETRLSR	CLNTFDLVAL	GVGSTLGAGV	YVLGAVARE	60
	NAGPAIVISF	LIAALASVLA	GLCYGEFGAR	VPKTSGLVY	SYVTVGELMA	PITGWNILIS	120
45	YIIGTSSAVR	AWSATFDLEI	GRPIGEFERT	HMTLNAFVGL	AEFNDIFAVI	IILILTGLLT	180
	LGVKESAMVN	KIFTICINVLV	LGFIMVSGFV	KGSVKMQLT	EEDFGNTSGR	LCLNNDTKEG	240
	KPGVGGFMFP	GFGSVLGSAA	TCFYAFVGF	CIATTGEEVK	NPQKAIFVGI	VASLLICFIA	300
	YFGVSAALTL	MMPYFCLDNN	SPLDPAFKHV	GWEGAKYAVA	VGSLCALAS	LLGSMFPMR	360
	VIYMAEDGL	LFPKLANVND	RTKTPIIATL	ASGAVAAVMA	PLFDLKDLDV	IMSIGTLAY	420
50	SLVAACVLVL	RYQPEQPNLV	YQMASTDEL	DPADQNELAS	TNDSQLGFLP	EAEMFSLKTI	480
	LSPKMEPSK	ISGLIVNIST	SLIAVLIITF	CIVTVLGRE	LTKGALWAVP	LLAGSALLCA	540
	VVTGVINRQP	ESKTKLSPKV	PFLPVLPILS	IPVNVYLMNQ	LDQGTWVRPA	VWMLIGFIY	600
	FGYGLWHSSE	ASLDADQART	PDGNLDQCK				629

Seq ID NO: C250 Protein Sequence
Protein Accession #: NP_002767.1

	1	11	21	31	41	51	
60							
	MRAPHLHLSA	ASGARALAKL	LPLLMAQLWA	AEAALLPOND	TRLDPPEAYG	PCARGSQPWQ	60
	VSLFNLGLSF	CAGVLVDQSW	VLTAAHCGNK	PLWARVGDH	LLLLQGEQLR	RTTRSVVHPK	120
	YEQSGSPILP	RRTDEHDLML	LKLARFVVP	PRVRALQLPY	RCAQPGDQCQ	VAGWGTTAAR	180
	RVKYNKGLTC	SSITILSPKE	CEVFPYGVVT	NNMICAGLDR	GQDPQCSDSG	GPLVCDLTLQ	240
65	GILSKGWYFC	GSAQHFAVYT	QICKYMSWIN	KVIRSN			276

Seq ID NO: C251 Protein Sequence
Protein Accession #: XP_095088.3

	1	11	21	31	41	51	
70							
	MTAAATAPRG	RVSPASPARS	TAGLPRAFLO	SLRTLDDILD	DWQRCVHLR	EIQSLWVEAR	60
	ELPSGVLBGL	SQRRGPQPGA	AVRSRRGGAV	PRGARAVPER	CAGTETRGR	RCSGLQLRGG	120
	GFRGCPADPC	ARGEHRRTI	TSGVDCGLLK	QMKLEQEK	VLLQGLEMA	QGRDWYQQQL	180
	QOVQERQCR	QQSRASADFG	AVGSPRPLGR	LLPKVQEVAR	WLGELLAEC	AGRALPTSSS	240
75	GPPCSALTST	SSPGWQQQII	LMLKEQNRL	TQEVTEKSER	ITQLEQKSAL	IKQLFEARAL	300
	SQQDGGLSA	GPHIEPLTRF	RLPVLTWAGA	LLSPHSPQLL	LPLSADSGGP	LHELDPWF	360
	AVLLWVPSG	KRTAARLHP	HQRPAEGAWQ	LQCGAERAAE	TCGTLPHPES	HKTTCPEDSL	420
	GGPCPQEGDR	SWSHLGAAPD	VAPAVAKVTP	NREDAAGSRH	GDICPLCPKG	LLTPFDIAIE	480
	FSLAENQCID	HAQONLYRDV	MLENYRNLFS	LGMTVSKFDL	IACLEQNKEP	QNIKRNEMAA	540
80	KHPVTCSHFN	QDLQPEQSIK	DSLQKVIPT	YKCGHENLQ	LKKCKYKGSF	CEVHKGGYND	600
	LNQCLSNQTN	KIFQTHKCVK	VFSKPSNSNR	HNARYTGKKH	LKCKYKGSF	CMPSHLNQHQ	660
	LIHTKEKSYK	CEEGKSPFNH	SSSGTTHKRI	LTGEKPYRCE	EGGKAFRWP	NLTRHKRIHT	720
	GEKPYACBEC	GQAFRRSSTL	TNHKRIHTGE	RPYKCEBCKG	AFSVSSALIY	HKRIHTGEKP	780
	YTCBEGKAF	NCSSTLWKTHK	LIHTGEKPYT	CEBEGRTFNC	SSTVKAHKRI	HTGEKPYKCE	840

5	ECDAKPKWHS SLAKHKIHT GEKPYKCSDS KALAKSSEVQ KVYSGDGENG IRVHKKKTQ 900									
	GMLVRNKNEN RTGLFQIRAA VRPNRDFSWG QQEGSLTDP1 QRKEEPLQN HYDHQNALED 960									
	QRNTGVGGLL TFRDVVIEFS LEBWQCLDHA QQNLYRDVML ENYRNLVSLG IAVSKPDLIT 1020									
	CLEQNKKEPN IKRNMVTKH PDLPELGLIK DSLQKVIPIR YKSGHDNLQ VKTCKSMGEC 1080									
	EVQKGGCNEV NQCLSTONK IPQTHKCKV FGKFSNSNRH KTRHTGKKHF KCKYKGSFC 1140									
10	MVSQHLHQHI IHTRENSYQC EECGKPFNC STLSKHKRIH TGEKPYRCE CGKAPTWSST 1200									
	LTHGRIHTG EKPYTCESG QAFSRSTLA NKKRIHTGEK PYTCESGKA PSLSSSLTYH 1260									
	KRIHTGEKPY TCESGKAFN CSSTLKHKI IHTGEKPYK KECGKAFAP STLNTHKRIH 1320									
	TGEKPYKCE CDKAPKSSS LANHKSMTG EKPYKCE 1357									
	Seq ID NO: C252 Protein Sequence Protein Accession #: NP_114433.1									
15	1 11 21 31 41 51									
	MASRMRLLLL LLSLAKTAGV LGDIIMRPS APGWFYHKS CYGYFRKLRN WSDABLECQS 60									
	YGNAGHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLVRWSG 120									
	KSMGGNKHCA EMSSNNFLT WSSNECNKRQ HFLCKYRP 158									
	Seq ID NO: C253 Protein Sequence Protein Accession #: XP_051860.2									
20	1 11 21 31 41 51									
	MDGVNLSTEV VYKKGQDYRF ACYDRGRACR SYRVRFLOGK FVRPKLVTI DTNVNSTILN 60									
	LEDNVQSWKP GDTLVIASTD YSMYQAEFQ VLPSCRCAFN QVKVAGKFMV LHIGEEIDGV 120									
	DMRAEVLGLS RNIIVMGEME DKCYPYRNHI CNFFDFDTPG GHKIFALGFK AAHLEGTELK 180									
	HMGQQLVGQY PIHPLAGDV DERGGYDFPT YIRDLISHT FSRCTVTHGS NGLLIKDVVG 240									
30	YNSLGHCFPT EDGPEERTPT DECLGLLVKS GTLLPSDRDS KMCKMITGDS YPGYIPKPRQ 300									
	DCNAVSTFW ANPNNNLINC AAAGSEETGF WFIHHVPTG PSVGMYSPTY SEHIPGLKPY 360									
	MNRASNYRA GMIDNGVKT TEASAKDKRP FLISISARYS PHQADAPLK REPARIHFI 420									
	AYKNQDRGAW LRGGDVWLD CRPADNGIGL TLASGTFPPY DQSGQETKN SLFVSGSNV 480									
	GTEMDNRIW GPGGLDHSR TLPIGQNPFI RGIQLYDGP NIQNTCFRKF VALEGRHTSA 540									
35	LAFRLNNAW SCPHNNVTGI AFEDVPITSR VFFGEPGPF NQLDMDGDKT SVFHDVDGVS 600									
	SEYPSGYLTK NDNMLVRHPD CINVFDWGA ICSGCYQMY IQAYKTSNLR MKIIRKDFPS 660									
	HPLYLEGALT RSTHYQQYQ VVTLQKGYTI HWDQTAPEL AIWLINFNKG DWIRVGLCYP 720									
	RGTFPSILSD VHNRLKQTS KTGVPVRTLQ MDKVEQSYPG RSHYYWDEDS GLIFLKLKAQ 780									
	NEREKFAFCS MKGCERIKI ALIPKNAGVS DCTATAYPK TERAVVDVPM PKLFGSQLK 840									
40	TDHFLVVKM ESSKQHPFHL WNDFAFIEVD GKYPSSSEDG IQVVVDGNQ GRVVSHTSFR 900									
	NSILQGIPIW LFNVATIPD NSIVLWASKG RYVSRGPWTR VLEKLADRG LKLKEQMAFV 960									
	GFKGSFRPIW VTLDTEHKA KIFQVVPFV VKKKKL 996									
	Seq ID NO: C254 Protein Sequence Protein Accession #: NP_055188.1									
45	1 11 21 31 41 51									
	MTALSSENC FOYQLRQTNQ PLDVNYLLFL IILGKILLNI LTLMRRKNT CQNFMEYPCI 60									
	SLAFVDLLLL VNISILYFR DFVLLSIRPT KYHICLFTQI ISFTYGLHY PVFLTACIDY 120									
	CLNFSKTKL SPKQKLFYF FTVILWISV LAYVLGDPAL YQSLKAQNA SRHCFFYVSI 180									
	QSYWLSPPMV MILFVAPITC WBEVTLVQA IRITSYMET ILYFPSSHS SYTVRSKKIP 240									
50	LSKLIVCLFS TWLPVLLQV IIVLLKVQIP AYIEMNIPWL YFVNSPLIAT VYWFNCHKLN 300									
	LKDGLPLDP FVWKKCCIP LTIPNLEQIE KPISIMIC 338									
	Seq ID NO: C255 Protein Sequence Protein Accession #: Eos sequence									
55	1 11 21 31 41 51									
	MALVLGSLLL LGLCGNSFG QPSSSTDAPK AWNYELPATN YETQDSHAG PIGILFELVH 60									
	IFLYVQPRD FPEDTLRKFL QKAYESKIDY DKIVVYEAGI ILCCVLGLL IIMLPLVGYP 120									
	FCMCRCCNK GSEMHRQKE NGPFLRCKFA ISLLVICII SIGIFYGFA NEQVTRIKR 180									
	SRKLADSNFK DLRTLLNETP EQIKYLAQY NTTDKRAFT LNSINSVLGG GILDRLRPN 240									
60	IPVLDEIKSM ATAIRKTKA LEMNNTLKS LHQQSTQLSS SLTSVKTSR SSLNDPLCLV 300									
	HPSSETCNSI RLSLSQLNSN PELROLPPVD AELDNVNVVL RTDLGLVQ GYQSLNDIPD 360									
	RVQRQTITV AGIKRVLSI GSDIDNVTR LPIQDILSAF SVYVNTESY IHRNLPLEE 420									
	YDSYWLGLL VICSLTLIV IFYYLGLLCG VGYDRHATP TTRGCVSNTG GVFLMVGVL 480									
	SFLFCWILMI IIVLTFVPGA NVEKLICBP TSKEFLRVLD TPYLLNEDW YLGLSKLPNK 540									
65	SKMLTFEQV YSDCKNRGT YGTLHLQNSF NISEHLNINE HTGSISELE SLKVNLIPL 600									
	LGAAGRNLQ DFAACGIDRM NYDSYLAQTG KSPAGVNLIS PAYDLEKAN SLFPGNLRNS 660									
	LKRDAQTIKT IHQQRVLPIS QSLSTLYQSV KILQRTGNL LERVTRILAS LDFACNPTN 720									
	NTSSVIIET KCGRTIIGY PEHYLQWIEP SISEKVASCK PVATALDTAV DVFLCSYIID 780									
	FLNLPWFEGIG KATVFLPAL IPAVKLAKY RRMDSQDVYD DVETIPMKN ENGNNGYHRD 840									
70	HVGIIHNPVM TSPSQH 856									
	Seq ID NO: C256 Protein Sequence Protein Accession #: NP_149038.1									
75	1 11 21 31 41 51									
	MKAIHLTL ALLSVNTATN QGNSADAVTT TETATSGPTV AAADTTEINF PETASTTANT 60									
	PSFPTATSPA PPIIHTHSSS TIPTAPPPII STHSSSTIPI PTAADSEST NVNSLATSDI 120									
	ITASSPNDGL ITMVPSETQS NNEMSPITD NQSSGPPTGT ALLETSTLNS TGFSNPQDD 180									
	PCADNSLCVK LNTSPCLCL EGYYSNSTC KKGKVPFGKI SVTVSETFDP ESKSMAYQD 240									

5 LHSEITSLFK DVFGTSVYQ TVILTVSTSL SPRSEMRADD KPVNVTIVTI LASTTSONEK 300
 TVTEKINKAI RSSSSNPLNY DLTLCDDYYG CNQTADDCLN GLACDCKSDL QRPNPQSPFC 360
 VASSLKCPDA CNAQHKQCLI KKSOGAPECA CVPGYQEDAN GNCQKCAPGY SGLDCKDKFQ 420
 LILTVGTIA GIVILSMIIA LIVTARSNNK TKHIEENLI DEDFQNLKLR STGPTNLGAE 480
 GSVFPKVRIT ASRDSQMNP YSRHSSMPRP DY 512

Seq ID NO: C257 Protein Sequence
 Protein Accession #: NP_001423.1

10 1 11 21 31 41 51
 | | | | |
 MTAGRRMEML CAGRVPALLL CLGFHLLQAV LSTTVIPSCI PGESSDNCTA LVQTEDNPRV 60
 AQVSIKCCSS DMNGYCLHQY CIYLVDMSON YCRCEVGYTG VRCEHPFLTV HQPLSKEYVA 120
 15 LTVILILFL ITVVGSTYYF CRWYRNRRSK EPKKEVERVT SGDPPELPQV 169

Seq ID NO: C258 Protein Sequence
 Protein Accession #: AAC63902.1

20 1 11 21 31 41 51
 | | | | |
 MDRSKENCIS GPKVATAPVG GPKRVLVTTQ IPCQNPLPVN SGQAQRVLCF SNSSQVRVPLQ 60
 AQKLVSHPK VQKQKQKQLQ ATSVPHFVSR PLANTQKSKQ PLPSAPENNP EEELASKQKN 120
 EESKGRQWAL EDFEIGRPLG KGFPGNVYLA REKQSKFILA LKVLFKQALE KAGVEHQLR 180
 25 EVEIQSHLEH PNILRLYGVF HDATRVYLIL EYAPLGTVYR ELQKLSKFE QRTATYITEL 240
 ANALSYCHSK RVHRDIKPE NLLLSGAGEL KIADFGWSVE APSSRRRTTLC GTLDYLPPEM 300
 IGRMHDEKV DLWSLGVLGY EPLVGKPPFE ANTYQETYKR ISRVEPTFPD FVTEGARDLI 360
 SRLKHNPSQ RMLREVLLEH PWITANSSKP SNOQNKESAS KQS 403

Seq ID NO: C259 Protein Sequence
 Protein Accession #: NP_037504.1

30 1 11 21 31 41 51
 | | | | |
 MSRTAYTVGA LLLLLGTLLP AABGKKKGSQ GAIPPPDKAQ HNDSEQTQSP QQPGRNRGR 60
 35 QGGRGTAMPQ BEVLESSQEA LHVTERKYLK RDWCKTQPLK QTIHEEGCNS RTIINRFCYG 120
 QCNSFYIPRH IRKEEGSFQS CSPCKPKKFT TMMVTLNCPE LQPPTKKRV TRVKQCRCIS 180
 IDLD 184

Seq ID NO: C260 Protein Sequence
 Protein Accession #: Eos sequence

40 1 11 21 31 41 51
 | | | | |
 MKVGVWLWLS FPTFTDGHGG FLGKNDGIKT KKEIVNKKK HLGPVBEYQL LLQVYTRDSK 60
 45 EKRDLNFKL LKPPPLWLS GLIRIIRAKA TTDNSLNGV LQCTCEDSYT WPPPSCLDPQ 120
 NCYLHTAGAL PSCECHLNL SQSVNFCERT KIWGTFKINE RPTNDLLNS SAIYSKYANG 180
 IEIQLKKAYE RIQGFESVQV TQPRNGSIVA GYEVVGSSSA SELLSAIEHV AEKAKTALHK 240
 50 LFPLEDGSFR VFGKAQCNDI VFGFGSKDDE YLPCSSGYR GNITAKCESS GWQVIRETCV 300
 LSLLLELNKN FSMIVGNATE AAVSSPVQNL SVIIRQNPST TVGNLASVVS ILSNISSLSL 360
 ASHFRVSNST MEDVISIADN ILNSASVTNW TVLLREEKYA SSRLLLETLEN ISTLVPPPAL 420
 55 PLNPSRKPID WKGIPVNSQ LKRGYSYQIK MCPQNTSIPI RGRVLIGSDQ FQSLPETII 480
 SMASLTGNI LPVSKNGNAQ VNGFVISTVI QNYSINEVFL PFSKIESNLS QPHCVFWDGS 540
 HLQWMDAGCH LVNETQDIPT CQCTHLTSFS ILMSPFPVST IFPVVKWITY VGLGISIGSL 600
 60 ILCLIEBALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSCVCTAA 660
 VFFTHFFYLS LFFWMLMGI LLAYRIILVF HMAQHLMA VGFCAGYGCP LIISVITIAV 720
 TQPSNTYKRR DVCWLNWSNG SKPLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR 780
 DDKATIRVG KSLILITPLL GLTWGFGIGT IVDSONLAWH VIFALLNAFQ GPFILCFGIL 840
 LSKLRQLLF NKLSALSSWK QTEKQNSDL SAKPKPKPKP NPLQNKHYA PSHTGDSSDN 900
 60 IMLTQVPSNE 910

Seq ID NO: C261 Protein Sequence
 Protein Accession #: NP_000575.1

65 1 11 21 31 41 51
 | | | | |
 MTSKLAVALL AAPLISAALC EGAVLPRSAK ELRCQCIKTY SKPFPKPKIK ELRVIESGPH 60
 CANTEIIVKL SDGRELCLDP KENWVQRVVE KFLKRAENS 99

Seq ID NO: C262 Protein Sequence
 Protein Accession #: NP_005594.1

70 1 11 21 31 41 51
 | | | | |
 MSTERSETT FDEDSQFNDE VVPYSDDSTB DELDDQGS AV EPEQNRVNR AEENREPFRK 60
 75 ECTWQVKAND RYHEQPHFM NTRFLCICKES KYANNAIKTY KYNAFTPIPM NLFEQFKRAA 120
 NLYFLALLIL QAVPQISTLA WYTLVPLLV VLGVTAKDL VDDVARHKMD KEINNRTCEV 180
 IKDGRPKVAK WKEIQVGDVI RLKKNDFVPA DILLSSSEP NSLCYVETAS LDGETNLKFK 240
 80 MSLEITDQYL QREDTLATPD GFIECEEPNN RLDKFTGTLE WRNTSFPLDA DKILLRGCVI 300
 RNTDFCHGLV IFAGADTKIM KNSGKTRPKR TKIDYLMNYM VYTIIPVVLIL LSAGLAIGHA 360
 YWEAQVGNSS WYLYDGEDDT PSYRGFLIFW GYIIVLNTMV PISLVSVSEV IRLGQSHFIM 420
 WDLQMYIAEK DTPAKARTTT LNEQLGQIHY IFSDKTGLT QNIMTFKKCC INGQIYGDRH 480
 DASQHNHNIQ EQVDFSWNTY ADGKLAFYDH YLIEQIQSGK EPEVRQFPFL LAVCHTMVD 540
 RTDQQLNYQA ASPDEGALVN AARNFGFAPL ARTQNTITIS ELGTERTYNV LAILDFNSDR 600
 KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMWPTKQBTQ DALDIPANET LRTLCLCYKE 660

5 ISEKEPTWNN KKFMAASVAS TNRDEALDKV YEEIEKDLIL LGATAIEDKL QDGVPEITISK 720
 LAKADIKIWN LTGDKKETAE NIGFACELLT EDTTICYGED INSLLEHARME NQRNRGGVYA 780
 KFAFFVQESF PPGQGNRALI ITGSWLNELL LEKKTGRNKI LKLFKPRTEB ERRMRTOQSKR 840
 RLEAKKEQRO KNFVDLACEC SAVICCRVTP KQKAMVVDLV KRYKKAITLA IGDGANDVNM 900
 10 IKTAHIGVGI SQQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKP LRYFFYKNPA 960
 FTLVHFWSYF FNGYSQAQATY EDWFITLYNV LYTSLPVLLM GLLDQDVSDK LSLRFPGLYI 1020
 VQQRDLFFNY KRFEVSLHGG VLTSMLFFPI PLQAYLQTVG QDGEAPSDYQ SFAVTIASAL 1080
 VITVNPQIGL DTSYMTFVNA PSIFGSIALY FGIMFDPHSA GIHVLFPSEAF OPTGTASNAL 1140
 15 RQPYINLTII LTVAVCLLPV VAIRFLSMTI WPSESDKIQK HRKRLKAEEQ WQRRQQVPRR 1200
 GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPLDAIVAD GTAERYRTGD S 1251

Seq ID NO: C263 Protein Sequence

Protein Accession #: XM_044533

15 1 11 21 31 41 51
 MLRTAMGLRS WLAAPWGALE PRPPLLLLLL LLLLLQPPFP TWALSFRISL PLGSEERPFPL 60
 RFEAEHISNY TALLLSRDGR TLYVGAREAL FALSSNLGFL PGSEYQELLW GADAEKKQCC 120
 20 SFGKGPQQRD CQNYIKILLP LSGSHLPTCG TAAFSMCTY INMENFTLAR DEKGNVLLED 180
 GKGRCPFDPN FKSTALVVDG ELYTGTVSSF QGNDPAISRS QSLRPTKTES SLANLQDPAP 240
 VASAYIPESL GSLQGDDDKI YFFPSETQGE FEFENTIVS RIARICKGDE GGERVLQQRW 300
 TSFLKAQLLC SRPDDGPPFN VLQDVFTLSP SPQDWRDRLF YGVFTSQWHR GTEGSAVCV 360
 FTMKDQVRVP SGLYKEVNRE TQQWYTVTHP VPTPRPGACI TNSARERKIN SSLQLPDRVL 420
 25 NFLKDHFLMD QQVRSMLLL QPQARYQVVA VHRVPGHLHT YDVLPLGTGD GRHLKAVSVG 480
 PRVHIIEELQ IFSSGQPVQN LLLDTHRGLL YAASHSGVVQ VPMANCSLYR SCGDCLLARD 540
 PYCAWSSSSC KPLSLYQPLQ ATRPWIQDIE GASAKDLCSA SSVSPSPFVP TGEKPCQVQV 600
 FQPNVTNTLA CPILLSNLATR LHLRNGAPVN ASASCHVLEP GDLLLVGTQQ LGFEQCSWLE 660
 EGFPQLVASY CEVVEDGVA DQTEGGGSPV VIISTSRVSA PAGGKASNGA DRSYWKELPV 720
 30 MCTLFVLAVL LPVLFLYLRH RNSMKVFLKQ GECASVHPKT CPVVLPPETR PLNLGLPPST 780
 PLDHRGQSL SDSPGGRVP TESEKRPLSI QDSPVEVSPV CPRPRVRLGS BIRDSV 837

Seq ID NO: C264 Protein Sequence

Protein Accession #: NP_008950.1

35 1 11 21 31 41 51
 MASQNRDPAA TSVAARKGA EPSGGAARGP VGKRLQOEML TLMMSGDKGI SAPPESDNLF 60
 KMGVTIHGAA GTVVEDLRYK LSLEFFSGYP YNAFTVKFLT PCYHPNVDQ GNICLDILKE 120
 40 KWSALYDVRT ILLSIQSLIG EPNIDSPLNT HAAELWKNPT AFKKYLQETY SKQVTSQBP 179

Seq ID NO: C265 Protein Sequence

Protein Accession #: NP_055399.1

45 1 11 21 31 41 51
 MGRGNGFLFG LLGAVMLLSS GHGEEQPPET AAQRCCQVVS GYLDDCTCDV ETIDRFNNYR 60
 LFPRQLKLE SYFRYKYVN LKRPCFPWMD ISQCGRRDCA VKPCQSDVP DGIKSASYKY 120
 SEEANNLYEE CQAEERLQAV DESLSEETQK AVLQNTKHDD SSDNPCEADD IQSPEAEYVD 180
 50 LLLNPERYTG YKGPDAWKIN NVIYEENCFK PQTIKRPLNP LASSQGTSEE NTFYSWLEGL 240
 CVEKRAPYRL ISGLHASINV HLSARYLLQE TWLEKKWGHN ITEFQQRFDG ILTEGEGPRR 300
 LKNLYPLYLI ELRLASKVLP PFERPDQQLP TGNKIQDBEN KMLLEILHE IKSFPLHFDE 360
 NSFPAGDKKE AHKLKEDFRL HFRNISRIMD CVGCFKCRLEW GKLQTQGLGT ALKILPSEKL 420
 55 IANMPESGPS YEFLTRQEI VSLPNAPGRI STSVKELENF RNLLQNIH 468

Seq ID NO: C266 Protein Sequence

Protein Accession #: NP_002879.1

60 1 11 21 31 41 51
 MQPRRQRLPA PWSGPRGPRP TAPLLALLLL LAPVAAPAGS GGPDDPGQPQ DAGVPRRLIQ 60
 QKARAALHFF NFRSGSPSAL RVLAEVQEGR AWINPKEGCK VHVVFSTERY NPESLLQEGE 120
 GRLGKCSARV PFRNQKPRPT INVTCTRLIE KKKRQQEDYL LYKQMKQLKN PLBIVSIPDN 180
 HGHIDPBLRL IWDLAPLGSS YVMWEMTTQV SHYYLAQLTS VRQWVRKT 228

Seq ID NO: C267 Protein Sequence

Protein Accession #: NP_005400.1

70 1 11 21 31 41 51
 MSVKGMAIAL AVILCATVVO GFPMFKRGRC LCIGPGVKAV KVADIEKASI MYPENNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF 94

Seq ID NO: C268 Protein Sequence

Protein Accession #: FGENSEH predicted

75 1 11 21 31 41 51
 MLRQVLRRGL QSPCHRLGLC VSRHPVFFLT VPAVLTITFG LSALNRPQPE GDLERLVAPS 60
 HSLAKIERSL ASSLPFLDQS KSQLYSDLHT PGRYGRVILL SPTGDNILLQ AEGILQTHRA 120
 80 VLEMKVNHKG YNYTFSHLCV LRNQDKKCVL DDIIISVLEDL RQAASVNKTT ARVQVRYFNT 180
 KLVCSFCML LPFKEAALHF LP 202

Seq ID NO: C269 Protein Sequence

Protein Accession #: NP_002429.1

	1	11	21	31	41	51	
5	MRLPLLLVFA	SVIPGAVLLL	DTRQFLIYNE	DHKRCVDAVS	PSAVQTAACN	QDAESQKFRW	60
	VSSSQIMSA	FKLCLGVPSK	TDWVAITLYA	CDSKSEFPKW	ECIONDTLLGI	KGEDLFFNYG	120
	NRQEKIMLY	KGSGLWSRWK	IYGTIDNLCS	RGYEAMTYLL	GNANGATCAF	PFKFNKNWYA	180
	DCTSAGRSBG	WLWCGTTTDD	DTDCLFGYCP	LKFESESLSW	NKDPLTSVSY	QINSKSAITW	240
	HQARKSCQQQ	NAELLSITEI	HEQTYLTGLT	SSLTSGLWIG	INSLSFNSGW	QWSDRSPFRY	300
10	LNWLPGPSA	EPGKSCVSLN	PGKNAKWENL	ECVQKLGYIC	KKGNTLLNSP	VIPSESDVPT	360
	HCPSSQWIFYA	GHCYKIHHRD	KKIQRDALTT	CRKEGGDLTS	IHTIEELDFI	ISQLGYEPND	420
	ELWIGLMDIK	IQMYFENSDG	TPVTFTKWLK	GEPSHENNRQ	EDCVVMKGKD	GYWADRGCEN	480
	PLGYICMOKS	RSQGPETVEV	EKGCRKGWKK	HHFYCYMIGH	TLSTFAEANK	TCNNENAVLT	540
	TIEDRYEQAF	LTSFVGLRPE	KYFWTGLSDI	QTKGTFQMTI	EEBVRPTHWN	SDMPGRKPGC	600
15	VAMRTGIAGG	LMDVLKDEK	AKFVCKHWAE	GVTHPPKPTT	TPEPKCPEDW	GASSRTSLCP	660
	KLYAKGKHEK	KTWFSRDFC	RALGGDLASI	NNKEBQQTIV	RLITASGSYH	KLFWLGLTYG	720
	SPSEGFTWSD	GSPVSYENWA	YGEPNNYQNV	BYCGELKGDP	TMSWINDINC	HLANNWICQI	780
	KQQTPKPEPT	PAPQDNPEVT	EDGWVIYKDY	QYVFSKEKET	MDNARAFCKR	NFGDLVSIQS	840
	ESEKFKLWKY	VNRNDAQSAY	FIGLLISLDK	KPAWMDGSKV	DYVSWATGEP	NFANEDENCV	900
20	TMYSNSGFWN	DINOCYFNAP	ICQRHNSIN	ATTVMPTMPS	VPSGCKEGWN	FYSNCKPKIP	960
	QMEEERKWN	QBARAKCIGF	GGNLVSIQNE	KEQAFITYHM	KDSTFSAWTG	LNDVNSEHTF	1020
	LWTDGRGVHY	TMWKGYPFG	RRSSLSYEDA	DCVVIIGAS	NEAGKWMDDT	CDSKRGYICQ	1080
	TRSDPSLTNP	PATIQTDGQV	KYKGSSYSLM	RQKQFQHEAE	TYCKLINSLI	ASILDPSYNA	1140
	PAWLQMETSN	ERVWIALNSN	LTDNQYTWD	KWRVRYTNWA	ADEPKLKSAC	VYLDLDGYWK	1200
25	TAHCNESFYF	LCKRSDEIPA	TEPPQLPGRC	PESDHTAMIP	FHGHCYTES	SYTRNMGQAS	1260
	LECLRMGSSL	VGIESAAESS	FLSYRVEPLK	SKTNFWGLP	RNVEGTWLWI	NNSFVSFVNW	1320
	NTGDPSSGRN	DCVALHASSG	PWSNIHCSSY	KGYICKRPKI	IDAKPTHELL	TTKADTRKMD	1380
	PSKPSSNVAG	VVIIIVILLIL	TGAGLAAYFF	YKKRRVHLPQ	EGAPENTLYT	NSQSSPGTSD	1440
	MKDLVGNIEQ	NEHSVI					1456

Seq ID NO: C270 Protein Sequence
Protein Accession #: Eos sequence

	1	11	21	31	41	51	
35	MVLLHWCLLW	LLFPLSSRTQ	KLPTRDEELF	QMQRDKAPF	HDSSVIPDGA	EISSYLFRTD	60
	PKRYFFVVEE	DNTFLSVTVT	PCDAPLEWKL	SLQELPEDRS	GEGSGDLEPL	EQKQKIINE	120
	EGTELFSYKG	NDVEYFISSS	SPSGLYQLDL	LSTEKDTHPK	VYATTTFESD	QPYPELPYDP	180
	RVDVTSLGRT	TVTILAWKPS	TASLLKQPIQ	YCVVINKEHN	PKSLCAVEAK	LSADDAFMA	240
40	PKPGLDSPFP	DFAHFGPPSD	NSGKERSFQA	KPSPKLGRHV	YSRPKVDIQK	ICIGNKNIPT	300
	VSDLKPDQYQ	YFQVFPVNIH	SNMSTAYVGT	PARTKEEAKQ	KTVLEKDGKI	TDVFPVKRGA	360
	KFLRFAPVSS	HQKVTFFIHS	CLDAVQIQVR	RDGKLLSQN	VEGIIQQQLR	GKPKAKYLVR	420
	LKGNKKGASM	LKILATTFTPT	KQSPFSLPED	TRIKAPDKLR	TCSSATVAVL	GTQERNKPCI	480
	YKKEVDNDYN	EDQKKEQNKQ	CLGPDIRKKS	EKVLCKYFHS	QNLQKAVTTS	TIKGLQPGKS	540
45	YLLDVYVIGH	GHSVKYQSK	VVKTRKFC				568

Seq ID NO: C271 Protein Sequence
Protein Accession #: AAH34229.1

	1	11	21	31	41	51	
50	MEKVQLEFEN	QEMKKLQPF	RSTRNKEKED	RESSEYWKKS	GKVGKLVNQS	YMSQNKGNV	60
	VKFSAGKVKL	KLLKEQIQEP	VKPTVNYKMA	NSSCEKPKI	NGKVCQGCE	KAALLVLEC	120
	GEDYCSGCPA	NVQKGALKL	HRTTLQARS	QILFNVLDVA	HQFIKDVNPD	EPKEENNSTK	180
	ETSKIQHKKF	SVLLQSSSE	VEITTMKRAQ	RTKPKKSLLC	EGSPDEEASA	QSPQEVLSQW	240
55	RTGNHDDNKK	QNLHAAVKDS	LEECEVQTNL	KIWREPLNIE	LKEDILSYME	KLWLKGRRT	300
	PQEQLFKCYQ	IRSHIEMKPL	VMHVSVMKKT	MKIVMVRPK	YNTQLFYCQ		349

Seq ID NO: C272 Protein Sequence
Protein Accession #: NP_078963.1

	1	11	21	31	41	51	
60	MEKLWLKKHR	RTPQEQLFPM	LSDTFFPHPE	TTGDAQCSQN	ENDESDGEE	TKVQHTALLL	60
	PVETLNIERP	EPKSLKIVELD	DTYEEEPERA	ENIVPYKVKL	ADADSQRSCA	PHDCQKNSFP	120
65	YENGIIHQHV	FDKGRDPLN	LCLRNSSTYY	KDNKSGETSN	TDFDNIVDPD	VYSSDIEKIE	180
	ESTSPERNLK	EKNIGLESNQ	KSDSCSVSLE	SKDTLIGRDL	EKAPIESKLS	QDIKESLELS	240
	NLYKRPSPEE	SKTTKSSLLL	QEIACRSKPI	TKQYQGLERP	FIFDTNERLN	LLPSHRLECN	300
	NSSTRITLAE	DREWIPDHSI	SEYADNAIVL	GVLQGAQSPS	SSRKQKQMGQ	KSQRPSTANF	360
	PLNSNVKESR	SCLSSSHPRS	REAAAQSSSR	AASEISEIEY	IDITDQNELS	LDDTTDQHTL	420
70	DNLEKELQVL	RSIADTSEKL	YSLTSEEPFD	FSSQSLNISQ	ISTDPLKTSH	VRGPCGVEEL	480
	SCSGRDTKIQ	SLLSLSSESST	DEEEDFLNK	QHVITLPMNK	ST		522

Seq ID NO: C273 Protein Sequence
Protein Accession #: NP_005399.1

	1	11	21	31	41	51	
75	MKVSALLCL	LLMTAANPQ	GLAQPDALNV	PSTCCPTFSS	KKISLQRLKS	YVITTSRCPO	60
80	KAVIFRTKLK	KEICADPKK	WVQNYMKHLG	RKARTLKT			98

Seq ID NO: C274 Protein Sequence
Protein Accession #: BAC05158.1

	1	11	21	31	41	51

1347

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10
15

MFLLTGGVSL	KSAAKNPDPT	WLQDKSWEEI	CRASEPPAPR	GLRQHFCEHI	YEWREIYDSK	60
EPHNAKPPAP	MDKNLNEIQ	IIILRCLRPD	KITPAITNYV	TDKLGKKFVE	PPPFDLTKSY	120
LDNSCTIPLI	FVLSPGADPM	ASLLKFANDK	SMSGNKFAQI	SLGQGGQPIA	AKMIKAAIEE	180
GTWVCLQNC	LAVSWMPMLE	KICEDFTSET	CNSSFRLWLT	SYFSSKPFVT	ILQNGVKMTN	240
EPPTGLRLNL	LQSYLTDVPS	DPEFFKGCGR	KELLFINEYD	TIPFEAISYL	TGECNYGGRV	300
TDDNDRLLLL	TMLADFYNLY	IVENPHYKFS	PSGNYFAPPK	GTIEDYIEFI	KKLPPTQHPE	360
IFGLHENVDI	SKDLQQTCTL	FESLLLTCGG	SKQTGASGST	DQILLEITKD	ILNKLPSDFD	420
IEALRKYPV	RYEBSMTVL	VQEMERFNNL	IIITIRNLRD	LEKAIKGVV	MDSALEALSS	480
SLLVGKYPEI	WAKRSYPSLK	PLGSYITDPL	ARLNFLQDNY	NSGKPCVFWL	SGFFPTQAPL	540
TGAMQNYARK	YTTIDLLGY	EFEVIPSPTS	DTSPEDGVYI	HGLYLDGARN	DRESGLLAEQ	600
YPKLLFDLNP	IIMLKPTQKS	RIIKSDAYVC	PLYKTSEKRG	TLSTTGHSTN	FVIAMLLKTD	660
QPTRHWIKRG	VALLCQLDD					679

Seq ID NO: C275 Protein Sequence
Protein Accession #: AAA60212.1

20
25

1	11	21	31	41	51	
MAESHLQWL	LLLLFTLCGP	GTAAWTTSSL	ACAQGPEPWC	QSLEQALQCR	ALGHCLQEVW	60
GHVGADDLCQ	ECEDIVHILN	KMAKEAIFQD	TMRKFLEQEC	NVLPLKLLMP	QCQVLDYDF	120
PLVIDYFQIQ	TDSNGICMHL	GLCKSRQPEP	EQEPGMSDFL	PKPLRDLPLD	PLDLKLVLV	180
LPGALQARPO	PHTQDLSEQQ	FPILPLPYCW	CRALIKRIQA	MIPKALAVA	VAQVCRVPL	240
VAGGICQCLA	ERYSVILLDT	LLGRMLPQLV	CRLVLRCSMD	DSAGPRSPGT	EWLPRDSECH	300
LCMSVTTQAG	NSSBQAIPQA	MLQACVGSWL	DREKCKQFVE	QHTPQLTLV	PRGWDARTTC	360
QALGVCGTMS	SPLQCIHSPD	L				381

Seq ID NO: C276 Protein Sequence
Protein Accession #: NP_631911.1

30
35

1	11	21	31	41	51	
MLGCGIPALG	LLLLLQGSAD	GNGIQGFFYP	WSECGDIWDR	ESCGGQAAID	SPNLCLRLRC	60
CYRNGVCYHQ	RPDENVRKHI	MWALVNTCSG	LLLLSCSICL	FWWAKRRDVL	HMPGLAGLPC	120
DMSKSVLLS	KHRGKKTPTS	TGSVPVALSK	ESRDVEGGTE	GEGTEEGRET	EGEESEED	177

Seq ID NO: C277 Protein Sequence
Protein Accession #: NP_473364.1

40
45

1	11	21	31	41	51	
MKLVTIFLLV	TISLCSYSAT	AFLINKVPLP	VDKLAPLPLD	NILPFMDPLK	LLLKTIGISV	60
EHLVEGLRKC	VNELGPEASE	AVKGLLEALS	HLV			93

Seq ID NO: C278 Protein Sequence
Protein Accession #: FGENSEH predicted

50
55
60
65

1	11	21	31	41	51	
MPLSYAYKNA	ETLAGRHTSS	WMSRGAYQRR	NTRAAGRPEE	CTDRNWHAGR	TRGIWLGQLE	60
ERCSDFVQVS	FFWVVRGLAG	SGAKLQTFTP	AQEGAPTQVR	QAEALLKCRQ	SGRPRGGAE	120
SERARDASML	SPLSAAMRNY	PTSSTIPPRR	SYSPTETIAHK	SYSCSLPDMK	ISMAESGPSL	180
DSLDILEDEG	SGSPFLVTHL	YFLGVVTTGM	EQLDFETGPN	IPDLQIYVKD	EVGVTDLQVL	240
TVQVTDVNEP	PGSQGNLAED	HLRADQPHFN	AHSHTYVRV	ATALARHLR	SSIGSPFLGT	300
FCVVVGMYF	LISPPKSRFM	SANGTLFSTT	ELDFEAGHRS	PHLIVEVRDS	GGLKASTELQ	360
VNIVNLDEVF	PRFTSPTRVY	TVLEELSPGT	IVANITAEDP	DDEGFPSHLL	YSITTVSKYF	420
MINQLTGTIQ	VAQRIDRDAG	ELRQNPITSL	EVLVKDRPYG	QGENRIQITF	IVEDVNDNPA	480
TQKFTFRSS	LHPALCSKTL	TMDTFLVDCF	HAADKDIPT	GRFTKERGLI	GLTVPHGWGS	540
LTIMAEGLKE	QVTSYMDGSR	QRDRACVGLK	LLIKPSDLMR	LSHYHENNSG	KTCPHDSISS	600
YQVPTTCRN	SRIQATNNE	TSSVTVTVNI	LEENDEKPIK	TPNSYFLALP	VDLKVGNTIQ	660
NFKLTCTDL	SSPRSFYRSI	GPGNVNNHFT	FSPNAGSNVT	RLLLTSRFDY	AGGFDKIWDY	720
KLLVVVTDN	LMSDRKAEK	LVETGTVTLS	IKVIPHPTTI	ITTTFRPRVT	YQVLRKNVYS	780
PSAWYVPFVI	TLGSILLGL	LVYLVVLLAK	AIHRHCPCKT	GKNKEPLTKK	GETKTAERDV	840
VVETIQMNTI	FDGEAIDPEP	EQASLELYAL	LPSCCDPSPV	TLRKVQVCGE	SEETGQCSGH	900
ITLPKIPVD	DPRKQETGLQ	GDPEVWTLCP	AVKVVVGSQ	AERCIRLALS	LKYSSD	957

Seq ID NO: C279 Protein Sequence
Protein Accession #: XP_168571.1

70
75

1	11	21	31	41	51	
MINQLTGTIQ	VAQRIDRDAG	ELRQNPITSL	EVLVKDRPYG	QGENRIQITF	IVEDVNDNPA	60
TQKFTFRSS	VPERTAKGTL	LLDLNKFCD	DDSEAPNNRF	NFTMPSGVGS	GSFPLQDPAG	120
SGKIVLIGDL	DYENPSNLAA	GNKYTVIIQV	QDVAPPYYKN	NVYVYILTSP	ENEFPLIFDR	180
PSYVFDVGER	RPAQGHLSGP	EEKRLLSICM	VRAVCHHFLG	HIASGSRVP	GRPIGQSHQP	240
TLPLQDWESQ	GTSDKERRNE	DCRERRRGNN	YPDEHYL			277

Seq ID NO: C280 Protein Sequence
Protein Accession #: NP_005257.2

80

1	11	21	31	41	51	
MGDWSFLGNP	LEEVHKHSTV	VGKVVLTIVL	IFRMLVLGTA	ABSSWGDEQA	DPRCDTIQPG	60
CQNVCYDQAP	FISHIRYVWL	QIIFVSTPSL	VYMGHAMHTV	RMQERKKLRE	AERAKEVRGS	120

GSYEYFPAEK AELSCWEEGN GRALQQTLL NTYVCSILIR TIMEVGFIVG QYPIYGIFLT 180
 TLHVCRRSPC PHFVNCYVSR PTEKNVFIVF MLAVAALSLL LSLAELYHLG WKIKRQRFVK 240
 PRQHMAKQQL SGPSVGIQVS CTFFPDFNQC LENGPGGKFF NPPSNMNASQ QNTDNLVTEQ 300
 VRGQEQTPEE GFIVQVRYGQK FEVPNGVSPG HRLPHGYHSD KRRLSKASSK ARSDDLSV 358

Seq ID NO: C281 Protein Sequence
 Protein Accession #: NP_055274.2

1 11 21 31 41 51
 MYLSICCCFL LMAPALTLMN LMYSVPBEEQ AGTVIGNIGR DARLQPLGP AERGGGGRSK 60
 SSGSYRVLENS APHLLDLDAD SGLLYTKQRI DRESLCRHNA KCQLSLEVFA NDKBICMIKV 120
 EIQQDINDAP SPSSDQIEMD ISENAAPGTR PPLTSAHDPD AGENGLRITYL LTRDDHGLPG 180
 LDVKSRRGDT KFPFLVIQKA LDREQQNHHT LVLTAIDGGE PPRSATVQIN VKVIDSDNS 240
 PVFEAPSYLV ELPENAPLGT VVIDLANATDA DEGPNGEVLY SFSSYVPDRV RELFSDPKT 300
 GLIRVKGSLD YEENGMLEID VQARDLGNP IPAHCKVTVK LIDRNDNAPS IGFVSVRQGA 360
 LSEMAPPGTV IALVRVTRDR SGKNGQLQCR VLGGGGTGGG GGLGGPGGSV PFKLEENYDN 420
 FYTVVTRDPL DRETQDEYNV TIVARDGGSP PLNSTKSPAI KILDENDNPP RPTKGLYVLQ 480
 VHNNIPGEY LGSVLAQDPD LGQNGTVSYS ILPSHIGDVS IYTYVSVNPT NGAIYALRSF 540
 NFEQTKAFEF KVLAKDSQAP AHLESNATVR VTVLDVNDNA PVIVLPTLQN DTABLQVPRN 600
 AGLGYLVSTV RALDSDFGES GRITYEIVDG NDDHLPEIDP SSGEIRTLHP FWEDVTPVVE 660
 LVVKVTDGK PTLASAKLI IRSVSGSLPE GVPRVNGEQH HNDMSLPLIV TLSTISILL 720
 AAMITIAVKC KRENKBIRTY NCRIAESHP QLGGGKGGKK KINKNDIMLV QSEVERNAM 780
 NVNINVSSPS LATSPMYFDY QTRLPLSSPR SEVMYLPKAS NNLTVPQGHG GCHTSFTGQG 840
 TNASETPATR MSTIQTDNFP AEPNYMGSRO QFVQSISVAP RLRTQKEPA 889

Seq ID NO: C282 Protein Sequence
 Protein Accession #: NP_005592.1

1 11 21 31 41 51
 MELCRSLALL GGSGLMFLCL TALSTDFWFE AVGPHTSAHS GLWPTGHGDI ISGYIHVTQT 60
 FSIAMVLWAL VSVSFLVLSC FPSLFPFGHG PLVSTTAAPA AAISMVVAMA VYTSEWDQP 120
 PHPIQTFFS WSYLGNVSA ILLCTGALS LGAHCGGPRP GYETL 165

Seq ID NO: C283 Protein Sequence
 Protein Accession #: NP_006424.2

1 11 21 31 41 51
 MATWALLLLA AMLIGNPGLV FSRLSPEYYD LARAHRLDEE KSCPCLAQEG PQGDLTKTQ 60
 ELGRDYRTCL TIVQKLKGM DKPTQRSVSN AATRVCRTGR SRWRDVCNRF MRRYQSRVTQ 120
 GLVAGETAQQ ICEDLRLCIP STGPL 145

Seq ID NO: C284 Protein Sequence
 Protein Accession #: NP_005594.1

1 11 21 31 41 51
 MKVSAALAV ILIATLACAP ASAPSYSSDT TPCCFAYIAR PLPRAHIKEY FYTSGKCSNP 60
 AVVPVTRKNR QVCANPEKKW VREYINSLEM S 91

Seq ID NO: C285 Protein Sequence
 Protein Accession #: NP_071437.1

1 11 21 31 41 51
 MAPGRAVAGL LLLAAAGLGG VAEGPGLAFS EDVLSVFGAN LSLSAAQLQH LLEQMGAASR 60
 VGVPEPGQLH FNQCLTAEEI FSLHGFSNAT QITSSKFSVI CPAVLQQLNF HPCEDRPKHK 120
 TRPSHSEVWG YGFLSVTIIN LASLLGLILT PLIKKSYFFK ILTFPVGLAI GTLFSNAIFQ 180
 LIPEAPGFDP KVDSYVEKAV AVFGGFYLLF FFERMLKMLL KTYGQNGHTH FGNDNPGPQE 240
 KTHQPKALPA INGVTYANP AVTEANGHIH FDNVSVSLQ DGKKEPSSCT CLKGPKLSEI 300
 GTIAWMITLC DALHNFIDGL AIGASCTLSL LQGLSTSIAT LCEEFPHELG DFVILLNAGM 360
 STRQALLFN LSACSCYVGL AFGILVGNF APNIIIPALAG GMFLYISLAD MPPEMNDMLR 420
 EKVTRKRTDP TFFMIQNAGM LTGFTAILLI TLVAGEIBLE 460

Seq ID NO: C286 Protein Sequence
 Protein Accession #: NP_004175.1

1 11 21 31 41 51
 MPNSEPASLL ELFNSTATQG ELVRSILKAGN ASKDEIDSAN KMLVSLKMSY KAAAGEDYKA 60
 DCPGPNAPT SNHGPDATFA EEDFVDPWTQ QTSKAGIDY DKLIVRFGSS KIDKELINRI 120
 ERATQQRPHH FLRRGIFFSH RDMNQVLDA ENKKPFYLYT GRGPSSEAMH VGHLLIFIFT 180
 KWLQDVFNVP LVIQMTDEK YLWKDLTLQ AYGDVAENAK DIIACGPDIN KTFIFSDLDY 240
 MGSSEGFYKN VVKIQKHVTF NQVKGIFPGT DSDCIGKISF PAIQAAFPSP NSFPQIFDRR 300
 TDIQCLIFCA IDQDPYFRMT RDVAPRIGYP KPALLHSTFF PALQGAQTKM SASDPNSSIF 360
 LTDTAQIKT KVNKHAFSGG RDTIEHRQF GGNCDVDVSF MYLTFLEDD DKLEQIRKDY 420
 TSGAMLTGEL KKALIEVLQF LIAEHQARRK EVTDEIVKEP MTPRKLSPDF Q 471

Seq ID NO: C287 Protein Sequence

Protein Accession #: NP_004929.1

	1	11	21	31	41	51	
5	MTVFRQENV	DYYDTGEEHG	SGQFAVVKKC	REKSTGLQYA	AKFIKKRRTK	SSRRGVSRED	60
	IEREVSIKE	IQHPNVITLH	EVENKTDVI	LILELVAGGE	LFDPLAEKES	LTREEATEFL	120
	KQILNGVYVL	HSLQIAHFDL	KPENIMLLDR	NVPKPRIKII	DPGLAHKIDF	GNEFPKNIPGT	180
	PEPVAPEIVN	YEPLGLEADM	WSIGVITYIL	LSGASPFLLG	TKQETLANVS	AVNYEFEDEY	240
10	PSNTSALAKD	FIRRLLVKDP	KKRMTIQDSL	QHPWIKPKDT	QQALSRKASA	VNMEKFKKFA	300
	ARKKWKQSVR	LISLQRLSR	SPLSRSNMSV	ARSDDTLDEE	DSFVMKAIH	AINDDNVPLG	360
	QHLGLSLSNY	DVNQPNKHGT	PPLIIAAGCG	NIQILQLLIK	RGSRIDVQDK	GGSNVYVWAA	420
	RHGHVDTLKF	LSGNKCPDLV	KDKSGEMALH	VAARYGHADV	AOVTCAASQA	IPISRTKEEE	480
	TPLHCAAWHG	YYSVAKALCE	AGCNVNIKNR	EGETPLLTAS	ARGYHDIVEC	LAEHGADLNA	540
15	CDKDGHIALL	LAVRRCCMEV	IKTLLSQGCF	VDYQDRHGNT	PLHVACKDGN	MPIVVALCEA	600
	NCNLDISNKY	GRTPLHLAAN	NGILDVVRYL	CLMGASVEAL	TTDGKTAEDL	ARSEQHEHVA	660
	GLLARLRDNT	HRGLPIQQLR	PTQNLQPRIK	LKLFQHSQSG	KTLVBSLKC	GLLRSFRRR	720
	RPLRSSTNSS	RFPPSPPLASK	PTVSVSINNL	YPCENVSVR	SRSMFPEPL	TKGMLEVFVA	780
	PTHHPHCSAD	DQSTKAIDIQ	NAYLVGVDG	SVNEFSGNFV	YFCCYDYFAA	NDPTSIHVVV	840
20	FSLBEPYBIQ	LNPVIFWLSF	LKSLVPVEEP	IAPGGGLKNP	LQVVLVATHA	DIMNVPRPAG	900
	GFPGYDKDTS	LKKEIRNRFG	NDLHISNKL	VLDAGASGSK	DMKVLNRHLQ	EIRSQIVSVC	960
	PMTHLCEKI	ISTLPSWRKL	NGPNQLMSLQ	QFVYDVQDQL	NPLASEEDLR	RIAQQLHSTG	1020
	EINIMQSETV	QDVLDDPRW	LCTNVLGKLL	SVETPRALHH	YRGRTYVEDI	QRLVPDSQVE	1080
	ELLQILDAMD	ICARDLSSGT	MVDVPALIKT	DNLHRSWADE	EDEVHVVYGV	RIVPVEHLTP	1140
25	PCGIFHKVQ	VNLCSNHIQ	STEGDADIRL	WVNGCKLANR	GAELLLVLLN	HGGGIEVQVR	1200
	GLETEKIKCC	LLLDVSCSTI	ENVMATTLPG	LLTVKHVYLS	QQLREHHEPV	MIYQPRDFPR	1260
	AQTLKETSLT	NTMGYKBSF	SSIMCPGCHD	VYSQASLGMD	IHASDLNLLT	RRKLSRLDDP	1320
	PDPLGKWCL	LAMNLGLPDL	VAKYNTNNGA	PKDFLPSPLH	ALLREWTYF	ESTVGTLMGK	1380
	LRELGRDAA	DLLLKASGVF	KINLDGNGQE	AYASSCNSGT	SYNSISSVVS	R	1431

Seq ID NO: C288 Protein Sequence
Protein Accession #: NP_002072.1

	1	11	21	31	41	51	
35	MELRARGWNL	LCAAAALVAC	ARGDPASKSR	SCGEVRQIYG	AKGFSLSQV	QAEISGEHLR	60
	ICPGQYTCCT	SEMEENLANR	SHAELETALR	DSSRVLQAML	ATQLRSFDDH	FQHLNDNSER	120
	TLQATFPQAF	GEIYTNARA	FRDLYSELRL	YYRGANLHLE	ETLAEFWARL	LERLFKQLHP	180
	QLLLPDDYLD	CLGKQAEALR	PFGAPRELRL	LRATRAFVAA	RSFVQGLGVA	SDVVRKVAQV	240
40	PLGPECSRVA	MKLIVYCAHCL	GVPGARPCPD	YCRNVLKGCL	ANQADLDAEW	RNLDSMVL	300
	TDKFWTSGV	BSVIGSVETW	LAEAINALQD	NRDTLTAKVI	QCCGNPKVNP	QPGPEEKRR	360
	RGLAPRERP	PSGTLKLV	EAKAQLRDVQ	DFWISLPGTL	CSEKMASTA	SDRCWNGMA	420
	RGRYLEPEVMG	DGLANQINNP	EVEVDITKPD	MTIRQQIMQL	KIMTNRLRSA	YNGNDVDFQD	480
	ASDDGSGSGS						490

Seq ID NO: C289 Protein Sequence
Protein Accession #: AAH30205.1

	1	11	21	31	41	51	
50	MIILIYFLLL	LWEDTQGWGF	KDGIFRNSIW	LERAAGVYHR	EARSQKYKLT	YAEAKAVCEP	60
	EGGLHATYKQ	LEAARKIGFH	VCAAGWMAKO	RVGYPIVKG	PNCQPGKGTI	IDYGIRLARS	120
	ERNWAYCYNP	HAKECGGVPT	DPKQIFKSPG	PFNEYEDNQI	CYWHIRLKYG	QRIHLSFLDF	180
	DLEDDEPGCLA	DYVEIYDSYD	DVHGFVGRYC	GDLEPDDIIS	TGNVMTLKPL	SDASVTAGGP	240
55	QIKYVAMDVF	SKSSQGGKTS	TSTGNKNPL	AGRPSHL			277

Seq ID NO: C290 Protein Sequence
Protein Accession #: NP_001973.1

	1	11	21	31	41	51	
60	MRANDALQVL	GLLESLARGS	EVGNSQAVCP	GTNLGLSVTG	DAENQYQTLV	KLYERCEVVM	60
	GNLEIVLTGH	NADLSFLQWI	REVTGYVLVA	MNEPSTLPLP	NLRVVRGTQV	YDGKFAIFVM	120
	LNMYNTSSHA	LRQLRLTQLT	EILSGGVYIE	KNDKLCHMDT	IDWRDIVRDR	DAEIVVKDNG	180
	RSCPPECHVC	KGRCWGPGSE	DOQTLTKTIC	APQCNGHCFG	PNPQCCHDE	CAGGCSGPQD	240
65	TDCPACRHFN	DSGACVPRCP	QPLVYNKLT	QLEPNPHTKY	QYGGVCVASC	PHNFVVDQTS	300
	CVRACPFDM	EVDKNGLKMC	EPCGGLCPKA	CEGTGSGSRF	QTVDSNIDG	FVNCTKILGN	360
	LDPLITGLNG	DPWHKIPALD	PEKLMVPRTV	REITGYLANIQ	SWPPHMGHNS	VFSNLTTIGQ	420
	RSLYNRGFSL	LIMKNLNVTS	LGFRSLKEIS	AGRIYISANR	QLCYHHSLNW	TKVLRGPTEE	480
70	RDLIKHNRPR	RDCVAEGKVC	DPLCSSGGCW	GGPGQCLSC	RNYSRGGVCV	THCNPLNGEP	540
	REFAEAECP	SCHPECQPMG	GTATCNGSGS	DTCAQCAHFR	DGPHCVSSCP	HGVLGAKGPI	600
	YKFDVQNEC	RPCHEHCTQG	CKGPELQDCL	QOTLVLIQKT	HLTMALTVIA	GLVVIPIMLG	660
	GTFLYWRGRR	IQNKAMRRY	LERGESIEPL	DPSEKANKVL	ARIFKETELR	KLKVLGSGVP	720
	GTVHKGVWIP	EGESI KIPVC	IKVIEDKSGR	QSFQAVTDHM	LAIGSLDHAH	IVRLGLGCPG	780
75	SSLQVLTQYL	PLGSLLDHVR	QHRGALGPQL	LLNWGVQIAK	GMYYLEEHGM	VHRNLAARNV	840
	LLKSPSQVQV	ADFGVADLLP	PDDKQLLYSE	AKTPIKWMAL	ESIHFGKYTH	QSDVVSYGVT	900
	VWELMTFAG	PVAGLRLLAEV	PDLEKGERL	AQPQICTLDV	YVMVVKCWM	DENIRPTFKE	960
	LANEFTRMAR	DPFRYLVIKR	ESGPGIAPGP	SPHGLTNKKL	EEVELEPELD	LDLDLEAED	1020
	NLATTTLGSA	LSLPVGTLMR	PRGSQSLSP	SSGYMPMNGQ	NLGGSCQESA	VSGSSERCPR	1080
80	PVSLHMPRPG	CLASESEGH	VTGSBAELQE	KVSMCRSRSR	SRSPRPRGDS	AYHSQRHSL	1140
	TFVTPLSPFP	LEEDVNGYV	MPDTHLKGTP	SSREGTLGSV	GLSSVLGTEE	EDEDEEYEM	1200
	NRNRHSPFP	PPRPSLEEL	GVEYMDVGS	LSASLGSTQS	CPLHVPVIMP	TAGTTPTDEY	1260
	EYMNRRDGG	GGGGDYAAMG	ACPASEQGYE	EMRAFQGPQH	QAPHVHYARL	KTLSLEATD	1320
	SAFDNPDYWH	SRLFPKANAQ	RT				1342

Seq ID NO: C291 Protein Sequence
Protein Accession #: NP_001207.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MAPLCPSPWL PLLIPAPAFG LTVQLLLSLL LLMPVHFQRL PRMQEDSPLG GGSSGEDDPL 60
GEEDLPSEED SPREEDPPGE EDLPGEEDLF GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG 120
DPQEPQNNAH RDKEGDDQSH WRYGGDFPWP RVSPACAGRF QSPVDIRPOL AAFCPALRPL 180
ELLGFLPLPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
VEGHRFPFBI HVHVLSTAFI RVDEALGRPG GLAVLAAPLE EGPEENSAYE QLLSRLEEIA 300
EEGSETQVPG LDLSALLPSD PSRYFQYEGS LTTTPCAQGV IWTVPNQTMV LSAQLHTLS 360
DTLNGPGDSR LQINFRATQP LNGRVIRASF PAGVDSPPRA AEPVQLNSCL AAGDILALVF 420
GLLFAVTSVA FLVQMRQRHR RGTKGGVSYR PAEVAETGA 459

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Seq ID NO: C292 Protein Sequence
Protein Accession #: NP_004198.1

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20      1      11      21      31      41      51
      |      |      |      |      |      |
MGGAVVDEGP TGKAPDGGW GWAFLFGCFV ITGPSYAFPK AVSVFFKELI QEFGIGYSDT 60
AWISSILLAM LYGTGPLCSV CVNRFPCRFP MLVGGFLFASL GMVAASPCRS IIQVYLTTGV 120
ITGLGLALNP QPSLIMLNRY FSKRRPMANG LAAAGSPVPL CALSPLGQLL QDRYWRGGFP 180
LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFRDRGFVL YAVAASVMVL 240
GLPVPPVFPV SYAKDLGVFD TKAAFLLTIL GFIDIFARPA AGFVAGLGKV RFYSVYLFSP 300
SMFFNGLADL AGSTAGDYGG LVVFCIFFGI SYGMVGAQGF EVLMAIVGTH KPSAIGLVL 360
LMEAVAVLVG PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLGNPFCCI RKKPKPEQPE 420
VAAAEKEKLE KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

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Seq ID NO: C293 Protein Sequence
Protein Accession #: NP_000349.1

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30      1      11      21      31      41      51
      |      |      |      |      |      |
MALFVRLAL ALALALGPAA TLAGPAKSPY QLVQLQHSRLR GRQHGPNVCA VQKVIGTNRK 60
YFTNCQWYQ RYICGKSTVI SYECCPGYEK VPGKGGCPAA LPLSNLYETL GUVGTTTQL 120
YTDRTAKLRP EMEGPGSFTI FAPSNEAWAS LPAEVLDSL V SNVNIKLNA LRYHMVGRRV 180
LTDLKHGHT LMSYQMSNI QIHHPNGIV TVNCARLLKA DHATNGVVH LIDKIVSTIT 240
NNIQIIEIE DTFETLRAAV AASGLNMLE GNGQYTLAP TNEAFKIPS ETLNRLIGDP 300
EALRDLNHN ILKSAMCABA IVAGLSVETL EGTTLVGCSS GDMLTINGKA IISNKDILAT 360
NGVTHYDEL LIPDSAKTLF ELAASDVST AIDLFRQAGL GNHLGSSERL TLLAPLNSVF 420
KDGTPPIDAH TRNLLRNHII KDQLASKYLY HGQTLSTLGG KKLRFVYVRN SLCIENS CIA 480
AHDKRGYGT LFTMDRVLT PMGTVMVLK GDNRFPSMLVA AIQSAGLTET LNRGVYTVF 540
APTNEAFRAL PPRERSRLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
LKNNVSVNKK EPVAEPDIMA TNGVVEVITN VLQPPANRPQ ERGDELADSA LEIFKQASAP 660
SRASQSRVRL APVYQKLLER MKH 683

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Seq ID NO: C294 Protein Sequence
Protein Accession #: NP_006527.1

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50      1      11      21      31      41      51
      |      |      |      |      |      |
MTQRSIAGPI CNLKFVTLV ALSSSELPFLG AGVQLQDNGY NGLLIAINPQ VPENQNLISN 60
IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH 120
GDDPYTLQYR GCGKEGKYIH PTPNPLANDN LTAGYGSRRG VFWHEWAHLR WGVFDEYNND 180
KPFYINGQNG IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
MEMQSLSSV EPCNASTHNO EAPNLQNM C SLRSKWDVIT DSADFHHSFP MNGTELPPPP 300
TPSLVQAGDK VVCLVLDVSS KMAEADRLIQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI 360
RAQLHQINSN DDKRLVSYL PTTVSAKTDI SICSLGKGF EVVEKLANGKA YGSVMILVTS 420
GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKPFVPDI SNSNSMIDAF 480
SRISSGTGD I FQHQIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL 540
FPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWITYTLN NTHSLQALK VTVTSRASNS 600
AVPPATVEAP VERDSLHPPH PVMYIANVKQ GFYFILNATV TATVEPETGD PVTLRLLDDG 660
AGADVINKDG IYSRYFFSPA ANGRYSKLVH VNHSPISTP AHSIPGSHAM YVPGYTANGN 720
IQMNAPRKSV GRNEERKNG FSRVSGGSGF SVLGVPAGPH PDVFPCKII DLEAVKVEE 780
LTLSTAPGE DFDQQAQTSY EIRMSKSLQN IQDDPNAIL VNTSKRNPQQ AGIREIFTFS 840
PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
LILKGVL TAM GLIGIICLII VVTHHTLSRK KRADKKENG T KLL 943

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Seq ID NO: C295 Protein Sequence
Protein Accession #: Eos sequence

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70      1      11      21      31      41      51
      |      |      |      |      |      |
MKFLLILLQ ATASGALPLN SSTSLKNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHFF REMPGGFPVR KHYITYRINN 120
YTPDMNRDQV DYAIRKAPQV WSNVTPLKFS KINTGMADIL VVFARGAHGD PHAFDGGKGI 180
LAHAFPGPGS IGDDAHFDED EFWTTHSGGT NLPLTAVHEI GBSLGLGHSS DPKAVMFPTY 240
KYVDINTFRL SADDIRGIQS LYGDPKFNQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300
FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIBAAEIEA RNQVFLKDD KYWLISNLRP 360
EPNYPKSIHS FGPFPFVKKI DAAVFNRFY RTYFFVDNQY WRDYERRQPM DPGYPKLITK 420
NFQIGPKID AVFYSKNKY YFPQGSNQFE YDPLLRITK TLKSNWFGC 470

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Seq ID NO: C296 Protein Sequence
Protein Accession #: Eos sequence

1 11 21 31 41 51
 5 MKPLLILLQ ATASGALPLN SSTSLKNNV LFGERYLEKP YGLEINKLPV TKMKYSGNLM 60
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RCGVPDVHHP REMPGGPVVR KHYITYRINN 120
 YTPDMNREDV DYAIRKAFQV WSNVTPLKFS KINTGMADIL VVFARGAHGD FFAFDGKGGI 180
 LAHAFGPGSG IGGDAHFDED EFWTHSGGT NLFLTAHVAI GHSGLGHSS DPKAVMPPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEPA LCDPNLSFDA VTTVGNKIFP 300
 10 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIRAAYEIEA RNQVPLFKDD KYWLISNLRP 360
 EFNYPKSIHS FGPNPVKKI DAAVFNPRFY RTYFFVDNQY WRVDERRQMM DPGYPKLITK 420
 NFQIGIGKID AVFYSKNKYY YFFQGSNQFE YDFLLQRITK TLKSNSWFGC 470

Seq ID NO: C297 Protein Sequence
 Protein Accession #: NP_008883.1

1 11 21 31 41 51
 15 MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFVSDQ HSLYPLLEAT DNDDIYGAAW 60
 IGIFVGLCLF CLSVLGI VGI MKSSRKILLA YPILMPIVYA FEVASCITAA TQRDFPTPNL 120
 20 FLKQMLERYQ NNSPFDNDQ WKNGVTKTW DRMLQDNCQ GVNQPSDWQK YTSAPRTENN 180
 DADYFWRQK CVMNKLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAWFGFAI 240
 LCWTFWVLLG TMFYWSRIEY 260

Seq ID NO: C298 Protein Sequence
 Protein Accession #: NP_001784.2

1 11 21 31 41 51
 25 MGLPRGPLAS LLLLQVCWLG CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
 QEPALFSTDN DFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 30 KGPPFQRLNQ LKSNKDRDTH IFYSITPGA DSPPEGVFAV EKETGWLILLN KPLDREEIAK 180
 YELPGHAYSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYYTN GVVAYSISHS EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 35 TMMDGDGSTT TAVAVVEILD ANDNAPMPDP QKYBAHVPEP AVGHEVQRLT VTDLDAPNSP 360
 ANRATYLLMG GDDGDHFTIT THFENSGIIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR 480
 DPAGNWLAMP DSGQVAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLLD 540
 VNDEGPVPEP RQITICNQSP VRQVLNITDK DLSFHTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 40 TVVLSLKKFL KQITFYDVHLS LSDHGNKEQL TVIRATVCDG HGHVETCPGP WKGGFILFVL 660
 GAVLALLFLL LVLLLVRKK RIKKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDITQLHR 720
 GLEARPEVLL RNDVARTIIP TMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEKSGSDAA SLSSLTSSAS DQDQDYDLYN EWGSRFKKLA DMYGGEEDD 829

Seq ID NO: C299 Protein Sequence
 Protein Accession #: NP_005620.1

1 11 21 31 41 51
 45 MAKSAENGI YSVSGDEKKG FLIAPGPDGA PAKGDGPGVL GTPGGR LAVP PRETWTRQMD 60
 FIMSCVGFAY GLGNVVRFPY LCKYNGGGVF LIPYVLIALV GGIPPIFLEI SLGQFMKAGS 120
 50 INVMNICPLF KGLGYASPMI VFYCNYYIM VLANGFYLYV KSFTTTLFPA TOGHTWNTPD 180
 CVEIPRHEDC ANASLANLTC DQLADRRSPV IEFWENKVLK LSGGLEVPGA LMWEVTLCLL 240
 ACNVLVYPCV WKGVKSTGKI VYFTATFPYV VLVLVLRGV LPLGALDGII YYLKFDSWKL 300
 55 GSPQWKIDAG TQIFPSYAIQ LGALTALGSY NRFNNNCYKD AIILALINSQ TSFPAGPVVF 360
 SILGFMAAQ GVHISKVAES GPGLAFTIAP RAVTLMFVAP LWAAALFFML LLLGLDSQFV 420
 GVEGPIITGLL DLLPASYYFR POREISVALC CALCFVIDLS MVTDDGMVYQ QLFDDYSASG 480
 TLLWQAFWE CVVVANVYGA DRFMDDIACH IGYRPPCWMK WCNWFFPTPLV CMGIFIPNVV 540
 60 YYEPLVYNT YVYFWNGEAM GWAPALSSML CVPLHLGLCL LRAKGTMAER WQHLTQPIWG 600
 LHLLEYRAQD ADVRGLTTLT FVSESSKVVV VESVM 635

Seq ID NO: C300 Protein Sequence
 Protein Accession #: NP_006507.1

1 11 21 31 41 51
 65 MEPSSKKLTG RLMLAVGGAV LGSLLQFGYNT GVINAPQKVI EEFYNQTVWH RYGESILPTT 60
 LITLWLSLVA IPSVGGMIGS FSVGLFVNRP GRRNSMLMMN LLAPVSAVLM GFSKLGKSPF 120
 MLILGRFIIQ VYCGLTGTPV PMYVGEVSPT AFRGALGTIL QIGIVVGILI AQVFGLDSIM 180
 70 GNKDLWPLLL SIIFIPALLQ CIVLFPCEPS PRFLINRNE ENRAKSVLKK LRGTADVTHD 240
 LQEMKEESRQ MMREKKVITL ELFRSPAYRQ PILIAVVLQL SQQLSGINAV FYSTSIFEK 300
 AGVQPPVIAT IGSQIVMTAF TVVSLPVVER AGRRTLHLIG LAGMAGCAIL MTIALALLEQ 360
 LPMWSTLSIV AIFGFAVFE VGPGFIPWFI VAELEFSQSPR PAIAVAGFS NWTSNFIVGM 420
 75 CFQYVQLCG PYVPIIFTVL LVLPFIPTYP KVPETKGRTP DEIASGFRQG GASQSDKTPE 480
 ELPHPLGADS QV 492

Seq ID NO: C301 Protein Sequence
 Protein Accession #: XP_035292.2

1 11 21 31 41 51
 80 MAGAGPKRRA LAAPAAEKEE EAREKQLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
 GTIIGSGIFV TPTGVLEKAG SPGLALVVWA ACGVPSIVGA LCYARLGTII SKSGGDYAYM 120
 LEVYGSLLPAF LKLWIELLII RPSSQYIVAL VPATYLLKPL PPTCPVPEEA AKLVACLCLV 180
 LLTAVNCSYV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSEGTKLDDV 240

5 GNIVLALYSQ LFAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
 STEQMLSEEA VAVDFGNYHL GVMSEIIPVF VGLSCFGSVN GSLFTSSRLP FVGSREGHLP 360
 SILSMIHQVL LTFVPSLVFT CVMTLIYAFS KDIFSVINFF SFFNMLCVAL AIIGMIWLRH 420
 RKPELEERPIK VMLALPVFFI LACLPLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWMMN 480
 KPNWLLQGIF STTVLQQLM QVVPQET 507

Seq ID NO: C302 Protein Sequence
 Protein Accession #: NP_005259.1

10 1 11 21 31 41 51
 MNWSIFEGLL SGVNYKYSTAP GRWLSSLVFI FRVLVYLVT A ERVNSDDHKO PDCNTRQPGC 60
 SNVCFDEFFP VSHVRLMALQ LILVTCPSLL VMHVAYREV QEKHREANG ENSGRLYLNP 120
 15 GKRGGLMWT YVCSLVFKAS VDIAPLYVFH SFYPKYILPP VVKHADPCP NIVDCFISKP 180
 SEKNIPTLFM VATAICILL NLVELIYLVS KRCHCLAAR KAQAMCTGHH PHGTTSSCKQ 240
 DLLSGDLIF LGSDSHPLF PDRPRDHVKK TIL 273

Seq ID NO: C303 Protein Sequence
 Protein Accession #: NP_005121.1

20 1 11 21 31 41 51
 MKICSLTLLS FILLAAQVLL VEGKKVKVNG LHSKVVSEQK DTLGNTQIKQ KSRPGNKGKP 60
 VTKDQANCRW AATEQEEGIS LKVECTQLDH EFSCVPAGNP TSCLKLDER VYWKQVARNL 120
 25 RSQKDICRYS KTAIVTRVCR KDFPESLSKL VSSTLFGNTK PRKEKTEMSF REHIKCKETT 180
 PSSLAVTQTM ATKAPCEVED PDMAQRKTA LEFCGETWSS LCTFFLSIVQ DTSC 234

Seq ID NO: C304 Protein Sequence
 Protein Accession #: AAH22542

30 1 11 21 31 41 51
 MCSEIILRQE VLKDGFRDL LIKVKPGESI EDLHTCRLLI KQDIPAGLYV DPYELASLRE 60
 RNITEAVMVS ENFDIEAPNY LSKESEVLIY ARRDSQCIDC FQAFPLPVHCR YHRPHSEDGE 120
 35 ASIVVNNPDL LMFCDQAGSR RMIRFRFDSF DKTIEFFILK CWAHSEVAAP CALENEDICQ 180
 WNMKMYKSVY KNVILQVPVG LTVHTSLVCS VTLLITILCS KKKKK 225

Seq ID NO: C305 Protein Sequence
 Protein Accession #: NP_004985.1

40 1 11 21 31 41 51
 MSLWQPLVLV LLVIGCCPAA PRQRQSTLVL FPGDLRTNLT DRQLASEYLY RYGYTRVAEM 60
 RGEKSLGPA LLLLQQLSL PETGELOSAT LKAMRTPRCG VPDLGRFQTF EGDLEWHHEN 120
 45 ITWIQNYSE DLPRAVIDDA FARAFALWSA VTPLTFTRVY SRDADIVIQF GVAEHGDGYP 180
 FDGKGLLAH APPPGGIQGG DAHFDDELW SLGKGVVPT RFGNADGAAC HFFPIFEGRS 240
 YSACTTDGRS DQLFWCSTTA NYDTDDRFGP CPSERLVTRD GNADGKPCQF PFIPOGQSYS 300
 ACTTDGRSDG YRWCAITANY DRDLKFGPCF TRADSTVMGG NSAGELCVFP FTFLGKEYST 360
 50 CTSEGRGDGR LWCATTSNFD SDKKWGFCDP QQYSLFLVAA HEFGHALGLD HSSVPEALMY 420
 PMYRFTEGFP LHKDDVNGIR HLYGPRPEPE PRPPTTTTPQ PTAPPTVCPT GPPTVHPSE 480
 PTAGPTGPPS AGPTGPTAG PSTATTVPLS PVDDACNVI FDAIARIGNQ LYLFDGKYW 540
 RPSSEGRSRP QGFPLIADKW PALPRKLDV FZEPLSKLP FFSGRQVWVY TGASVLGPRR 600
 LDKLGLGADV AQVTGALRSR RGKMLPSGR RLWRPDKAQ MVDPRSASEV DRMPFGVPLD 660
 55 THDVPQYREK AYPQQRFPY RVSSRSELNQ VDQGVYTYD ILQCPED 707

Seq ID NO: C306 Protein Sequence
 Protein Accession #: NP_000204

60 1 11 21 31 41 51
 MAGPRPSPNA RLLLAALISV SLSGTLANRC KKAPVKSCTE CVRVKDCAY CTDEMFRDRR 60
 CMTQAEALLA GCQRESIVVM ESSFQITEET QIDTTLRRSQ MSPQGLRVL RPGERHFP 120
 EVFEPLESFV DLYILMDFSN SMSDDLNLK RMGQNLARVL SGLTSDYITG FGKPVVKVSV 180
 65 PQTDMRPEKL KEPWFNSDPP FSPKRVISLT EDVDEFRNKL QGERISGNLD APEGGFDAIL 240
 QTAVCTRDIG WRPDSTHLLV PSTESAFHYE ADGANVLGI MSRNDERCEL DTTGTYYTQYR 300
 TDQYPSVPTL VRLLAGHNII PIPAVTNYSE SYERLHTYF PVSSLGVLQE DSSNIVELLE 360
 EAPNRIRSNL DIRALDSPRG LRTEVTSKMF QKTRTGSFHI RRGVGVYQV QLRALHVDG 420
 THVCQLPEDQ KGNHLKPSF SDGLKMDAGI ICDVCTCELQ KEVRSARCSF NGDFVCGQCV 480
 70 CSBGWSGQTC NCSTGSLSDI QPCLREGEDK PCSGRGECQC GHCVCYGEGR YEGQPCYDN 540
 PQCPRTSGFL CNDRGRCSMG QCVCEPGWTG FSCDCPLSNA TCIDSNGGIC NGRGHCEGR 600
 CHCHQQLYTT DTICEINYS A IHFGLCEDLR SCVQQAAGT GEKKGRTCEE CNFKVMVDE 660
 LKRASEVVVR CSFDEDDDC TYSYTMEDG APGPNSTVLV HKKDCPCPGS FWWLIPLLLL 720
 LLLPLALLLL LCWKYCACCK ACLALLPCCN RGHMVGFKEH HYMLRENLMA SDELDTPLMR 780
 75 SGNLKGREDV RWKVTNNMQR PGFATHAASI NPTELVPYGL SLRLARLCTE NLLKPDTRC 840
 AQLRQEVEN LNEYVRIQSG VHKLQOTKPR QQPNAKKQD HTIVDTVMA PRSAKPALLK 900
 LTEKQVQRLA PHDLKVAPGY YTLTADQDAR GMVEPQEGVE LVDVRVPLFI RPEDDEKQL 960
 LVEAIDVPAG TATLGRRLVN ITIIEQARD VVSFEQPEFS VSRGDQVARI FVIRRVLDGG 1020
 KSQVSYRTQD GTAQGNRDYI FVEGELLFPQ GEAWKELQVK LLELQEVDSL LRGRQVRFP 1080
 80 VOLSNPKFGA HLGQPHSTTI IIRDFDELDR SFTSQMLSSQ PPFHGDLAG QNPNKAAGS 1140
 RKIHFWLPP SGKPMGYRVK YWIQGDSSE AHLLDSKVP VELTNLYPYC DYEMKVCAYG 1200
 AQEGGYSLL VSGTHQEV SEPGRAPNV VSTVTQLSW AEPAETNGEI TAYEVCYGL 1260
 NDDNRPIGPM KCVLDNPKN RMLLIENLRE SQPYRYTVKA RAGAGWGER EAIINLATQP 1320
 KRPMSPITIP DIPVDAQSG EDYDSFLMYS DDVLRSPSGS QRPVSVDSTG CGWKPEPLLG 1380
 EELDLRRVTM RLPELIPRL SASSGRSSDA BAPTAPRTTA ARAGRAAAMP RSATPGPPGE 1440

5
 15
 20

HLVNGRMDFA	PGSTNSLHR	MTTTSAAAYG	THLSPHVPHR	VLSTSTLSTR	DYNSLTRSEH	1500
SHSTTLPRDY	STLTSVSSH	SRLTAGVPDT	PTRLVFSALG	PTSLRVSWQE	PRCERPLQGY	1560
SVBYQLNGG	ELHRLNIPNP	AQTSVVVEDL	LPNHSYVFRV	RAQSQEGWGR	EREGVITIES	1620
QVHPQSPCLP	LPQSAFTLST	PSAPGELVFT	ALSPDSLQLS	WERPRRPNGD	IVGYLVTCEN	1680
AQGGGPATAF	WDGDSPEER	LTVPGLSENV	PYKFKVQART	TEGFGPEREG	IITIESQDGG	1740
PPFQLGSRAG	LFQHPQLSEY	SSITTTHTSA	TEPFLVDGLT	LGAQHLEAGG	SLTRHVTQEF	1800
VSRTLTTSST	LSTHMDQPPF	QT				1822

Seq ID NO: C307 Protein Sequence
 Protein Accession #: NP_076404.1

15
 20

1	11	21	31	41	51	
MGFNLTAKL	PNNELHQGES	RNSGNRSDBG	GKNTTLHNEF	DTIVLPVLYL	IIFVASILLN	60
GLAVNIPFPI	RNKTSPFIPYL	KNIVVADLIM	TLTFPPFRIHV	DAGFGPWYFK	FILCRYTSVL	120
FYANMYTSIV	FLGLISIDRY	LKVVKFPGDS	RMYSITFTKV	LSVCVWVIMA	VLSLPNIILT	180
NGQPTEDNIH	DCSKLSPLG	VKMTAVTYV	NSCLFVAVLV	ILIGCYIAIS	RYIHKSSRQF	240
ISQSSRRKKH	NQSIKRVVAV	PFTCFPLPYHL	CRIPFTFSLH	DRLLDESAQK	ILVYCKEITL	300
FLSACNVCLD	PIIYFFMCRS	FSRRLFKKSN	IRTRSESIRS	LQSVRRSEVR	IYYDYTDV	358

Seq ID NO: C308 Protein Sequence
 Protein Accession #: NP_065840.1

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1	11	21	31	41	51	
MVWCLGLAVL	SLVISQGADG	RGKPEVVSIV	GRAEESVVLG	CDLLPPAGRP	PLHVIEWLRP	60
GFLLPPIQIF	GLYSRIDPD	YVGRVRLQKG	ASLQIEGLRV	EDQGWYECRV	FFLDQHIPPED	120
DFANGSWHL	TNNSPPQEQE	TPPAVLEVG	LEPVTLCRVA	RGSPLPHVTW	KLRGKDLGGQ	180
QQQVQVQNGT	LRIRRVERGS	SGVYTCQASS	TEGSATHATQ	LLVLGPPFIV	VPPKQSTVNA	240
SQDVSLACHA	EAYPANLTY	WFQDNINVFH	ISRLQPRVQI	LVDGSLRLLA	TQPDADAGCYT	300
CVPSNGLIHP	PSASAYLTVP	CMFQVIRCFV	RANPPLLFSV	WTKDQKALQL	DKFPQWSQGT	360
EGSLIIAALGN	EDALGEYSCT	PYNSLGTAGP	SPVTRVLLKA	PPAFIERPKE	EYFQEVGREL	420
LIPCSAQGGP	PFVVSMTKVG	RGLQGGQAQVD	SNSSLILRPL	TKEAHGHWEK	SASNAVARVA	480
TSTNVYVLGT	SPHVVTNVSV	VALPKGANVS	WEPGFQGGYL	QRFSVWYTPL	AKRPDRMHHD	540
WVSLAVPVGA	AHLLVPGQLP	HTQYQFSVLA	QNKLGSGPFS	EIVLSAPEGL	PTTAPAPGLE	600
PTIIPFPLSP	PRGLVAVRTP	RGVLLHWDFF	ELVPKRLDGY	VLEGRQSGSQ	WEVLDPAVAG	660
TETELIVPGL	IKDVLVEFRL	VAFAPGSFVSD	PSNTANVSTS	GLEVYPSRTQ	LPGLLPQFVL	720
AGVVGVCFL	GVAVLVSILA	GCLLNRRRAA	RRRKRLRLQD	PPLIFSPYTK	SAAPSALGSG	780
SPDSVAXLKL	QGSFVPSLRQ	SLWGDPACT	PSPHPDPPSS	RGPLPLEPIC	RGPDGRFVMG	840
PTVAAPQERS	GREQAEPRTP	AQRLARSFDC	SSSSPSGAPQ	PLCIEDISPV	APPPAAPPPSP	900
LPGPGLLQY	LSLPPFREM	VDGDWFPLEB	PSPAAPPDYM	DTRRCPTSSF	LRSPTFPVS	960
PRESLPGAVV	GAGATAEPPY	TALADWTLRE	RLPLGLLPAA	PRGSLTSQSS	GRGSASFRLP	1020
PSTAPSAAGS	YLSFAPGDT	SWASGPERNP	RREHVTVSK	RRNTSVDENY	EWDEPTPGDM	1080
ELLETLHLGL	ASSRLRPEAE	TELGVKTPBE	GCLLNTAHVT	GPEARCAALR	EEFLAFRRRR	1140
DATRRLPAY	RQVPFPEQA	TLL				1163

Seq ID NO: C309 Protein Sequence
 Protein Accession #:

50
 55

1	11	21	31	41	51	
MLTKPLQGGP	APPGTTPPP	GGKDREAFEA	EYRLGPLLGK	GGPGTVFAGH	RLTDRLQVAI	60
KVIPRNRVLG	WSPLSDSVTC	PLEVALLWKV	GAGGGHPGVI	RLLDWFETQE	GFMLVLERPL	120
PAQDLFDYIT	EXGPLEGSPS	RCFFGQVAA	IQHCHSRGVV	HRDIKDBNLT	IDLRRGCAKL	180
IDFGSGALLH	DEPYTDFDGT	RVYSPPEWIS	RHQYHALPAT	VMSLGILLVD	MVCGDIPFER	240
DQEILEAEHL	FPAHVSFDC	ALIRRCCLAPK	PSSRPSLEBI	LLDPWMQTPA	EDVTPQLQR	300
RPCPFGLVLA	TLSLAWFLGA	FNGQKSHPM	MSQG			334

Seq ID NO: C310 Protein Sequence
 Protein Accession #: NP_002501.1

60
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1	11	21	31	41	51	
MECLYYFLGF	LLLAARLPD	AAKRPHDVLG	NERPSAYMRE	HNQLNGWSSD	ENDWNEKLYP	60
VWKRGDMRWK	NSWKGGRVQA	VLTSDSPALV	GSNITPAVNL	IFPRCQKEDA	NGNIVYEKNC	120
RNEAGLSADP	YVYNWTAWSE	DSDGENTGQ	SHHNVPFDGK	PFPHPGWRR	WNFIYVFHTL	180
GQYFQKLGR	SVRVSVNTAN	VTLGQPLMEV	TVYRRHGRAY	VPIAQVKDQV	VVTQIIPVFV	240
TMFQKDRNS	SDETFLKDLF	IMFDVLHDP	SHFLNYSITN	YKWSFGDNTG	LPVSTNHTVN	300
HTYVLNGTFS	LNLTVKAAAP	GPCPPPPPPF	RPSKPTPSLG	PAGDNPLELS	RIPDENCQIN	360
RYGHFQATIT	IVEGILEVNI	IQMTDVLMPV	PWPESSLIDF	VVTCQGSIPT	EVCTIISDPT	420
CEITQNTVCS	PVDVDEMCLL	TVRRTFNGSQ	TYCVNLTGID	DTSLALTSTL	ISVFDKDPAS	480
PLRMANSALI	SVGCLAIFVT	VISLLVYKX	KEYNPIENSP	GNVVRSGKLS	VPLNRAKAVF	540
PPGNQEKDPL	LKNQEFKGV					560

Seq ID NO: C311 Protein Sequence
 Protein Accession #: Eos seq

80

1	11	21	31	41	51	
MRILKRFLAC	IQLLCVCLD	WANGYYRQQR	KLVEEIGNSY	TGALNQKNWG	KKYPTCNSPK	60
QSPINIDEDL	TQVNVNKKL	KPQGWKDTSL	ENTFIHNTGK	TVEINLTNDY	RVSQGVSEMV	120
PKASKITFW	GKCNMSDGS	EHSLEGGKFP	LEMQIYCFDA	DRPSSFEAV	KGKGLRALS	180
ILFEVGTEN	LDFKAIIDGV	ESVSRFGKQA	ALDPPILLNL	LPNSTDKYYI	YNGSLTSPCC	240
TDTVDNIVFK	DTVSISESQL	AVFCBVLTMQ	QSGYVLMMDY	LQNNFRBQY	KFSRQVFSY	300

5	TGKEEIHAEV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEPLTDGQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPPE	420
	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPHPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSTGAESL	NTVSIITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLME	PHYSTFAYFP	720
	TEVTTHAPT	SSRQDLVST	VNVVYSQTTQ	PVYNBASNS	HESRIGLAEG	LESEKKAIVP	780
10	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	PLYEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTTE	PEEVQSCSTD	LGITADSSNH	PDNKHQNRVI	NIVAYDHSRV	900
	KLAQLAEKDG	KLITYINANY	VDGYNRPKAY	IAAQGPLKST	AEDFWRMIWB	HNVEVIMVIT	960
	NLVEKGRRC	DQYWPADGSE	EYGNFLVTQK	SVQVLAYTVP	RNPTLRNTKI	KKGSQKGRPS	1020
	GRVVTQYHYT	QWPDGMPPEY	SLPVLTFVRK	AAAYAKRHAVG	FVVVHCSCAGV	GRGTGYIVLD	1080
15	SMLQQIQHES	TVNIFGLKH	IRSQRNYLVQ	TEEQVVFHID	TLVEAILSKE	TEVLDSHHA	1140
	YVNALLPGP	AGKTKLEKQF	QLLSQSNIQQ	SDYSAALKQC	NREKNRTSSI	IPVERSERVGI	1200
	SSLSGEGTGP	INASYIMGYI	QSNBFIITQH	PLLHTIKDFW	RMIWDHNAQL	VVMIPDQGNM	1260
	AEDEFVYWPN	KDEPINCESP	KVTLMABEKK	CLSNEEKLII	QDFILEATQD	DYVLEVRHFQ	1320
	CPKWNPDSP	ISKTFELISV	IKERAAANRDG	PMIVHDEHGG	VTAGTFALCT	TLMHQLEKEN	1380
20	SVDVYQVAKM	INLMRPGVFA	DIEQYQFLYK	VILSLVSTRQ	EENPSTSLDS	NGAALPDGNI	1440
	AESLESLSV						1448

Seq ID NO: C312 Protein Sequence
Protein Accession #: XP_031379

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	QSPINIDEDL	TQVNVNKLKL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
30	PKASKITHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPERAV	KGKGLRALS	180
	ILFEVGTEN	LDPKAIDGV	ESVSREFGKQA	ALDPFILLNL	LPNSTDKYVI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHAEV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEPLTDGQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPPE	420
35	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPHPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSTGAESL	NTVSIITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLME	PHYSTFAYFP	720
	TEVTTHAPT	SSRQDLVST	VNVVYSQTTQ	PVYNBASNS	HESRIGLAEG	LESEKKAIVP	780
40	LNTTPAASS	DSALHATFVP	PSVDVSFESI	LSSYDGAPLL	PFSSASPSSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPFLHASL	PVAGGDLLE	PSLAQYSDVL	STTHAASETL	EFGSESGVLY	900
	KTLMFSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVTYQG	960
	SLFSGPSHIP	IPKSSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLFDT	DGLTALNISS	1020
45	PVSVAREFTYT	TSVFGDDNKA	LKSEIIYGN	ETELQIPSPN	EMVYPSSESTV	MPNMYDNVVK	1080
	LNASLQETSV	SISSTKGMFP	GLAHTTTKV	PDHEISQVPE	NNFSVQPTHT	VSOASGDTSL	1140
	KPVLSANSEP	ASSDPASSEM	LSPSTQLLFY	ETSASFSTEV	LLQPSFQASD	VDTLLKTVLP	1200
	AVPSDILVE	TPKVDKISST	MLHLIVSNSA	ESSENLHSTS	VPVFDVSPTS	HMHASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVPSLYSND	ELFQTNALIE	NOAHPPKGRH	VFATPVLSD	1320
	EPLNTLNLK	IHSDEILTST	KSSVTGKVFA	GIPTVASDTP	VSTDHVSPIG	NGHVAITAVS	1380
50	PHRDGSVTST	KLLFPFKATS	ELSHSAKSDA	GLVGGGEDGD	TDDGDDDDDD	DRGSDGLSH	1440
	KCMSCSYRE	SQEKVMNDSD	THNSLMDQN	NFISYSLSEN	SEEDNRVTSV	SSDSQTMDR	1500
	SPGKSPSANG	LSQKNDGKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDEBSG	SGQGTSDSLN	1560
	ENETSTDFSP	ADTNEKDADG	LLAAGDSEIT	PGFPQSPTSS	VTSENSEVPH	VSEAEASNS	1620
	HESRIGLAEG	LESEKKAIVP	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	PLYEDSTSPR	1680
55	VISTPPTPIF	PISDDVGAIP	IKHFPKHVAD	LHASSGFTTE	FETLKEFYQE	VQSCVTDLGI	1740
	TADSSNHPDN	KHKRNRYINIV	AYDHSRVKLA	QLAEKDGKLT	DIYNANYVDG	YNRPKAYIAA	1800
	QGPKLSTAE	FWRMIWEHNV	EVIVMITHLV	EKGRRKCDQY	WPADGSEYQ	NFLVTQKSVQ	1860
	VLAYYTVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFVRKAAY	1920
	AKRHAVGFPV	VHCSAGVGR	GTIVLDSML	QQIQHEGTVN	IFGFLKHRS	QRNYLVQTEE	1980
60	QYVFIHDTLV	BAILSKETEVE	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKQCNRB	KNRTSSIIIP	ERSRVGISSL	SGEGTDYINA	SYIMGYQSN	EFIIHQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDQGNMAED	EFVYWNKDE	PINCESFKVT	LMAEBHKCLS	2160
	NEEKLIQDF	ILEATQDDYV	LEVRFHQCPK	WPNPDSPISK	TFELISVIKE	EAANRDGPMI	2220
	VDEHGGVTA	GTFCALTITL	HQLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVL	2280
65	SLVSTRQEN	PSTSLDSNGA	ALPDGNIAES	LESLSV			2315

Seq ID NO: C313 Protein Sequence
Protein Accession #: NP_002842

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	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKRWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNKLKL	KFGQWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	PKASKITHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRFSSPERAV	KGKGLRALS	180
75	ILFEVGTEN	LDPKAIDGV	ESVSREFGKQA	ALDPFILLNL	LPNSTDKYVI	YNGSLTSPPC	240
	TDTVDWIVFK	DTVSISESQL	AVFCEVLTMQ	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSY	300
	TGKEEIHAEV	CSSEPENVQA	DPENYTSLLV	TWERPRVVD	TMIEKFAVLY	QQLDGEDQTK	360
	HEPLTDGQD	LGAILNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLPPE	420
80	LIGTEEIIKE	EEEGKDIEEG	AIVNPGRDSA	TNQRKKEPQ	ISTTTHYNRI	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVNTSL	NSTSQPVTKL	ATEKDISLTS	QTVTELPHPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSTGAESL	NTVSIITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSEMG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLME	PHYSTFAYFP	720
	TEVTTHAPT	SSRQDLVST	VNVVYSQTTQ	PVYNBASNS	HESRIGLAEG	LESEKKAIVP	780

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PLVIVSALTF ICLVVLGVIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840
PIKHPFKHVA DLHASSGFTF EFETLKEFYQ EVQSCSTDGL ITADSSNHDP NKHKRYININ 900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMWEHN 960
VEVIVMITNL VEGRRKCDQ YWADGSEY GNFLVTQKSV QVLAAYTVRN FTLRNTKIKK 1020
GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL FVLTFVRKAA YAKRHAVGPV VVHCAGVGR 1080
TGTYIVLDSM LQIQHEGTN NIPGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIIP 1200
VERSRVGISS LSGEGTDYIN ASYIMGYYS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
MIPDQGNMAE DEFVYVWPKD EPINCESPKV TLMAEHKCL SNEEKLIQD FILEATQDDY 1320
VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
MHQLEKENSF DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
AALPDGNIAE SLESIV 1456

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Seq ID NO: C314 Protein Sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
MRILKRFLAC IQLLCVCRLD WANGYYRQQR KLVEEIGWSY TGALNQKNWG KKYPTCNSPK 60
QSPINIDEDL TQVNVNLKKL KPGQWDTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
MVPKASKITF HWGKNMSSD GSEHSLGQK FLEMQIYCF DADRPSSFE AVKGKGLRA 180
LSILFEVGT EENLDFKAIID GVESVSRPGK QAALDPFILL NLLPNSTDKY YIYNGSLTSP 240
PCTDTHWIFV KDTVSISESQ LAVFCEVLTM QSGYVLMMD YLQNNFREQQ YKFSRQVPSS 300
YTGEKEIHFA VCSSEPNVQ ADPENYTSLL VTWERPRVYV DTMEKFAVL YQLDGEDQTK 360
KHEFLTDGYQ DLGAILNLL PMSYVLQIV AICTNGLYK YSDQLIVDMP DNPFLDLFPE 420
ELIGTEBIK EEEGKDIEE GAIVNPGRDS ATNQIRKKEP QISTTTHYNR IGTYNEAKT 480
NRSPTRGSEF SGKGDVNTS LNSTSQPVTK LATEKDILST SQVTTELPH TVEGTSASIN 540
DGSKTVLRSF HNNLSGTAE LNTVSITEYE EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600
SENISQGYIF SSENPEITDY DVLIPESARN ASEDSTSSGS EESLKDPSME GNWFPSSDT 660
ITAQPDVGSQ RESFLQNTY EIRVDESEKT TKSFSAGPVM SQGPSVTDL MPHYSTPAYF 720
PTEVTPHAPT PSSRQDLVST TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAIV 780
PLVIVSALTF ICLVVLGVIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840
PIKHPFKHVA DLHASSGFTF EFETLKEFYQ EVQSCSTDGL ITADSSNHDP NKHKRYININ 900
VAYDHSRVKL AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMWEHN 960
VEVIVMITNL VEGRRKCDQ YWADGSEY GNFLVTQKSV QVLAAYTVRN FTLRNTKIKK 1020
GSQKGRPSGR VVTQYHYTQW PDMGVPEYSL FVLTFVRKAA YAKRHAVGPV VVHCAGVGR 1080
TGTYIVLDSM LQIQHEGTN NIPGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
VLDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIIP 1200
VERSRVGISS LSGEGTDYIN ASYIMGYYS NEFIITQHPL LHTIKDFWRM IWDHNAQLVV 1260
MIPDQGNMAE DEFVYVWPKD EPINCESPKV TLMAEHKCL SNEEKLIQD FILEATQDDY 1320
VLEVRHFQCP KWPNDPSPIS KTFELISVIK EEAANRDGPM IVHDEHGGVT AGTFCALTTL 1380
MHQLEKENSF DVYQVAKMIN LMRPGVFADI EQYQFLYKVI LSLVSTRQEE NPSTSLDSNG 1440
AALPDGNIAE SLESIV 1456

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Seq ID NO: C315 Protein Sequence
Protein Accession #: Eos sequence

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1 11 21 31 41 51
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QSPINIDEDL TQVNVNLKKL KPGQWDTSL ENTFIHNTGK TVEINLTNDY RVSGGVSEMV 120
FKASKITFWH GKNMSSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEAV KKGKGLRALS 180
ILFEVGT EENLDFKAIIDG BSVSRPGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240
TDTVDWIFVK DTVSISESQ AVFCEVLTMQ QSGYVLMMD YLQNNFREQQ YKFSRQVPSS 300
TKGEIHFAV CSSEPNVQA DPENYTSLLV TWERPRVYV DTMEKFAVL YQLDGEDQTK 360
HEFLTDGYQD LGAILNLLP NMSYVLQIVA ICTNGLYK YSDQLIVDMP DNPFLDLFPE 420
LIGTEBIKE EEEGKDIEE GAIVNPGRDS ATNQIRKKEP QISTTTHYNR IGTYNEAKT 480
NRSPTRGSEF SGKGDVNTS LNSTSQPVTK LATEKDILST SQVTTELPH TVEGTSASIN 540
DGSKTVLRSF HNNLSGTAE LNTVSITEYE EESLLTSFKL DTGAEDSSGS SPATSAIPFI 600
ENISQGYIFS SSENPEITDY DVLIPESARN SEDSTSSGS EESLKDPSME GNWFPSSDT 660
TAQPDVGSQ RESFLQNTY EIRVDESEKT TKSFSAGPVM SQGPSVTDL MPHYSTPAYF 720
TEVTPHAPT PSSRQDLVST TVNVVYSQTT QPVYNEASNS SHESRIGLAE GLESEKKAIV 780
LVIVSALTFI CLVVLGVIL IYWRKCFQTA HFYLEDSTSP RVISTPPTPI FPISDDVGAI 840
IKHFPKHVAD LHASSGFTF EFETLKEFYQ EVQSCSTDGL ITADSSNHDP NKHKRYININ 900
AYDHSRVKLA AQLAEKDGKL TDYINANYVD GYNRPKAYIA AQGPLKSTAE DFWRMWEHN 960
EVIVMITNLV EGGRRKCDQ YWADGSEY GNFLVTQKSV QVLAAYTVRN FTLRNTKIKK 1020
SQKGRPSGRV VTQYHYTQW PDMGVPEYSL FVLTFVRKAA YAKRHAVGPV VVHCAGVGR 1080
GTYIVLDSM LQIQHEGTN NIPGFLKHIR SQRYLVQTE EQYVFIHDTL VEAILSKETE 1140
LDSHIHAYV NALLIPGPAG KTKLEKQFQL LSQSNIQQSD YSAALKQCNR EKNRTSSIIIP 1200
SRVAGTILLS QSNIIQSDYS AALKQCNREK NRTSSIIIPVE RSRVGISLS GEGTDYINAS 1260
YIMGYYSNE FIITQHPLH TIKDFWRMI DHNAQLVVM PDQGNMAE DEFVYVWPKD 1320
INCESPKVIT MAEHLKCLN EELIQQDFI LEATQDDYV EVRHFQCPK PNPDPSPISK 1380
FELISVIKEE AANRDGPMIV HDEHGGVTAG TFCALTTLMH QLEKENSVDV YQVAKMINLM 1440
RPGVPADIEQ YQFLYKVI LSGTRQEE NPSTSLDSNG AALPDGNIAE SLESIV 1494

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Seq ID NO: C316 Protein Sequence
Protein Accession #: Eos sequence

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FKASKITFWH GKNMSSDGS EHSLEGQKFP LEMQIYCFDA DRPSSFEAV KKGKGLRALS 180
ILFEVGT EENLDFKAIIDG BSVSRPGKQA ALDPFILLNL LPNSTDKYI YNGSLTSPPC 240

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5	1	11	21	31	41	51	
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPEASNSSH	420
	ESRIGLAEG	ESKKAIVPL	VIVSALTPIC	LVVLVGILY	WRKCPQTAHF	YLEDSTSPRV	480
	ISTPPTPIFP	ISDDVGAIP	KHFPKHVADL	HASSGFTBEF	ETLKEFYQEV	QSCTVDLGIT	540
	ADSSNHDPNK	HKNRNINIVA	YDHSRVKLAQ	LAEKDGKLT	YINANYVDGY	NRPKAYIAAQ	600
	GPLKSTAEDP	WRMIWEHNV	VIVMITNLVE	KGRRKCDQYM	PADGSEBYGN	FLVTQKSVQV	660
	LAYYTVRNFT	LRNTKIKKGS	QKGRPSGRV	QYHYTQWPD	MGVPEYSLPV	LTFVRKAAYA	720
10	KRHAVGPVVV	HCSAGVGRTG	TYIVLDSMLQ	QIQHEGTVNI	PGFLKHIRSQ	RNYLVQTEBQ	780
	YVFIHDTLVE	ALLSKETEV	DSHIHAYVNA	LLIPGPAGKT	KLEKQFQLLS	QSNIQQSDYS	840
	AALKQCNREK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	YIMGYQSN	FIITQHPLH	900
	TIKDFWRMIW	DHNAQLVVM	PDGQNMAEDE	FVYWPKNDEP	INCRSPKVT	MAEEHKCLSN	960
	EEKLIQDFI	LEATQDDYVL	EVRRHPCPKW	PNDPSISK	FELISVIKEE	AANRDGPMIV	1020
15	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	RPGVFADIEQ	YQFLYKVLIS	1080
	LVSTRQEENP	STSLDSNGAA	LPGNIAESL	ESL			1113

Seq ID NO: C317 Protein Sequence
Protein Accession #: Eos sequence

20	1	11	21	31	41	51	
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	QSPINIDEDL	TQVNVNLLKL	KPQGWKDTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
	FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRPSSFEBAV	KGKGLRALS	180
25	ILFEVGTEN	LDFAKIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPPE	420
	LIGTEEIIKE	EEEGKOIEEG	AIVNPGRDSA	TNQIRKKBPQ	ISTTTHYNR	GTKYNEAKTN	480
30	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAEASL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTPAYFP	720
	TEVTPHAFIP	SSRQQLVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAIVP	780
35	LVIVSALTPI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTTE	FETLKEFYQE	VQSCVDLGI	TADSSNHDPN	HKNRNINIV	900
	AHDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAED	FWRMIWEHNV	960
	EVIVMITNLV	EKGRRKCDQY	WPADGSEBYG	NFLVTQKSVQ	VLAYTTRNF	TLRNTKIKKG	1020
40	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFRKAAY	AKRHAVGPVV	VHCSAGVGRT	1080
	GTIVVLDLML	QIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	EALISKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQL	TLSPRLCEG	TISAHCNLPL	PGLTDPPTSA	1200
	SRVARTILLS	QSNIQQSDYS	AALKQCNREK	NRTSSIIPE	RSRVGISSLS	GEGTDYINAS	1260
	YIMGYQSN	FIITQHPLH	TIKDFWRMIW	DHNAQLVVM	PDGQNMAEDE	FVYWPKNDEP	1320
45	INCRSPKVT	MAEEHKCLSN	EEKLIQDFI	LEATQDDYVL	EVRRHPCPKW	PNDPSISK	1380
	FELISVIKEE	AANRDGPMIV	HDEHGGVTAG	TFCALTTLMH	QLEKENSVDV	YQVAKMINLM	1440
	RPGVFADIEQ	YQFLYKVLIS	LVSTRQEENP	STSLDSNGAA	LPGNIAESL	ESL	1493

Seq ID NO: C318 Protein Sequence
Protein Accession #: Eos sequence

50	1	11	21	31	41	51	
	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	QSPINIDEDL	TQVNVNLLKL	KPQGWKDTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
55	FKASKITFHW	GKCNMSSDGS	EHSLEGQKFP	LEMQIYCFDA	DRPSSFEBAV	KGKGLRALS	180
	ILFEVGTEN	LDFAKIIDGV	ESVSRFGKQA	ALDPFILLNL	LPNSTDKYI	YNGSLTSPPC	240
	TDTVDMIVFK	DTVSISESQL	AVFCEVLTMO	QSGYVLMMDY	LQNNFREQQY	KFSRQVFSSY	300
	TGKEEIEHAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYQD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGYK	SDQLIVDMPT	DNPELDLPPE	420
60	LIGTEEIIKE	EEEGKOIEEG	AIVNPGRDSA	TNQIRKKBPQ	ISTTTHYNR	GTKYNEAKTN	480
	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVTKL	ATEKDLSLTS	QTVTELPPT	VEGTSASLND	540
	GSKTVLRSPH	MNLSGTAEASL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
	TAQPDVGSGR	ESFLQNTYTE	IRVDESEKTT	KSPSAGPVMS	QGPSVTDLEM	PHYSTPAYFP	720
65	TEVTPHAFIP	SSRQQLVST	VNVVYSQTTQ	PVYNEASNSS	HESRIGLAEG	LESEKKAIVP	780
	LVIVSALTPI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	VISTPPTPIF	PISDDVGAIP	840
	IKHFPKHVAD	LHASSGFTTE	FETLKEFYQE	VQSCVDLGI	TADSSNHDPN	HKNRNINIV	900
	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	QGPKLSTAED	FWRMIWEHNV	960
70	EVIVMITNLV	EKGRRKCDQY	WPADGSEBYG	NFLVTQKSVQ	VLAYTTRNF	TLRNTKIKKG	1020
	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFRKAAY	AKRHAVGPVV	VHCSAGVGRT	1080
	GTIVVLDLML	QIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	QYVFIHDTLV	EALISKETEV	1140
	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQL	QSNIQQSDY	SAALKQCNRE	KNRTSSIIPE	1200
	ERSRVGISSL	SGEGTDYINA	SYIMGYQSN	EFIITQHPLH	HTIKDFWRMI	WDHNAQLVVM	1260
75	IPDQGNMAED	FVYWPKNDEP	PINCESFKVT	LMAEEHKCLS	NEEKLIQDF	ILEATQAWRS	1320
	DGRNFLCSN	PYAPTRKRKF	RGCLPGSQDD	QSEARSLC			1359

Seq ID NO: C319 Protein Sequence
Protein Accession #: XP_002914.4

80	1	11	21	31	41	51	
	MKDIDIGKEY	IIPSPGYRSV	RERTSTSGTH	RDREDSKFR	TRPLECQDAL	ETAARAEGLS	60
	LDASHMSQLR	ILDEHPFKGK	YHGLSALKP	IRTTSKHQHP	VDNAGLFSCM	TFSWLSLAR	120
	VAHKKGELSM	EDVWLSKHE	SSDVNCRRL	RLWQEBELNEV	GPDAASLRRV	WVIFCRTRLI	180

	LSIVCLMITQ	LAGFSGPAPM	VGHLLLEYTQA	TESNLQYSLL	LVLGLLLTEI	VRSWSLALTW	240
	ALNYRTGVRL	RGAILTMAPK	KILKLNRIKE	KSLGELINIC	SNDGQRMFEA	AAVGSLLAGG	300
	PVVAILGMIY	NVILIGPTGP	LGSAVFILFY	PAMMFASRLT	AYFRKCVAA	TDERVQKMNE	360
5	VLTYIKPIKM	YAWKAFPSQS	VQKIREEERR	ILEKAGYPQS	ITVGVAPIVV	VIASVVTFSV	420
	HMTLGPDLTA	AQAPTUVTVF	NSMTFALKVT	PFSVKSLSEA	SVAVDRFKSL	FLMEEVHMIC	480
	NKPASPHIKI	EMKNATLAWD	SSHSSIQNSP	KLTPKMKDK	RASRGKKEKV	RQLQRTTEQA	540
	VLAQKQGHLL	LDSDERPSPE	EEEGKHIHLG	HLRLQRTLHS	IDLEIQEGKL	VGICGSVSGG	600
	KTSLISAILG	QMTLLEGSIA	ISGTFAYVAQ	QAWILNATLR	DNILFGKEYD	EERYNSVLNS	660
10	CCLRPDLAIL	PSSDLTEIGE	RGANLSSGQR	QRISLARALY	SDRSIYILDD	PLSALDAHVG	720
	NHIFNSAIRK	HLKSKTVLTV	THQLQYLVDG	DEVIFMKEGC	ITERGTHEEL	MNLNGDYATI	780
	FNLLLGGETP	PVEINSKKET	SGSQKKSQDK	GPKTGSVKKE	KAVKPEEGQL	VQLEEKGGQS	840
	VPWSVYGVYI	QAAGGFLAPL	VIMALFMLNV	GSTAFSTWNL	SYNIKQSGSN	TTVTRGNETS	900
	VSDSMKDNPH	MQYYASIAL	SMAVMLILKA	IRGVVPVKGT	LRASSRLHDE	LFRRILRSPM	960
	KFFDTTPTGR	ILNRPDKMD	EVDVRLPFQA	EMFIQNVILV	FFCVGMIAVG	FPWFLVAVGP	1020
15	LVILFSLVLI	VSRVLIRELK	RDLNITQSPF	LSHITSSIQG	LATIHAYNKG	QEFLHRYQEL	1080
	LDDNQAPFFL	FTCAMRWLAV	RDLISIALI	TTTGLMIVLM	HQIIPPAYAG	LAISYAVQLT	1140
	GLPQFTVRLA	SETEARPTSV	ERINHYIKTL	SLEAPARIKN	KAPSPDWPQE	GEVTFENAEM	1200
	RYRENLPVLV	KKVSFTIKPK	EKIGIVGRGT	SGKSSLSGML	FRVLVLSGGC	IKIDGVRISS	1260
20	IGLADLRSLK	SIIPQEPVLF	SGTVRSNLDP	FNQYTEDQIW	DALERTHMKC	CIAQLPLKLE	1320
	SEVMENGDNF	SVGERQLLCI	ARALLRHCKI	LILDEATAAM	DTETDLLIQE	TIREAPADCT	1380
	MLTIAHRLHT	VLGSDRIMVL	AQQQVVEFDT	PSVLLSNDSS	RFYAMFAAAE	NKVAVKG	1437

Seq ID NO: C320 Protein Sequence

Protein Accession #: NP_005679.1

25	1	11	21	31	41	51	
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30	1	11	21	31	41	51	
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	1	11	21	31	41	51	
35	1	11	21	31	41	51	
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	1	11	21	31	41	51	
	1	11	21	31	41	51	
40	1	11	21	31	41	51	
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	1	11	21	31	41	51	
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	1	11	21	31	41	51	
50	1	11	21	31	41	51	
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	1	11	21	31	41	51	
	1	11	21	31	41	51	

Seq ID NO: C321 Protein Sequence

Protein Accession #: NP_005553.1

55	1	11	21	31	41	51	
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60	1	11	21	31	41	51	
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	1	11	21	31	41	51	
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65	1	11	21	31	41	51	
	1	11	21	31	41	51	
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	1	11	21	31	41	51	
70	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
75	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	
	1	11	21	31	41	51	

Seq ID NO: C322 Protein Sequence
Protein Accession #: NP_066924.1

80	1	11	21	31	41	51	
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	1	11	21	31	41	51	
	1	11	21	31	41	51	

QIQCKVFDSL LNLSTLQAT RALMVVGILL GVIAIFVATV GMKCMKCLEL DEVQKMRNAV 120
 IGGAIFFLAG LAILVATAMY GNRIVQEFYD PMTPVNARYE FGQALPTGWA AASLCLLGGA 180
 LLCCSCPRKT TSYTPRPRYP KPAPSSGKDY V 211

5 Seq ID NO: C323 Protein Sequence
 Protein Accession #: AAM77876

10 1 11 21 31 41 51
 MSSWIRWHPG AMARLWGFCW LVVGFWRAP ACPTSCCKSA SRIWCSDPSP GIVAPPRLEP 60
 NSVDPENITE IPIANQKRL E IINEDDVEAY VGLRNLITVD SGLKPFVAHA FLKNSNLQHI 120
 NPTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPASN LAAPNLVTEE GKSTILSCSV AGDPVPMYV DVGNLVSKHM 240
 15 NETSHTQGS L RITNISSDDS GKQISCAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLV LFLKLARHS KFGMKGFVLF HKIPLDG 477

20 Seq ID NO: C324 Protein Sequence
 Protein Accession #: NP_006171.1

25 1 11 21 31 41 51
 MSSWIRWHPG AMARLWGFCW LVVGFWRAP ACPTSCCKSA SRIWCSDPSP GIVAPPRLEP 60
 NSVDPENITE IPIANQKRL E IINEDDVEAY VGLRNLITVD SGLKPFVAHA FLKNSNLQHI 120
 NPTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPASN LAAPNLVTEE GKSTILSCSV AGDPVPMYV DVGNLVSKHM 240
 30 NETSHTQGS L RITNISSDDS GKQISCAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLV LFLKLARHS KFGMKGFVLF ISNDDDSASP 480
 LHHSNGSNT PSSSEGGPDA VIIGMTKIPV IENPQYFGIT NSQLKPDFTV OHIKRENIVL 540
 KRELGEAGFG KVFLAECYNL CPEQDKILVA VKTLKADSDN ARKDPHREAE LLTNLQHEHI 600
 VKFYGVCEG DPLIMVFYFN KHGDLNKFLR AHGPDVAVLMA EGNPTELTQ SQMLHIAQQI 660
 35 AAGMVYLAQ HFVHRDLATR NCLVGENLLV KIGDPGMSRD VYSTDYRVVG GHTMLPIRM 720
 PPESIMYRKF TTESDVWSLG VVLNEIFTYG KQFWYQLSNN EVIECITQGR VLQRPRTCPQ 780
 EYVBLMLGCH QREPHMRKNI KGIHTLLQNL AKASPVYLDI LG 822

40 Seq ID NO: C325 Protein Sequence
 Protein Accession #: Eos sequence

45 1 11 21 31 41 51
 MSSWIRWHPG AMARLWGFCW LVVGFWRAP ACPTSCCKSA SRIWCSDPSP GIVAPPRLEP 60
 NSVDPENITE IPIANQKRL E IINEDDVEAY VGLRNLITVD SGLKPFVAHA FLKNSNLQHI 120
 NPTRNKLTSL SRKHFRHLDL SELILVGNPF TCSCDIMWIK TLQEAQSSPD TQDLYCLNES 180
 SKNIPLANLQ IPNCGLPASN LAAPNLVTEE GKSTILSCSV AGDPVPMYV DVGNLVSKHM 240
 50 NETSHTQGS L RITNISSDDS GKQISCAEN LVGEDQDSVN LTVHFAPTIT FLESPTSDDH 300
 WCIPPTVKGN PKPALQWFFN GAILNESKYI CTKIHVTNHT EYHGCLQDN PTHMNGDYT 360
 LIAKNEYGKD EKQISAHFMG WPGIDDGANP NYPDVIYEDY GTAANDIGDT TNRSNEIPST 420
 DVTDKTGREH LSVYAVVVIA SVVGFCLLV LFLKLARHS KFGMKGFVLF HKIPLDG 477

55 Seq ID NO: C326 Protein Sequence
 Protein Accession #: NP_570843.1

60 1 11 21 31 41 51
 MPLKHYLLLL VGCQAWGAGL AYHGCPSECT CSRASQVECT GARIVAVPTP LPWNAMSLQI 60
 LNTHITELNE SPFLNISALI ALRIEKNELS RITPGAPRNL GSLRYLSLAN NKLQVLFGL 120
 FQGLDSLES L LSSNQLLQI QPAHPSQCSN LKELQLHGNH LEYIPDGAFD HLVLTKLNL 180
 GKNLSLTHSP RVFQHLGNLQ VLRLYENRLT DIPMGTFDGL VNLQELALQO NQIGLLSPGL 240
 FHNHNLRQL YLSNNHISQL PPSIFMQLPQ LNRLTLFGNS LKELSLGIFQ PMPNLRRLWL 300
 YDNHISLPP NVFSNLRQLQ VLILSRNQIS PISPGAFNGL TELRELSLHT NALQDLGDNV 360
 65 FRMLANLQNI SLQNNRLRQL PGNIPANVNG LMAIQLNQNN LENLPLGIFD HLGKLCRL 420
 YDNFPCOSD ILPLRNLWLL NQPRLGTDIV PVCFSFANVR GQSLIINVN VAVPSVHVPE 480
 VPSYPETPWY FDTFSYPDTT SVSSTTELTS PVEDYDILT IQVTDDRNVN GMTQAQSGLA 540
 IAAIVIGIVA LACSLAACVG CCCCKKRSQA VLMQMKAPE C 581

70 Seq ID NO: C327 Protein Sequence
 Protein Accession #: NP_002649.1

75 1 11 21 31 41 51
 MRALLARLLL CVLVVSDSKG SNEHLQVPSN CDCLAGGTCV SNKYFSNIHW CNCPKKFGGQ 60
 HCEIDSKSTC YEONGHFYRG KASTDTMGRP CLPWSATVL QQTYHAHRSD ALQLGLGKH 120
 YCNFNDNRRL PWCYVQGLK PLVQECMVHD CADGKXPSSP PEELKFOCGQ KTLRPRFKII 180
 GGEFTTIENQ PWAATYRRH RGGSVTVVCG GSLISPCWVI SATHCFIDYP KKEEDYIVYLG 240
 RSLRNSNTQG EMKFEVENLI LHKDYSADTL AHRNDIALLK IRSKEGRCAQ PSRTTIQTICL 300
 80 PSMYNDPQFG TSCBITGFGK ENSTDYLYPE QLKMTVVKLI SHRECCQPHY YGSEVTTKML 360
 CAADPQWKT D SCQDSGGPL VCSLQGRMTL TGIVSWGRGC ALKDKPGVYT RVSHPLPWIR 420
 SHTKRENGLA L 431

Seq ID NO: C328 Protein Sequence
 Protein Accession #: XP_087254.1

	1	11	21	31	41	51	
5	MQFRECSING	MKYQINGRL	VPEGTPDSS	EGNLSYSSSL	SHLNLNLSLT	TSSSFRTSPE	60
	NETELIKEHD	LFFRAVSLCH	TVQISNVQTD	CTGDGFWQSN	LAPSQLEYA	SSPDEKALVE	120
	AAARIGIVFI	GNSEETMEVK	TLGKLERYKL	LHILEFDSDR	RRMSVIVQAP	SGEKLLFAKG	180
	AESSILPKCI	GGEIEKTRIH	VDEPALKGLR	TLCIAYRKFT	SKEYEBIDKR	IFEARTALQO	240
	REEKLAAPVQ	PIEKDLILIG	ATAVEDRLQD	KVRETIBALR	MAGIKVWVLT	GDKHETAVSV	300
10	SLSCGHFHR	MNILELINQK	SDSECAEQLR	QLARRITEDH	VIQHGVLVDG	TSLSLALREH	360
	EKLPMFECRN	CSAVLCCRMA	PLQKAKVIRL	IKISPEKPIT	LAVGDGANDV	SMIQEAHVGI	420
	GIMGKEGRG	ARNSDYAIAI	FKFLSKLLFV	HGHFYIIRIA	TLVQYFFPKN	VCFITPQFLY	480
	QPYCLFSQQT	LYDSVYLTLY	NICFTSLPIL	IYSLLEQHV	PHVLQNKPTL	YRDISKNRLL	540
	SIKTFLYWTI	LGFSHAFIFP	FGSYLLIGKD	TSLLQNGQMF	GNWTFGTLVF	TVWVITVTVK	600
15	MALETHFWT	INHLTWGSI	IFYFVPSLPY	GGILWPFLGS	QNMVFVFIQL	LSSGSANFAI	660
	ILMVVTCPLF	DIKKVDFDRH	LHPTSTKAQ	LTETNAGIKC	LDSMCCFPFG	EACASVGRM	720
	LERVIGRCSP	THISRSWSAS	DPFYTNDRSI	LTLSTMDSST	C		761

Seq ID NO: C329 Protein Sequence
Protein Accession #: XP_087461.1

	1	11	21	31	41	51	
20	MLPFLAALLA	AACPPLPPVRG	GAADAPGLLG	VPSNASVNAS	SAASPSPRGC	WPRRPPGPPS	60
	ARARRRRRR	RRLCNISVQR	QMLSSLLVRW	GRPRGPOCDL	LLFSTNAHGR	APFAAAFRHV	120
25	GPPLLIHLG	LAAGGAQDQL	RLCVGCGWVR	GRRTGRRLPA	AAPSAATA	GAPTALPAYP	180
	AAEPGGLWL	QGEPLHFCCL	DFSLEELQGE	PGWRLNRKPI	ESTLVACFMT	LVIIVWSVAA	240
	LINPVPIIAG	FLPNGMEQRR	TTASTTAATP	AAVPAAGTAA	AAAAAAAAAA	AVTSGVATK	299

Seq ID NO: C330 Protein Sequence
Protein Accession #: XP_051522.2

	1	11	21	31	41	51	
35	MDLHLFDYSE	FGNFSDISWP	CNSSDCIVVD	TVMCPNMPNK	SVLLYTLSPF	YIFIFVIGMI	60
	ANSVVVWVNI	QAKTTGYDTH	CYILNLAIAD	LWVVLTPVW	VVSLVQHNQW	PMGELTCKVT	120
	HLIFSNLPG	SIFFLTCMSV	DRYLSITYFT	NTPSSRKKMV	RRVCILVWL	LAFCVSLPDT	180
	YYLKTVTAS	NNETYCRSFY	PEHSIKEWLI	GMELVSVVLG	FAVPFSIIAV	FYFLLARAI	240
	ASSDQEKHS	RKIIFSYVVV	FLVCWLPYHV	AVLLDIFSIL	HYIPFTCRLE	HALFTALHVT	300
40	QCLSLVHCCV	NPVLYSFINR	NYRYELMKAF	IFKYSAKTGL	TKLIDASRV	ETEYSALEQS	360
	TK						362

Seq ID NO: C331 Protein Sequence
Protein Accession #: NP_000341.1

	1	11	21	31	41	51	
45	MGFVRQIQLL	LWKNWTLRKR	QKIRFVVELV	WPLSLFLVLI	WLRNANPLYS	HHECHFPNKA	60
	MPSAGMLPWL	QQIFCNVNNP	CFQSPTPGES	PGIVSNYNNS	ILARVYRDFQ	BLLMNAPESQ	120
	HLGRIWTELH	ILSQFMDTLR	THPERIAGRG	IRIRDILKDB	ETLTLEFLIKN	IGLSDSVVVL	180
50	LINSQVRPEQ	FAHGVPDLAL	KDIACEALL	ERFIIFSQR	GAKTVRYALC	SLSQGTILQWI	240
	EDTLYANVDF	FKLFRVLPTL	LDSRSQGINL	RSWGILSDM	SPRIQEFTHR	PSMDLLWVT	300
	RPLMQNGGPE	TFTKLMIILS	DLLCGYPGGG	GSRVLSFNWY	EDNNYKAFLO	IDSTRKDPIY	360
	SYDRRTTSPC	NALIQSLESN	PLTKIAMRAA	KPLLMGKILY	TPDSPAARRI	LKNANSTFEE	420
	LEHVRKLVKA	WEEVGPQIWW	FFDNSTQNM	IRDTLGNPTV	KDFLNRLQGE	EGITAEAILN	480
55	FLYKGPRESQ	ADDMANFDWR	DIPNITDRTL	RLVNQYLECL	VLDKFESYND	ETQLTORALS	540
	LLEENMFWAG	VVFPMYPMPT	SSLPPHVKYK	IRMDIDVVEK	TNKIKDRYWD	SGPRADPVED	600
	FRYINGGPAY	LQDMVEQGIT	RSQVQAEAPV	GIYLQQMYP	CFVDDSPMI	LNRCFPFIMV	660
	LAWIYSVSM	VKSIVLEKEL	RLKETLKNQG	VSNVAVINCTW	FLDSFSIMSM	SIFLLTIFIM	720
	HGRILHYSDD	FILFLFLAF	STATIMLCFL	LSTFFSKASL	AAACSGVIYF	TLYLPHILCF	780
60	ANQDRMTABL	KKAVSLLSFV	AFGFGTEYLV	RFEEQGLGLQ	WSNIGNSPTE	GDEFSPLLSM	840
	QMMLDAACY	GLLAWYLDQV	FPGDYGTPLP	WYFLLQESYV	LSGEGCSTRE	ERALEKTEPL	900
	TEETEDPEHP	EGIHDSFFER	EHPGWVPGVC	VKNLVKIFEP	CGRPAVDRLN	ITPYENQITA	960
	FLGHNGAGKT	TTLISLTGLL	PPTSGLTVLVG	GRDIETSLDA	VRQSLGMCQP	HNILPHHLTV	1020
	AEHMLFYAQL	KGKSQBEAQL	EMBALEDITG	LHHKRNBEAQ	DLSGGMQRKL	SVAIAPVGDA	1080
65	KVVILDEPTS	GVDPYSRRSI	WDLKKYRSG	RTIIMPTHM	DEADHQGDRI	AIIAQGRLYC	1140
	SGTFLFLKNC	FGTGLYLTIV	RKMKNIQSOR	KQSEGTCSGS	SKGFSSTCPA	HVDDLTPQV	1200
	LDGDVNELMD	VVLHHVPEAK	LVEICIGELI	FLLPKNFKH	RAYASLFREL	EETLADIGLS	1260
	SPGISDTPLE	EIFLKVTEDS	DSGFLPAGGA	QQKRENVNPR	HPCLGPREKA	GQTPQDSNVC	1320
	SPGAPAAHPE	GQPPPEPECP	GQPLNTGTQL	VLQHVQALLV	KRFQHTIRSH	KDPLAQIVLP	1380
70	ATFVFLALML	SIVILPFGEY	PALTLPWYIY	GQYTFFSMD	EPGSEQPTVL	ADVLLNKGEF	1440
	GNRCLKEGWL	PEYPCGNSTP	WKTSPVSPNI	TQLPQKQKWT	QVNPSPSCRC	STREKLTMLP	1500
	ECPEGAGLPL	PPORTQSRSTE	ILQDLTDENI	SDPLVKTYPA	LIRSSLSKSP	WVNEQRYYGI	1560
	SIGGKLFPVP	ITGEALVGFL	SDLGRIMNVS	GGPITREASK	EIPDFLKHLE	TEDNIKVWFN	1620
	NKGWALVSLL	LNVAHNAILR	ASLPKDRSP	EYGITVISQP	NLTKELQSE	ITVLTTSVDA	1680
75	VVAICVIPS	SVFPASFLVY	LIQERNVSKS	HLQFISGVSP	TTYWVTNFWL	DIMNYSVSAG	1740
	LUVGIPIGFQ	KKAYTSPENL	PALVALLLLY	GWAVIPMMY	ASFLFDVPST	AYVALSCANL	1800
	FIGINSSAIT	FILELFDNNR	TLRFNAVLR	KLLIVFPFHC	LGRGLIDLAL	SQAVTDVYAR	1860
	FGBEHSANFP	HWDLIGKNLF	AMVVEGVVYF	LLTLLVQRHF	FLSQWIAEPT	KSPIVDEDDT	1920
	VABERQRIIT	GGNKTDLRL	HELTKIYLTG	SSPAVDRLCV	GVRPGECFGL	LGVNGAGKGT	1980
80	TFKMLTGDIT	VTSGDATVAG	KSILTNISEV	HQNMGYCPQF	DAIDELLTGR	EHLVLYARLR	2040
	GVPAEIEKV	ANNSIKSLGL	TVYADCLAGT	YSGGNKRKLS	TAIALIGCPP	LVLLDEPTTG	2100
	MDQARRMLW	NVIVSIRKG	RAVVLTSISM	EECEALCTRL	AIMVKGAFRC	MGTIQHLKSK	2160
	FGDGYIVTK	IKSPKDDLLF	DLNPVVEQFQ	GNFPGSVQRE	RHYNMLQFQV	SSSSLARIFQ	2220
	LLSHKSDSL	IESYSVTQIT	LDQVFNFAK	QQTESHDLPL	HPRAAGASRQ	AQD	2273

Seq ID NO: C332 Protein Sequence
Protein Accession #: NP_006662.2

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5      1      11      21      31      41      51
      |      |      |      |      |      |
MVPHAILARG RDVCRRNGLL ILSVLSVIVG CLLGFFLRTR RLSPQBIISYF QPPGELLMRM 60
LKMMLPLVV SSIMSGLASL DAKTSSRLGV LTVAYYLWTT FMAVIVGIFM VSIIHPGSAA 120
QKETTEQSGK PIMSSADALL DLIRNMFPAN LVEATPKQYR TKITPVVKSP KVAPEEAPPR 180
10    RILIYGQBBE NGSHVQNFAL DLTPPPEVVY KSEPGTSDGM NVLGIVVFFSA TMGIMLGRMG 240
      DSGAPLVSPC QCLNESVMKI VAVAVWYFPF GIVFLIAGKI LEMDDPRAVG KKLGFYSVTV 300
      VOGLVLHGLF ILPLLYFFIT KKNPIVPFIRG ILQALLIALA TSSSSATLPI TFKCLLENNH 360
      IDRRIRFVL FVGATINMDG TALYEAVAAI FIAQVNNYEL DFGQIITISI TATAASIGAA 420
      GIPQAGLVTM VIVLTSVGLP TDDITLIIAV DWALDRFRMT INVLDALAA GIMAHICRDK 480
15    FARDTGTEKL LPCETKPVSL QEIVAAQQNG CVKSVABASE LTLGPTCPHH VPVQVERDEE 540
      LPAASLNHCT IQISELETNV

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Seq ID NO: C333 Protein Sequence
Protein Accession #: NP_005680.1

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20    1      11      21      31      41      51
      |      |      |      |      |      |
MVTVGNYCEA EGPVGPANMQ DGLSPCFFFT LVPSTRMALG TLALVLALPC RRRERPAGAD 60
      SLSWAGAPRI SPYVLQLLLA TLQAALFLAG LAGRVGTARG APLPSYLLLA SVLESILAGAC 120
25    GLWLLVVERS QARQRLAMGI WIKFRHSPLG LLLWTVAFAA ENLALVSWNS PQWWWARADL 180
      GQQVQFSLWV LRYVVSGLPF VGLWAPGLR POSYTLQVHE EDQDVERSQV RSAAQQTWR 240
      DFGRLRLLS GYLWPRGSPA LQLVVLICLG LMGRLERLNV LVPIFYRNIV NLLTEKAPWN 300
      SLAWTVTSYV FLKFLQGGGT GSTGPFVSNLR TFLWIRVQQF TSRRVELLIF SHLHELRLRW 360
30    HLGRRTGSLV RIADRTSSV TGLLEYLVFN VIPTLADIII GIIFYSMFFN AWFGLIVFLC 420
      MSLYLTLTIV VTEWRTKFRR AMNTQENATR ARAVDSLLNF BTVKYNAES YEVEERYRAI 480
      IKYQGLEWKS SASGLVLLNQI QNLVIGLGLL AGSLLCAYFV TEQKLQVGDY VLFGTYYIQL 540
      YMPLNWFQTY YRMIQTNFID MENMFDLLKE ETEVKDLPGA GPLRFQKGR IEFENVHFSYA 600
      DGRETLQDVS FVTMPGQTIA LVGPGAGKKS TILRLLPFRY DISSGCIRID QQDISQVTOA 660
35    SLRSHIGVVP QDTVLFPNDI ADNIRYGRVT AGNDEVEAAA QAAGIHDAIM AFPEGYRTQV 720
      GERGLKLSGG EKORVAIART ILKAPGIILL DEATSALDTS NERAIQASLA KVCANRTTIV 780
      VAHRLSTVVN ADQILVIKDG CIVERGRHEA LLSRGGVYAD MWQLQQGQES TSEDTKPQTM 840
      ER

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Seq ID NO: C334 Protein Sequence
Protein Accession #: NP_000667.1

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40    1      11      21      31      41      51
      |      |      |      |      |      |
MLLETQDALY VALELVIAAL SVAGNVLVCA AVGTANTLQT PTNYFLVSLA AADVAVGLFA 60
45    IPFAITISLG PCTDFYGLCF LACFVLVLTO SSIFSLLAVA VDRYLAICVP LRYKSLVTGT 120
      RARGVIAVLW VLAPGIGLTP FLGWNKDSA TNNCTEPWDG TTNESCLLVK CLFENVVEMS 180
      YMVYFNFPGC VLPPLLIMLV IYIKIFLVAC RQLQRTLMED HSRTTLQREI HAAKSLAMIV 240
      GIFALCNLPV HAVNCVTLPQ PAQGNKPKW AMNMAILLSH ANSVVNPIVY AYRNRDRFRT 300
50    FHKIISRYLL CQADVKSNG QAGVQPALGV GL

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Seq ID NO: C335 Protein Sequence
Protein Accession #: NP_443164

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55    1      11      21      31      41      51
      |      |      |      |      |      |
MGIGARGAWA ALLLGTLQVL ALLGAHESA AMAETLQHPV SDHTNETSNS TVKPTTSVAS 60
      DSSNTTITTM KPTAASNTTT PGMVSTNMTS TTLKSTPKTT SVSQNTSQIS TSTMTVTHNS 120
      SVTSAASSTV ITTTHMSEAK KGSKPTDGSF VGGIVLTLGV LSILYIGCKM YSRRRGIRYR 180
60    TIDEHDAII

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Seq ID NO: C336 Protein Sequence
Protein Accession #: NP_004186.1

```

65    1      11      21      31      41      51
      |      |      |      |      |      |
MAQHGMAGAP RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTARCC RVHTTRCCRD 60
      YPGECCSEW DCMCVQPEFH CGDPCCTTCR HHPCPPGQGV QSQGKFSFGF QCIDCASGTF 120
      SGGHEGHCKP WTDCTQFGFL TVPPGNKTEN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL 180
70    TSAQLGLHIW QLSQCMWPR ETQLLLEVFP STEDARSCQF PEEBERGERSA EEKGRLGDLW 240
      V

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Seq ID NO: C337 Protein Sequence
Protein Accession #: BAC03767.1

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75    1      11      21      31      41      51
      |      |      |      |      |      |
MGCDGRVSGL LRRNLQPTLT YWSVFFSFGI CIAFLGPTLL DLRCQTHSSL PQISWVFFSQ 60
      QLCLLGSAL GGVFKRTLQ SLNALFTSSL AISLVFAVIP PCRDVKVLAS VMALAGLAMG 120
      CIDTVANMQL VRMYQKDSAV FLQVLHFFVG FGALLSPLLA DPFLSEANCL PANSTANTTS 180
80    RGHLPFVSRV LQQHVDKAP WSNQTPPGLT PKDGAGTRVS YAFWIMALID LPVPMVAVML 240
      LSKERLLTCC PQRRPILLSA DELALETQPP EKEDASSLPP KFQSHLGHEE LPSCCQRKNL 300
      RGAPYSFFAI HITGALVLFM TDGLTGAYSA FVYSYAVEKP LSVGHKVAGY LPSLPWGFIT 360
      LGRLLSIPIS SRMKPATMVF INVVGVVTFP LVLLIFSYNV VFLFVGTASL GLFLSSTFPS 420
      MLAYTEDSLQ YKGCATTIVLV TGAGVGEMVL QMLVGSIFQA QGSYSFLVCG VIFGCLAPTF 480

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YILLLPFHRM HPGLPSVPTQ DRSIGMENSE CYQR

514

Seq ID NO: C338 Protein Sequence
Protein Accession #: NP_002194.1

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1	11	21	31	41	51	
MGPERTGAAP	LPILLVLALS	QGILNCCLAY	NVGLPEAKIF	SGPSSEQFGY	AVQOPINPKG	60
NWLLVGSFWS	GFPENRMGDV	YKCPVDLSTA	TCEKLNQTS	TSIPNVTEMK	TNMSLGLILT	120
RNMGTGGFLT	CGPLWAQCCG	NQYYTTGVCS	DISPDFQLSA	SFSPATQPCP	SLIDVVVCD	180
ESNSIYFMDA	VKNFLKFPVQ	GLDIGPTKTQ	VGLIQYANNP	RVVFNLTYSK	TKEEMIVATS	240
QTSQYGGDLT	NTFGAIQYAR	KYAYSAAAGG	RRSATKVMVV	VTDGESHGDS	MLKAVIDQCQ	300
HDNLRFGIA	VLGYLNRNAL	DTKNLIKEIK	AIASIFTERY	FFNVSDAAL	LEKAGTLGEQ	360
IPSEGTIVQG	GNFQMEMSQ	VGFSADYSSQ	NDILMLGAVG	AFGMSGTIVQ	KTSHGHLIFP	420
KQAFDQILQD	RNHSVLGYS	VAAISTGEST	HFVAGAPRAN	YTGQIVLYSV	NENGNITVIQ	480
AHRGDQIGSY	PGSVLCSDV	DKDTITDVLL	VGAPMYMSDL	KKEEGRVYLF	TIKKGILGQH	540
QFLEGPEGIE	NTRFGSAIAA	LSDINMDGFN	DVIVGSPLEN	QNSGAVIYN	GHQGTIRTQY	600
SQKILGSDGA	FRSHLQYFGR	SLDGYGDLNG	DSITDVSIGA	FGQVQLWSQ	SIADVAIEAS	660
FTPEKITLVN	KNAQILKLC	PSAKFRPTKQ	NNQVAIVYNI	TLADGPFSSR	VTSRGLFKEN	720
NERCLQKNMV	VNQAQSCPEH	IYIYQEPSDV	VNSLDLRLVDI	SLNPGTSPA	LEAYSETAKV	780
FSIPFHQDQ	EDGLCISDLV	LDVRQIPAAQ	EQPFIVSNQN	KRLTFSTVLK	NKRESAYNTG	840
IYVDFSENLE	PASFSLPVDG	TEVTCQVAAS	QKSVACDVGY	PALKREQVQT	FTINFDFNLQ	900
NLQNQASLSF	QALSESQEEEN	KADNLVNLKI	PLLYDAEHL	TRSTNINFE	ISSDGNVPSI	960
VHSPEDVGP	FIFSLKVTG	SVPVSMATVI	IHIPQYTKK	NPLMYLTGVQ	TDKAGDISCN	1020
ADINPLKIQG	TSSSVSKPSE	NFRHTKELNC	RTASCNVTC	WLKDVHMKGE	YFVNVTIRW	1080
NGTFASSTFQ	TVQLTAAAEI	NTYNPEIYVI	EDNTVTIPLM	IMKPDEKAEV	PTGVIIISII	1140
AGILLLLALV	AILWKIGFFK	RKYKMTXNP	DEIDETTELS	S		1181

Seq ID NO: C339 Protein Sequence
Protein Accession #: NP_113648.1

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1	11	21	31	41	51	
MYRPRARAAP	EGRVRGCAVP	STVLLLLLAYL	AYLALGTGVF	WTLEGRAAQD	SSRSFQDKW	60
ELLQNFCTLD	RPALDSLIRD	VVQAYKNGAS	LLENNTSMGR	WELVGSFFFF	VSTITTIGYG	120
NLSPTMAAR	LPCIFFALVG	IPLNLVVLNR	LGHLMQGGVN	HWASRLGGTW	QDDPKARWLA	180
GSGALLSGLL	LPALLPPLL	SHMBGWSYTE	GFYFAPITLS	TVGFGDYVIG	MNPSQRYPLW	240
YKMWVSLWIL	FGMAWLALII	KLILSQLETF	GRVCSCHHS	SKEDPKSQSW	RQGPDRPEPS	300
HSPQGGCYPE	GPMGIQIHL	PSAHAAGCGK	DS			332

Seq ID NO: C340 Protein Sequence
Protein Accession #: NP_004145.1

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1	11	21	31	41	51	
MEWDNGTGQA	LGLPPTTCVY	RENFKQLLLP	PVYSAVLAAG	LPLNICVITQ	ICTSRRALTR	60
TAVYTLNLAL	ADLLYACSLP	LLIYNVAQGD	HWPFQDFACR	LVRFLFYANL	HGSILFLTCI	120
SFQRYLGICH	PLAPWHKRG	RRAAWLVCVA	VWLAVTTQCL	PTAIFPAATGI	QRNRTVCYDL	180
SPPALATHYM	PYGMALTVIG	FLLEPFAALLA	CYCLLACRLC	RQDGPASFVA	QERRGKAARM	240
AVVAAAFAP	SLEPPHITKT	AYLAVRSTPG	VPCTVLEAPA	AAYKGTREFFA	SANSVLDPIL	300
FYPTQKQFRR	RPHELLQKLT	AKWQRQGR				328

Seq ID NO: C341 Protein Sequence
Protein Accession #: NP_009128.1

55
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65
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75
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1	11	21	31	41	51	
MQRPGPRLWL	VLQVMGSCAA	ISSMDMERPG	DGKCQPIEIP	MCKDIGYNTM	RMPNLMGHEN	60
QREAAIQLHE	FAPLVEYGCH	GHLRFFLCSL	YAPMCTEQVS	TPIPACRVMC	EQARKKCSPI	120
MEQNFKFPD	SLDCRKLPNK	NDPNYLCMEA	PNGSDEPTR	GSGLPFPLFR	PQRPHSAQEH	180
PLKDGPGRG	GCDNPGKPHH	VEKSASCAPL	CTPGVDVYWS	REDKRFVAVW	LAIWAVLCFP	240
SSAFTVLTP	IDPARFRYPE	REIIFLSMCY	CVYSVGYLIR	LPAGAESIAC	DRDSGQLYVI	300
QEGLESTGCT	LVFLVLYYPG	MASSLMWVVL	TLTWFLAAGK	KMGHEAIEAN	SSYFHLLAANA	360
IPAVKTILIL	VMRRVAGDEL	TGVCYVGSMD	VNALTGFLVI	PLACYLVIGT	SFILSGFVAL	420
FHIRRVMTG	GENTDKLEKL	MVRIGLFSVL	YTVPATCVIA	CYFYERLAMD	YWKILAAQHK	480
CKMNQTKTL	DCLMAASIPA	VEIFMVKIFM	LLVVGITSGM	WIWTSKTLQS	WQVCSRRLLK	540
KKSRRKPASV	ITSGGIYKKA	QBPQRTTHGK	YEIPAQSPTC	V		581

Seq ID NO: C342 Protein Sequence
Protein Accession #: NP_005752.1

70
75
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1	11	21	31	41	51	
MEVSRRKAPP	RPFRPAAPLP	LLAYLLALAA	PGRGADEPVM	RSEQAIGAIA	ASQEDGVFVA	60
SGSCLDQLDY	SLEHSLRLY	RDQAGNCTEP	VSLAPPARFR	PGSSFSKLL	PYREGAAGLG	120
GLLLTGWTFD	RGACEVRPLG	NLSRNSLRNG	TEVVSCHPQG	STAGVVYRAG	RNRNRYLAVA	180
ATYVLPETET	ASRCNPAASD	HDATIALKDT	EGRSLATQEL	GRLLKCEGAG	SLHFVDAFLW	240
NGSIYFPYYP	YNYTSGAATG	WPSMARIAQS	TEVLFQGGAS	LDGHHGHPDG	RRLLSSSLIV	300
EALDVWAGVP	SAAAGEGQER	RSPTTALCL	FRMSEIQARA	KRVSWDFKTA	ESHCKEGDQP	360
ERVQPIASST	LIHSDLTSVY	GTVMNRITVL	FLGTGQGQLL	KVILGENLTS	NCPEVIYBIK	420
ESTPVFKLV	PDPVNIYIY	LTAGKEVRR	RVANCKHKS	CSECLTATDP	HCGHCHSLQR	480
CTPGQDCVHS	ENLENWLDIS	SGAKCKPKIQ	IIRSSKEKTT	VTMVGFSFPR	HSKQMVKNVD	540
SSRELQCNKS	QPNRTCTCSI	PTRATYKQVS	VNVNMFSPGS	WNLSDRFNPT	NCSLKECPA	600
CVETGCAWCK	SARRCIHPTT	ACDPSDYERN	QECCPVAVEK	TSGGGRPKEN	KGNRTNQALQ	660
VFYKSIIEPQ	KVSTLGKSNV	IVTGANFTRA	SNITMLKGT	STCDKDVIVQ	SHVLNDTHMK	720

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10
15

FSLPSSRKEM KDVCIQFDGG NCSSVGSLSY IALPHCSLIF PATTWISGQ NITMMGRNPD 780
VIDNLIISHE LKGNINVSEY CVATYCGFLA PSLKSSKVRT NVTVKLRVQD TYLDCOGLQY 840
REDPRFTGYR VESSEVTELE VKIQKENDNF NISKKDIBIT LPHGENGQLN CSFENITRNQ 900
DLTTILCKIK GIKTASTIAN SSKKVRVKLG NLELYVEQES VPSTWYPLIV LPVLLVIVIF 960
AAVGVTTRHS KELSRRQSQQ LELLESELRK EIRDFGRLQ MDKLDVVDSE GTVPFLDYKH 1020
FALRTFFPES GGTHIFTED MNRDANDKN ESLTALDALI CNKSLVTVI HTLEKQKNPS 1080
VKDRCLFASF LTIALQTKLV YLTSILEVLT RDLMEQCSNM QPKMLRRTS SVVEKLLTNW 1140
MSVCLSGFLR ETVGEPFYL VTTLNQKINK GPDVITCKA LYTLNEDWLL WQVPEFSTVA 1200
LNVVFEKPE NESADVCRNI SVNVLDCTI GQAKEKIFQA FLTKNGSPYG LQINEIGLEL 1260
QMGTRQKELL DIDSSSVILE DGITKLNTIG HYEISNGSTI KVPKIANFT SDVEYSDDH 1320
HLILPDSEAF QDVQGRHRG KHKPKVKEMY LTKLLSTKVA IHSVLEKLF RSIWLPNSRA 1380
PFAIKYFPFP LDAQAENKKI TDPDVVHIWK TNSLPLRFVW NILKNPQFV DIKKTPHIDG 1440
CLSVIAQAFM DAPSLTEQQL GKEAPTNNLL YAKDIPTYKE EVKSYKPAIR DLPPLSSSEM 1500
EEPLTQESKK HENEFNEEVA LTBIIKYIVK YPDEILNKLE RERGEEAQK QLLHVKVLFD 1560
EKKCKWM 1568

Seq ID NO: C343 Protein Sequence
Protein Accession #: NP_002176.1

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30

1 11 21 31 41 51
MTILGTTFGM VPSLLQVVSQ ESGYAQNGDL EDAELDDYSF SCYSQLEVNG SQHSLTCAFE 60
DPDVNTNLE PEICGALVEV KCLNFRKLQ IYPIBTKKFL LIGKSNICVK VGEKSLTCK 120
IDLTTIVKPE APFDLSVIYR EGANDFVVT NTSHLQKKYV KVLMDVAYR QEKDKNKWH 180
VNLSSSTLTL LQRKLQPAAM YEIKVRSIPD HYFKGFSEW SPSYFRTPE INNSSGEMDP 240
ILLTISILSF FSVALLVILA CVLWKKRIKP IVWPSLPDHK KTLHLCKCP RKNLNVSPNP 300
ESFLDQIHR VDDIQRDEV EGFQDTPFP QLESEKQRL GGDVQSFNCP SEDVVVTPE 360
FGRDSSLTCL AGNVSACDAP ILSSRSRLDC RESGKNGPHV YQDLLSLGT TNSTLPPPF 420
LQSGILTLN VAQGPILTS LGSNQEEAYV TMSSFYQNK 459

Seq ID NO: C344 Protein Sequence
Protein Accession #: NP_002713.1

35

1 11 21 31 41 51
MAAARLCLSL LLLSTCVALL LQPLLGAQGA PLEPVYPGDN ATPQMAQYA ADLRRYINML 60
TRPRYGRKHK EDTLAPSEWG SPHAAPREL SPLDL 95

Seq ID NO: C345 Protein Sequence
Protein Accession #: NP_115934.1

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45

1 11 21 31 41 51
MTWRHHVRL FTVSLALQII NLGNSYQREK HNGGREEVTK VATQKHRSQ LNWTSSTHFE 60
VTGSAGWGP EEPFYSRAF GEGASARPC CRNGGTCVLG SFCVCPAHT GRYCEHDQRR 120
SECGALEHGA WTLRACHLCR CIFGALHCLP LQTPDRCDPK DFLASHAGP SAGGAPSLLL 180
LLPCALLHRL LRPDAPAHPR SLVPSVLQRE RRCGRPGLG HRL 223

Seq ID NO: C346 Protein Sequence
Protein Accession #: NP_006524.1

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1 11 21 31 41 51
MARSLVCLGV IILLSAFSGP GVRGGPMFKL ADRKLCADQE CSHPISTMAVA LQDYMAPDCR 60
FLTIRGQVV YVFSKLKGRG RLFWGGSVQG DYYGDLAARL GYFPSSIVRE DQTLKPGKVD 120
VKTDKNDPYC Q 131

Seq ID NO: C347 Protein Sequence
Protein Accession #: Eos sequence

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65

1 11 21 31 41 51
MTQVTEKSTE HPEKITSTTE KTIRTPEKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60
TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120
TSRTKLSSIT SEATGNESH YLNKDGSKQG IHAGQMGEND SPPAWAIVIV VLVAVILLV 180
FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQNLGMGQ IPSPR 235

Seq ID NO: C348 Protein Sequence
Protein Accession #: NP_543146.1

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75

1 11 21 31 41 51
MTQVTEKSTE HPEKITSTTE KTIRTPEKPT LYSEKTICTK GKNTFVPEKP TENLGNITLT 60
TETIKAPVKS TENPEKTA AV TKTIKPSVKV TGDKSLTTTS SHLNKTEVTH QVPTGSFTLI 120
TSRTKLSSIT SEATGNESH YLNKDGSKQG IHAGQMGEND SPPAWAIVIV VLVAVILLV 180
FLGLIFLVSY MMRTRRTLTQ NTQYNDAEDE GGPNSYPVYL MEQNLGMGQ IPSPR 235

Seq ID NO: C349 Protein Sequence
Protein Accession #: FGENSEH predicted

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1 11 21 31 41 51

Seq ID NO: C350 Protein Sequence
Protein Accession #: FGENSESH predicted

Seq ID NO: C351 Protein Sequence
Protein Accession #: AAH35671.1

75	1	11	21	31	41	51	
	MVPGARGGGA	LARAAGRGLL	ALLLAVSAPL	RLQAEELGDG	CGLHVTYQDS	GMTSKNYPG	60
	TYPNHTVCEK	TITVPKGKRL	ILRLGLDIE	SQTCASDYLL	FTSSSDQYQG	YCGSMTVPKE	120
	LLLNTSEMTV	RFESGSHISG	RGLFLTAYSS	HDHDLTLC	RASHYLKTEY	SKFCPAGCRD	180
	VAGDISGNMV	DOYRDTSLLC	KAAIHAGIYA	DELGGQISVL	QREGISRYEG	ILANGVLSRD	240
80	GLSLDKRFLP	TSNGCSRSL	PFPDQIGRST	SSWQSVNESG	SLQVMSFQQA	RLDQDQPSWA	300
	SGDSSNNHKP	REWLIDLGE	KKKITGIRAT	GSTQSNFNY	VKSFVMNFVI	NNKWKTYKRG	360
	IVNNEKVPK	GNNSPRDPVQ	NNPFPIVAR	YVRVVPQTH	QRIALKVELI	GCQITQGNDS	420
	LVWRKTSQST	SVSTKQKEDT	ITRPIPSEET	STGAINITVA	IPLVLVLVLV	PAGMGIPFAA	480
	RKKKKKGSFY	GSAREAKTDC	WKQIKYPFAR	HOSARETISY	DNEKENTOLR	DLTSDMAG	539

Seq ID NO: C352 Protein Sequence
Protein Accession #: Eos sequence

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MGFGAGQRLR PVFAPRSSAE EAARPGQLRL GIRRGEAELA KLAPSGVMVP GARGGGALAR 60
AAGRGLALL LAVSAPLRLO AEELGDGCGH LVTYQDSGTM TSKNYPGTYP NHTVCEKIT 120
VPKGRLLILR LGDLIESQT CASDYLLFTS SSDQYGPYCG SMTVPKELLN NTSEVTVRFE 180
SGSHISGRGF LITYASSDHP DLITCLERAS HYLKTEYSKF CPAGCRDVAG DISGNMVDGY 240
RDTSLCKAA IHAGIIADEL GGQISVLQRK GISRYEGILA NGVLSRDGSL SDKRFLFTSN 300
GCSRSLSEFP DQIRASSSW QSVNESGDQV HWSFGQARLQ DQGPSWASGD SSNNHKPREW 360
LEIDLGEKKK ITGIRTGTST QSNFNFYVKS FVMNFKNNNS KWKTYKGIWN NEEKVPQGN 420
NFRDPVQNNP IPIVARYVR VVPQTNHORI ALKVELIGCQ ITQNDLSLVW RKTSQSTSVS 480
TKKEDETITR PIPSEETSTG INITTVAIPL VLLVVLVAFG MGIFAPFRKK KKGSPYGSA 540
EAKPTDCNKQ IKYPPARHQS AEFTISYDNE KEMTQKLDLI TSDMAG 586

Seq ID NO: C353 Protein Sequence
Protein Accession #: FGENSEH predicted

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MFQRQERFLD LSSAEAVAAW ILHQHPDIIN KGDGCGHLVT YQDSGTMTSK NYPGTYPNHT 60
VCEKITIVPK GKRLILRLGD LDIESQTCAS DYLLFTSSSD QYGMQKEET EVLCLSVAGA 120
QRVDIPVQLL PSFLEGWKGH ADARGPYCGS MTVPKELLN TSEVTVRFBG SGSHISGRGFL 180
LTYASSDHPD LITCLERASH YLKTEYSKFC PAGCRDVAGD ISGNMVDGYR DTSLLCKAAI 240
HAGIIADELG GQISVLQRKG ISRYEGILAN GVLSRDGSLG DKRFLFTSNG CSRSLSEFPD 300
GQIRASSSWQ SVNESGDQVH WSPGQARLQD QGPSWASGDS SSNNHKPREWL EIDLGEKKKI 360
TGIRTGTSTQ SNMNFVVKSF VMNFKNNNSK WKTYKGIWN NEEKVPQGNPN PRDPVQNNFI 420
PIVARYVRV VVPQTNHORIA LKVELIGCQI TQNDLSLVWR KTSQSTSVST KKEDETITRP 480
IPSEETSTDA MPQIVGDHT QMISQRENLG PDEGKIPFKG TAESMVRVVF AVVVNDLGML 540
FLAHTPEEDI DHYCWKQIKY PFARHQSASF TISYDNEKEM TQKLDLITSD MADYQQPLMI 600
GTGTVTRKGS TFRPMDDAE EAGVSTDAGG HYDCPQAGR HEYALPLAPP EPEYATPIVE 660
RHLVRAHTPS AQSGYRVFGP QPGHKHSLSS GGFSPVAVGQ AQDGDYQRPH SAQPADRGYD 720
RPAKVALSAT BSGHPSQKPF PTHPGTSDSY SAPRDCLTPL NQTAMTALL 769

Seq ID NO: C354 Protein Sequence
Protein Accession #: NP_004607.1

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MAGVSACIKY SMFTFNFLFW LOGILILALA IWVRVSNDSD AIFGSEDVGS SSVAVDILI 60
AVGAIMILG FLGCCGAIKE SRCLLLFFI GLLLILLQV ATGILGAVFK SKSDRIVNET 120
LYENTKLISA TGESEKQFQE AIIVQBEFK CCGLVNGAAD WGNPFQHYPE LCACLDKQRP 180
CQSYNGQVY KETCISFIKD FLAKNLIIVI GISPLGLAVIE ILGLVFSMVL YCQIGNK 237

Seq ID NO: C355 Protein Sequence
Protein Accession #: NP_004608.1

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41
51
MCTGGCARCL GGTLIPLAPF GFLANILLFP PGGKVIDDND HLSQEIWFPG GILGSGVIMI 60
PFALVILGLK NNDCCGCCGN EGCGKRFAMP TSTIPAVVGF LGAGYSFIIS AISINKPKC 120
LMANSTWGYF PHDGDYLNDE ALWNKCREPL NVVFWNLTLF SILLVVGSIQ MVLCAIQVNV 180
GLLGLTLCGDC QCCGCCGSDG PV 202

Seq ID NO: C356 Protein Sequence
Protein Accession #: NP_002372.1

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MPRPAPARRL PGLLLLWPL LLLPSAAPDP VARPGFRLE TRGPGGSPGR RPSFAAFDGA 60
PASGTSEPRG ARGAGVCKSR PLDLVPIIDS SRSVRPLEFT KVKTFFVSRII DTLDIGPADT 120
RVAVVNYAST VKIEFQLQAY TDQSLKQAV GRITPLSTGT MSGLAIQTAM DEAPTEAGA 180
REPSSNIPKV AIIVTDGRFQ DQVNEAARA QASGIELYAV GVDRADMASL KMMASEPLEE 240
HVFFVETYG VIEKLSRFQE TPCALDPCVL GTHCQHVCI SDGEGKHCE CSQGYTLNAD 300
KKTCSALDRG ALNTEGCEHI CVNDRSGSYH CECYEGYTLN EDRKTCASQD KCALGTHGCG 360
HICVNDRTGS HHCBCYEGYT LNADKKTCSV RDKCALGSHG CQHICVSDGA ASYHCDCYPG 420
YTLNEDKKTG SATEZARRLV STEDACGCEA TLAFOQKRVSS YLQRLNTKLD DILEKLKINE 480
YQIHR 486

Seq ID NO: C357 Protein Sequence
Protein Accession #: NP_057723.1

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11
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31
41
51
MARGSLRRL RLLVLGLWLA LLRSVAGEQA PGTAPCSRGS SWSADLDKCM DCASCRARPH 60
SDFCLGCAA PPAPFRLNP ILGALSILTP VLGLLSGLLV WRCRRREKF TPIETETGG 120
GCPAVALIQ 129

Seq ID NO: C358 Protein Sequence
Protein Accession #: NP_001810.1

1 11 21 31 41 51
 5 MQPTLLLSLL GAVGLAAVNS MPVDNRNHNH GMVTRCIIEV LSNALSKSSA PPITPECRQV 60
 LKTSRKDVKD KETTENENTK FEVRLLRDPA DASEAHSSSS RGEAGAPGEE DIQGPTKADT 120
 EKWAEGGGHS RERADEPQWS LYPDSQSVSE EVKTRHSEKS QREDEEEEGG ZNYQKGERGE 180
 DSSEKHLLEE PGETQNAFLN ERKQASAIKK EELVARSETH AAGHSQEKTH SREKSSQESG 240
 EEAGSQENHP QESKQPPRSQ EEESEGEEDA TSEVDKRRTR PRHHHGRSRP DRSSQGGSLP 300
 SEEGKHPQEE SEESNVSMAS LGEKRDHST HYRASEEEPE YGEEIKGYPG VQAPEDLEWE 360
 10 RYRGSGSEY RAPRPQSEES WDEEDKRNYP SLELDQMAHG YGEESEESRG LEFGKGRHHR 420
 GRGGEPRAPY MDTRREEKRF LGEGHHRVQE NQMDKARRHP QGAWKELDRN YLNYGEEGAP 480
 GKWQQGGDLQ DTKENREEAR FQDKQYSSHH TAEKRKRLGE LFNPHYDPLQ WKSSHFERRD 540
 NMNDFLEGE EENELTLNEK NFFPEYNVDW WEKKPFSEDV NMWYEKRNLA RVPKLDLKRQ 600
 YDRVAQLDQL LHYRKKSAEF PDFYDSEEPV STHQEAENEK DRADQTVLTE DEKKELLENLA 660
 15 AMDLELQKIA EKFSQRG 677

Seq ID NO: C359 Protein Sequence
 Protein Accession #: XP_093082.1

1 11 21 31 41 51
 20 MKLLCEGLKQ PNCVLQTLRW YRCLISSASC GALAAVLSTS QWLTELEFSE TKLEASALKL 60
 LYGGLKDPNC KLOKLNQPS LSVTAAKLPV GMVNCSSGFS GSLVQSHFGY QODSSPKCDL 120
 CKLLWPSTRV AAADKCGSPK SPLSEGLNWA GRLEAVEEVL GLGLVLVQPD PASQGGHCE 180
 25 NYGSPRDLVD LEVKAEPRLR KGGMDLQRP LQVLLCKIF SLKLFLEFIAL PNSPGQSVV 240
 QVTIPDGFVN VTGGSNVTLI CIYTTTVASR EQLSIQWSPF HCKEMEPIS PWEEGKWPDV 300
 EAVKGTLDGQ QAEQLIYFSG GQQAIVAGQF KDRITGSNDP GNASITISHM QPADSGIYIC 360
 DVNNPPDFLG QNQGILNVSV LVKPSKPLCS VQGRPETGHT ISLSCLALG TPSPVYVWHK 420
 LEGRDIVPKV ENFNPTTGL VIGNLTNFEQ GYYQCTAINR LGNSSCEIDL TSSHPVEGII 480
 30 VGALIGSLVG AATIIISVCF ARNKAKAKAK ERNSKTI AEL EPMTKINFRG ESEAMPREDA 540
 TQLEVTLPSS IHETGPDITQ EPDYBPKPTQ EPAPEPAPGS EPMAPVDLDI ELELEPETQS 600
 ELEPEPEPEP ESEPGVVVEP LSEDEKGVVK A 631

Seq ID NO: C360 Protein Sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 35 MVFAFWKVF ILSCLAGQVS VVQVTIPDGF VNVTVGSNVT LICIIYTTVA SREQLSIQWS 60
 FFHKMEMEPI SSPWEEGKWP DVEAVKGTLD GQQAELQIYF SQGGQAVAIG QFKDRITGSN 120
 40 DPGNASITIS RMQPADSGIY ICDVNNPPDF LGQNGQILNV SVLVKPSKPL CSVQGRPETG 180
 HTISLSCLSA LGTSPFVYVW HKLEGRDIVP VKENFNPTTG ILVIGNLTNF EQGYQCTAI 240
 NRLGNSSCEI DLTSSHPVEG IIVGALIGSL VGAAIISVV CFARNKAKAK AKERNKTI A 300
 45 ELEMTKINP RGSSEAMPRE DATQLEVTLP SSIHETGPD TQEPDYEPKP TQEPAPAP 360
 GSEFMVAVPD LBLELEPET QSELEPEPEP EPSEPGVVV EPLSEDEKGV VKA 413

Seq ID NO: C361 Protein Sequence
 Protein Accession #: NP_003011.1

1 11 21 31 41 51
 50 MVSRMVSTML SGLLFWLASG WTPAFAYSFR TPDVSEADI QRLHGVMEQ LGIARPRVEY 60
 PAHQAMNLVG PQSIEGGAHE GLQHLGPPGN IPNIVAEITG DNIPKDFSED QGYFDPNPF 120
 PVGKTDDGCL ENTFTDAEFS REFQLHQHLE DPEHDYPGLG KWNKCLLYEK MKGGERRRKR 180
 55 SVNPLYGQR LNNVAKKSV PHFSEDEKDP E 211

Seq ID NO: C362 Protein Sequence
 Protein Accession #: NP_076926.2

1 11 21 31 41 51
 60 MTTMQGMEQA MPGAGPGVPQ LGNMAVIRSH LWKGLQEKEL KGEPKVLGVV QILTALMSLS 60
 MGITMCMAS NTYGSNPISV YIGYTIWGSV MFIISGSLSI AAGIRTTKGL VRGSLGMNIT 120
 SSVLAASGIL INTFSLAFYS FHHFYCNYYG NSNNCHGTMS ILMGLDGMVL LLSVLEFCIA 180
 65 VSLSAFGCKV LCCTPGGVVL ILPSHSHMAE TASPTPLNEV 220

Seq ID NO: C363 Protein Sequence
 Protein Accession #: NP_002082.1

1 11 21 31 41 51
 70 MRGSELPLVL LALVLCAPR GRAVPLPAGG GTVLTKMYPR GNHMAVGHLM GKXSTGESSS 60
 VSEKSLKQQ LREYIRWEEA ARNLLGLIRA KENRNHQPPQ FKALGNQPS WDSSESSNPK 120
 DVGSKGVGR LSAPGSQREG RNPQLNQ 148

Seq ID NO: C364 Protein Sequence
 Protein Accession #: NP_036393.1

1 11 21 31 41 51
 80 MDLQGRGVPS IDRLRLVLLM FHTMAQIMAE QEVNLSGLS TNPEKDIFVV RENGTTCLMA 60
 EPAAKPIVY DVWASNYVDL ITEQADIALT RGAEVKGRCG HSQSELQVFW VDRAYALKML 120
 FVKESHNMKS GPBATWRLSK VQPVYDSSEK THPKDAVSAG KHTANSHHLS ALVTPAGKSY 180
 EQQAQTISL ASSDPQKTVT MILSAVHIQ FDIISDFVFS EHHKCFVDER EQLEETPLI 240
 LGLILGLVIM VTLAIYHVH KMTANQVQIP RDRSQYKMG 280

Seq ID NO: C365 Protein Sequence
Protein Accession #: NP_003217.1

5 1 11 21 31 41 51
| | | | |
MLGLVLALLS SSSAEETVGL SANQCAVPAK DRVDCGYPHV TPKECNNGRC CPDSRIPGVP 60
WCFKPLTRKT ECTF 74

10 Seq ID NO: C366 Protein Sequence
Protein Accession #: NP_002984.1

15 1 11 21 31 41 51
| | | | |
MSLPSSRAAR VPGPSGSLCA LLALLLLLTTP PGPLASAGPV SAVLTELRCCT CLRVTLRVNP 60
RTIGKLQVFP AGPQCSKVEV VASLKNKGQV CLDPEAPFLK KVIQKILDSG NKKN 114

20 Seq ID NO: C367 Protein Sequence
Protein Accession #: NP_005233.2

25 1 11 21 31 41 51
| | | | |
MRSPSAAWLL GAAILLAASL SCSGTIQGTN RSSKGRSLIG KVDGTSHVTG KGVTVETVFS 60
VDEFSASVLT GKLTITVFLPI VYTIIVFVGL PSNGMALWVF LFRTKKKHPA VIYMANLALA 120
DLLSVIWFPL KIAYHIHANN WIYGEALCNV LIGFFYGNNY CSILFMTCLS VQRYWVIVNP 180
MGHSRKKANI AIGISLAIWL LILLVTIPLY VVKQTIFIPA LNTTCHDVL PEQLLVGDMP 240
NYFLSLAIGV FLFPAPLTAS AYVLMIRMLR SSAMDENSEK KRKRAIKLIV TVLAMYLICF 300
TPSNLLLVQH YPLIKSQGQS HVALYIIVAL CLSTLNSCID PFVYVYVSHD FRDHAKNALL 360
CRSVRTVKVM QVSLTSKKHS RKSSSYSSSS TTVKTSY 397

30 Seq ID NO: C368 Protein Sequence
Protein Accession #: NP_003460.1

35 1 11 21 31 41 51
| | | | |
MAEAKTHWLG AALSILPLIF LISGAEEASF QRNQLLQKEP DLRLNVQKF PSPMIRALE 60
YIENLRQAH KESSSPDYNP YQGVSVPLQQ KENGDESHLP ERDLSSEEDW MRIILEALRQ 120
AENEPQSAFK ENKPYALNSE KNPPMDMSDD YETQQWPERK LKHMQFPFPMY EENSNDNPFK 180
RTNEIVEEQW TPQSLATLES VPQELGKLTG PNNQKRERMD EEQKLYTDEE DDIYKANNIA 240
YEDVVGGEW NPVEEKIESQ TQEEVRDSKE NIGKNEQIND EMKRSGQLGI QEEDLRKESK 300
DQLSDDSKV IAYLKRLVNA AGSGRLQNGQ NGERATRLFE KPLDSQSIYQ LIEISRNLQI 360
FPEDLIEMLK TGKPKNGSVE PERELDLPVD LDDISEADLD HPDLFQNRML SKSGYPKTPG 420
RAGTEALPDG LSVEDIILNL GMESAANQKT SYFPNPNQKE KVLPRLPYGA GRSRSNQLPK 480
AAWIPHVNR QMAYENLNK DQELGEYLAR MLVKYPEIIN SNQVKRVPGQ GSSEDDLQEE 540
EQIEQAIEKH LNQSSQBEDT KLAPVSKRFP VGPPKNDTTP NRQYWEDELL MKVLEYLNQE 600
KAEKGREHIA KRAMENM 617

50 Seq ID NO: C369 Protein Sequence
Protein Accession #: NP_112217.1

55 1 11 21 31 41 51
| | | | |
MPCQRSWLA NLSVVAQLLN FGALCYGRQP QPGPVRFPDR RQEHFIKGLP EXHVVGPVRV 60
DASGHFLSYG LHYPIITSSRR KRDLDGSEDW VYYRISHEEK DLFFNLTVNQ GFLSNSYIME 120
KRYGNLSHVK MMASAPLCH LSGTVLQOGT RVGTAALSAC HGLTGFFQLP HGDFPIEPVK 180
KHPLVEGGYH PHIVYRRQKV PETKEPTCGL KDSVNISQKQ ELWREKWERH NLPSRSLRR 240
SISKERWVET LVVADTMIE YHGSENVESY ILTIMNMVGT LFHNPISIGNA IHIVVRLIL 300
LEEEBQGLKI VHAAKTLSS FCKWQKSINP KSDLPVHHD VAVLLTRDI CAGFNRPCE 360
LGLSHLSGMC QPHRSNINE DSGLEPLAFTI AHELGHSPGI QHDGKENDCE PVGRHPYIMS 420
RQLQYDPTPL TWSKCSSEYI TRFLDRGWGF CLDDIPKKKG LKSKVIAPGV IYDVHHCQQL 480
QYGFNATFCQ EVENVCQTLN CSVKGFCSRK LDAAADGTQC GEKKWCMAGK CITVGGKPPES 540
IPGGWGRWSP WSHCSRTOGA GVQSAERLCN NPEPKFGGKY CTGERKRYRL CNVHPCRSEA 600
PTFRQMOCSE FDTVPYKNEI YHWFFIFNPA HPCELYCRPI DGQFSEKMLD AVIDGTPCFE 660
GGNSRNVGIN GICKMVGCDY EIDSNATEDR CGVCLGDGSS CQTVRKMFQK KEGSGYVDIG 720
LIPKGARDIR VMEIEGAGNF LAIRSEDPEK YYLNGGFIQ WNGNYKLAGE VFQYDRKGDL 780
EKLWATGPTN ESWVIQLLFQ VTNPGIKYEY TIQKDGLEND VBQMYFWQYG HWTECSVTG 840
TGIRRTAHK IKKGRGMVKA TPCDPETQPN GRQKKCHEKA CPPRNWAGEW EACSATCGPH 900
GEKKRTVLCI QTMVSDEQAL PPTDQHLK PKTLLSCNRD ILCPSDWTVG NWSECSVSCG 960
GGVRIKSVTC AKNHDEPCDV TRKPNRSLC GLQCCPSSRR VLKPNKGTIS NGKNPPTLKP 1020
VPPPTSRPRM LTTPTGPESM STSTPAISSP SPTTASKEGD LGGKQWQDSS TQPELSSRYL 1080
ISTGSTSQPI LTSQSLGIQ SEENVSSSDT GPTSEGLVA TTTSGSGLSS SRNPITWFTV 1140
PFYNTLTGKP EMBIHSGSGE EREQPEDKDE SNFVIWTKIR VPGNDAPVES TEMPLAPPLT 1200
PDLRSRSMWP PFSTVMEGLL PSQRPTTSET GTPRVGEMVT EKPANTLLPL GGDHQPEPSG 1260
KTANRNHKL PNNMNTKSS EPVLTEEDAT SLITEGFLN ASNYKQLTNG HGSANWIVGN 1320
WSECSITCGL GAYWKRVECT TQMSDCAAI QRPDPAKRCH LRPCAGWKGV NWSKCSRNC 1380
GGFKIRIQE VDSRDHNLRL PFHCQFLAGI PPPLSMSCNP EPCEANQVEP WSQCSRSCG 1440
GVQERGVPFC GGLCDWTKRP TSTMSCNEHL CCHWATGNWD LCSTSCGGG QKRIVQCVPS 1500
BGNKTEDDQ CLCDHKPRPP EPKCNQOQAC KKSADLLCTK DKLSASFQCT LKAMKCSVP 1560
TVRAECCFSC PQTHITHQR QRRQLLQKS KEL 1593

80 Seq ID NO: C370 Protein Sequence
Protein Accession #: NP_001053.1

1 11 21 31 41 51

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MRQSHQLPLV GLLLFSPFIPS QLCCEICEVSE ENYIRLKPILL NTMIQSNYNR GTSAVNVVLS 60
LKLVGIGIQIT LMQKMIQIQK YNVKSRISDV SSGELALILL ALGVCRNAEE NLIYDYHLTD 120
KLENFQOABI ENMEAHNGTP LTNYYQLSLD VLALCLFNGN YSTAEVNVHF TPENKNYYFG 180
SQFSVDTGAM AVLALTCVKK SLINGQIKAD EGSLKNISYI TKSILVEKILS EKKENGLIGN 240
TFSTGEAMQA LRVSSDYNE NDWNCQQTIN TVLTEISQGA PSNFNAAAQV LPALMGKTFP 300
DINKSSSCVS ASGNFNISAD EPITVTIPDS QSYISVNVSV RINETYFTNV TVLNGSVPLS 360
VMEKAQKMD TIFGPTMEER SWGPYITCIQ GLCANNNDRT YWELLSGGEF LSQGAGSYVV 420
RNGENLEVRW SKY 433

Seq ID NO: C371 Protein Sequence
Protein Accession #: NP_004582.1

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1 11 21 31 41 51
MCCTKSLLLA ALMSVLLHLH CGESEASNF DCCLGYTDRI LHPKFIVGFT RQLANEGCDI 60
NAIIFHTKKK LSVCANPKQT WVKYIVRLLS KKVKNM 96

Seq ID NO: C372 Protein Sequence
Protein Accession #: NP_037403.1

25
30
1 11 21 31 41 51
MAGSPLLMGP RAGGVGLLV LLLGLFRPPP ALCARPVKEP RGLSAASPPL AETGAPRRFR 60
RSVPGEAAG AVQELARALA HLEAERQER ARAEAQEAED QQARVLAQLL RVWGAPRNSD 120
PALGLDDDFD APAAQLARAL LRARLDPAAL AAQLVPAPVP AAALRPFPFV YDDGPAGPDA 180
EEAGDETDPV DPPELLRYLLG RILAGSADSE GVAAPRRLRR AADHDVGSEL PPEGVLGALL 240
RVKRLTTPAP QVPARLLLP 260

Seq ID NO: C373 Protein Sequence
Protein Accession #: NP_002236.1

35
40
1 11 21 31 41 51
MLQSLAGSSC VRLVERHRSR WCFGFLVLGY LLYLVFGAVV FSSVELPYED LLRQELRKLK 60
RRFLEEHECL SEQQLEQFLG RVLEASNYGV SVLSNASGNW NWDFTSALFF ASTVLSTTGY 120
GHTVPLSDGG KAPCIYYSVI GIPPTLLELT AVVQRITVHV TRRPVLYFHI RWGFSKQVVA 180
IVHAVLLGFV TVSCFFPIPA AVFSVLEDDW NFLESFYPCF ISLSTIGLGD YVPGGYNQK 240
PRELYKIGIT CYLLGLLIAM LVVLETFCLE HELKKPRKMP YVKDKDEDEQ VHIEHDQLS 300
FSSITDQAG MKEDQKQNEP FVATQSSACV DGPANH 336

Seq ID NO: C374 Protein Sequence
Protein Accession #: NP_005463.1

45
50
1 11 21 31 41 51
METTINGTETW YESLHVLKA LNA TLHSNLL CRPGPGLGPD NQTEERRASL PGRDDNSYMY 60
ILFVMLFAV TVGSLILGYT RSRKVDKRSO PYHVIYKNRV SMI 103

Seq ID NO: C375 Protein Sequence
Protein Accession #: NP_005236.1

55
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1 11 21 31 41 51
MGRHLALLLL LLLLFQHFQD SDGSQRLEQT PLQFTHLEYN VTQENSAAK TYVGHVPKMG 60
VYITHPAWEV RYKIVSGDSE NLFKAEYIL GDFCFRLRRT KGGNTAILNR EVKDHVTLIV 120
KALEKNTNVE ARTKVRVQVL DTNDLRPLFS PTSYSVSLPE NTAIRTSIAR VSATDADIGT 180
NGEFPYSPKD RTDMFAIHPT SGVIVLTGRL DYLETLYEM ETLAADRGMK LYGSSGISSM 240
AKLTVHEBQA NECAPIVITAV TLPSELDSD PAYAIVTDD CDQGANGDIA SLISVAGDIL 300
QQFRTVRSFP GSKEKVKKAI GDIDWDSHPF GYNLTQAKD KGTTPQFSSV KVIHVTSPQF 360
KAGPVKFEKD VYRAEISEFA PPNTFVVMVK AIPAYSHLY VFKRTPGKAK FSLNNTGLI 420
SILEPVKRRQ AAHFLELVTT SDRKASTKVL VKVLGANSNP PRPTQTAYKA AFDENVPIGT 480
TIMSLSAVDP DEGENGYVYI SIANLNHVFP AIDHFTGAVS TSENLDYELM PRVYTLRIRA 540
SDWGLPYRRE VEVLATITLN NLNDNTPLFE KINCEGTIPR DLGVGEQITT VSAIDADELQ 600
LVQYQIEAGN ELDLPFLNPN SGVLSLKRSL MDGLGAKVSF HSLRITATDG ENFATPLYIN 660
ITVAASHKLV NLQCEETGVA KMLAEKLLQA NKLHNQGEVE DIFDSDHSVN AHIPQFRSTL 720
FTGIQVKENQ PVGSSVIFMN STDLDTGPNQ KLVYAVSGGN EDSCFMIDME TGMLKILSPL 780
DRETTDRYTL NITVYDLGIP QKAAMRLLEV VVVDANDNPP EFLQESYFVE VSEDKEVHSE 840
IIQVEATDKD LGPNGHVTYS ILTDTDTFSI DSVTGNNIA RPLDRELQHE HSLKIEARDQ 900
AREEPQLFST VVVKVSLDVD NDNPTTFIPP NYRVKVRDL PEGTVIMWLE AHDPLDQSG 960
QVRYSLLDHG EGNFVDVRLS GAVRIVQQLD FEKKQVYNLT VRAKDKGKPV SLSTCYVEV 1020
EVVDVNNELH PPVFSSFVEK GTVKEDAFVG SLVMTVSAHD EDAGRGEIR YSIRDGSGVG 1080
VPKIGBETGV IETSDRLDRE STSHYNLTVP ATDQGVVPLS SPIBIYIEVE DVNDNAPQTS 1140
FVYVPEIME NSPKDVSVVQ IEAFDPDSSS NDKLMYKITS GNPQGFFSIH PKTGLITTS 1200
RLKDRQDEE HLELVTVTDN GSPPKSTIAR VIVKILDEND NKPQFLQKFI KIRLFEREKP 1260
DRERNARREP LYRVIAATDK EGNPAISYS IEDGNEHGKE FIEPKTGVS SKRPSAAGEY 1320
DILSIKAVDN GRPQKSSSTR LHIEWISKPK QSLEPISFEE SPPTFTVMES DPVAMHIGVI 1380
SVEPPGIFLW FDTIGGNYS HFDVDKGTGT IIVAKPLDAB QKSNNLTVE ATDGTITILT 1440
QVFIKVIDTN DHRPQFSTSK YEYVIPEDTA PETEILQISA VDQDEKNKLI YTLQSSRDPL 1500
SLKKFRLDPA TGSLYTSEKL DHEAVSFAHL TVMVRDQDVP VKRNFARIVV NVSDTNDHAP 1560
WFTASSYKGR VYSSAAVGSV VLQVTALDKD KGRNAEVLVS IESGNIGNIG NSFMIDPVLG 1620
SIKTAKEKLD RSNQAEYDLW KATDKGSPPM SEITSVRIFV TIADNASPKF TSKEYSVELS 1680
ETVSIKSPVG MVTAKSQSSV VYEIKDGTG DAFDINPHSG TIITQKALDP ETLPIYTLII 1740
QGTNMAGLST NITVLVHLQD ENDNAPVFMQ AETGLISES ASINSVVLTD RNVPLVIRAA 1800

	DADKDSNALL	VYHIVEPSVH	TYFAIDSSSTG	AIHTVLSLDY	EETSIPHFTV	QVHDMGTPRL	1860
	PABYAANVTV	HVIDINDCPV	VPAKPLYEAS	LLLFTYKGVK	VITVNATDAD	SSAFSGLIYS	1920
	ITEGNIGKKF	SMDYKTGALT	VQNTTQLRSR	YELTVRASDG	RFAGLTSVKI	NVKESKESHL	1980
5	KFTQDVVSAY	VKENSTEAST	LAVITAIGSP	INEPLFYHIL	NPDRRPKISR	TSQVLSSTGT	2040
	PPDREQQEAP	DVVVEVIEEH	KPSAVAHVVV	KVIVEDQNDN	APVPVNLPHY	AVVKVDTEVG	2100
	HVIRYVTAVD	RDSGRNGEVH	YYLKEHHEHF	QIGPLGEISL	KKQFELDTLN	KEYLVTVAK	2160
	DGGNPAFSAB	VIVPITVMNK	AMPVFEKPFY	SABIAESIQV	HSPVVHVQAN	SPBSGLKVPYS	2220
	ITDGDPPFSQ	TINFNTGVIN	VIAPLDFEAB	PAYKLSIRAT	DSLTAHAHEV	FVDIIVDDIN	2280
10	DNPPVFAQQS	YAVTLSEASV	IGTSVVQVRA	TDSDSEPNRG	ISYQMFQNH	KSHDHPHVD	2340
	STGLISLLRT	LDYEQSRQHT	IFVRAVDGGM	PTLSSDVIVT	VDVTDLANGP	PLFPEQQIYA	2400
	RISEHAPHGH	FTVCVKAYDA	DSSDIDKLQY	SILSGNDHKK	FVIDSATGII	TLNLHRHAL	2460
	KPFYSLNLVS	SDGVFRSSSTQ	VHVTVIGGNL	HSPAFLQNEY	EVELAENAPL	HTLVMEVKTT	2520
	DGDSGIYGHV	TYHIVNDFAK	DRFYINERGO	IFTLEKLDRE	TPAEKVISVR	LMAKDAGGKV	2580
15	AFCTVNVILT	DDNDNAQFPR	ATKYEVNIGS	SAAGTSVVVK	SASDADEGSN	ADITYAIEAD	2640
	SESVKENLEI	NKLSGVITTK	ESLIGLENEF	PTFFVRAVDN	GSPSKESVVL	VYVKILPPEM	2700
	QLPKFSEPFY	FTVCSEDPV	GTEIDLIRAE	HSGTVLYSLV	KGNTPESNRD	ESFVIDRQSG	2760
	RLKLEKSLDH	ETTKWQPSI	LARCTQDDHE	MVASVDVSIQ	VKDANDNSPV	FESSPYEAPI	2820
	VENLPGSSRV	IQIRASDADS	GTNGQVMYSL	DQSQSVEVIE	SPAINMETGW	ITTLKELDHE	2880
20	KRNVQIKV	ASDHGEKIQ	SSTAIVDVTV	TDVNDSPPRF	TABIKGTVS	EDDPQGGVIA	2940
	ILSTTDADSE	EINRQVITYI	TGGDPLQQFA	VETIQNEWKV	VYKPLDREK	RDNYLLTITA	3000
	TDGTFSSKAI	VEVKVLDAND	NSPVCCKTLY	SDTIPEDVLP	GKLIQMSAT	DADIRSNABI	3060
	TYTLLSGSAG	KFKLNPDTGE	LKTSTPLDRE	EQAVYHLLVR	ATDGGGRPCQ	ASIVVTTLEDV	3120
	NDNAPEFSAD	PYAITVFENT	EPGTLTTRVQ	ATDADAGLNR	KILYSLIDSA	DQPSINELS	3180
25	GIQLKEKPLD	RELQAVYTLS	LKAVDQGLPR	RLTATGTIVV	SVLDINDNPP	VFEYREYGAT	3240
	VSEDILVGTE	VLOVYAASRD	IEANAEITYS	IISGNEHGKF	SIDSKTGAVP	IENLDYESS	3300
	HEYILTVEAT	DGGTPSLSDV	ATVNVNVTDI	NDNTPVFSQD	TYTTVISED	VLEQSVITVM	3360
	ADDADGPSNS	HIHYSIIDGN	QSSSFTIDPV	RGEVKVTKLL	DRETISGYTL	TVQASDNGSP	3420
	PRVNTTVMNI	DVSDVNDNAP	VFSRGNYSVI	IQENKPVGFS	VLQVLVTTED	SSHNGPPFPF	3480
30	TIVTGNDKFA	FVNVPQGVLL	TSSAIKRKEK	DHYLLQVKVA	DNGKPOLSSL	TYIDIRVIEE	3540
	SIYPPAILPL	EIPITSSGEE	YSGGVIGIKH	ATDQDVYDTL	TYSLDPQMDN	LPSVSSTGGK	3600
	LIAHKKLDIG	QYLLNVSVTD	GKPTTVADIT	VHQRQVTQEM	LNHTIAIRFA	NLTPREFVTV	3660
	YWRNFORALR	NILGVRNNDI	QIVSLQSSEP	HPHLDVLLFV	EKPQSAQIST	KQLLHKINS	3720
	VTDLIELIGV	RILNVFQKLC	AGLDCPWKFC	DEKVSVDSEV	MSTHSTARLS	FVTPRHHRRA	3780
35	VCLCKEGRCP	PVHHCCEDDP	CPEGSECVSD	PWEEKTCVC	PSGRFGQCPG	SSMTLTGNS	3840
	VYKRLTENE	NKLEMLTMR	LRTYSTHAVV	MYARGTDYSI	LEIHGRLQY	KFDGCGSGPI	3900
	VSVQSIQVND	QWHAVALVE	NGNYARLVLD	QVHTASGTAP	GLTKTLNLDN	YVFPFGHRIQ	3960
	QGRHGRSPQ	VGNFGRCMD	SIYLNQQLP	LNSKPRSYAH	IEESVDVSPG	CPLTATEDCA	4020
	SNPCQNGGVC	NPSAGGYIC	KCSALYIGTH	CEISVNPCCS	NPCLYGGTCV	VDNQGFVQCQ	4080
40	RGLYTGGRQC	LSPYCKDEPC	KNGGTCFDSL	DGAVQCQDSG	FRGERCQSDI	DECSGNPCLH	4140
	GALCENTHGS	YHCNCSEYR	GRHCEDAAPN	QYVSTPWNIG	LAEGIGIVVF	VAGIFLLVTV	4200
	FVLCRKMRIS	KKGKQAEKPD	KHLGPATAPL	QRFPYDSKLN	KNYSDIPPQ	VVPRIPIVTP	4260
	SIPSDSRNNL	DRNSFEGSAI	PEHPEPSTFN	PESVHGHRKA	VAVCSVAPNL	PPPPPSNSPS	4320
	DSDSIQKPSW	DFDVTDTKVD	LDPCLSKKPL	EEKPSQPYSA	RESLSEVQSL	SSPQSESCDD	4380
45	NGYHWDTSW	MPSVPLFDIQ	EPFNYEVIDE	QTFLYSADFN	AIDTDYYPGG	YDIESDFPPP	4440
	PEDFPADEL	PFLPPEFSNQ	FESIHPPRDM	PAAGSLGSSS	RNRQRFNLNQ	YLPNFYPLDM	4500
	SEPTKGTGTE	NSTCREPHAP	YPPGYQRHFE	APAVESMPMS	VYASTASCSD	VSACCEVESE	4560
	VMSDYESGD	DGHFEETVTP	PLDSQQHTEV				4590

Seq ID NO: C376 Protein Sequence
Protein Accession #: NP_055035.1

	1	11	21	31	41	51	
55	MCYKGCARCI	GHSVLGLALL	CIAANILLYF	PNGETKYASE	NHLSRFVWFF	SGIVGGGLLM	60
	LLPAPVPIGL	EQDDCCGCCG	HENCGKRCAM	LSSVLAALIG	IAGSGYCVIV	AALGLAEGPL	120
	CLDSLQGWNY	TPASTEGQYL	LDTSWSECT	EPKHIVEMNV	SLPSILLALG	GIEFILCLIQ	180
	VINGVLGIC	GFCCSHQQQY	DC				202

Seq ID NO: C377 Protein Sequence
Protein Accession #: NP_003750.1

	1	11	21	31	41	51	
65	MSTENVEGKP	SNLGERGRAR	SSTFLRVVQP	MFNHSIFTSA	VSPAARIRP	ILGEEDDSPA	60
	PPQLPTELDE	LLAVDQQEMR	WKETARWIKP	EEKVEQGER	WSKPHVATLS	LHSLFELRTC	120
	MEKGSIMLDR	EASSLPQVLE	MIVDHQIETG	LLKPELKDKV	TYTLLRKHRH	QTKKSNLRS	180
	ADIGKTVSSA	SRMFTNPDNG	SPAMTHRNLT	SSSLNDISDK	PEKDQLKNKP	MKKLPDRAEA	240
	SNVLVGEVDF	LDTPPIAFVR	LQAVMLGAL	TEVPVPTPL	FILLGPKGKA	KSYHEIGRAI	300
	ATLMSDEVEH	DIAYKAKDRH	DLIAGIDEFL	DEVIVLPGE	WDPAIRIEPP	KSLPSSDKRK	360
70	NMYSGGENVQ	MNGDTPHDGG	HGGGSHGDCE	ELQRTGRFCG	GLIKDIKKA	PFFASDFYDA	420
	LNIALSAIL	FIYLATVTNA	ITPGGLGDA	TDMQGVLES	FLQTAVSQAI	PCLFAGQPLT	480
	ILSSTGPVLV	PERLLNPFK	DNNFDYLEFR	LWIGLWSAPL	CLILVATDAS	FLVQYPTTRT	540
	EEGFSSLSIF	IFIYDAPKRM	IKLADYYPIN	SNPKVGYNTL	FSCTCVFPDP	ANISISNDTT	600
	LAPEYLPTMS	SDMYENTTF	DWAFLSKKEC	SKYGGNLVGN	NCFVFPDITL	MSFILFLQTY	660
75	TSSMALKKFK	TSPYPPTTAR	KLISDPAIL	SILIFCVIDA	LGVVDTPKLI	VPSEFKPTSP	720
	NRGWFVPPFG	ENPWWCLAA	AIPALLVTIL	IFMDQQITAV	IVNRKSHKLL	KGAGYHLDLP	780
	WVAILMVLV	LMALPMYVAA	TVISIAHIDS	LKMETETSAP	GEQPKFLGVR	EQRVIGTLVF	840
	ILTLGSLVMA	PILKPIPMFV	LYGVFLYMGV	ASLNGVQFMD	RLKLLMLPLK	HQPDFIYLRH	900
80	VPLRRVHLPT	FLQVLCALL	WILKSTVAAI	IFPVHIALV	AVRKGMDFLP	QSHDLFLDD	960
	VIPEKDKKKK	EDEKCKKKKK	GSLDSNDNDS	DCPYSEKVP	IKIPMDIMEQ	QFPLSDSKPS	1020
	DRERSPTFLE	RHTSC					1035

Seq ID NO: C378 Protein Sequence
Protein Accession #: NP_000949.1

1 11 21 31 41 51
 5 MSTPGVNSSA SLSPDRINSP VTIPAVMFIF GVVGNLVAIV VLCKSRKEQK ETTFFYTLVCG 60
 LAVTDLLGTL LVSPVTIATY MKGQWPGGQP LCEYSTFILL FFSLSGLSII CAMSVERYLEA 120
 INHAYFYSHY VDKRLAGLTL FAVYASNVL FALFNMGGLS SRLQYFDTW C FIDWTINVT 180
 HAAYSVMYAG PSSFLILATV LCNVLVCGAL LRMHRQFMRR TSLGTBQHHA AAAASVASRG 240
 HPAASPALPR LSDFRRRRSF RRIAGAEIQM VILLIATSLV VLICSIPLVV RVFVNQLYQP 300
 10 SLEREVSXNP DLQAIRIASV NPILDPIYI LLRKTIVLSKA IERIKCLPCR IGGSRRRERSG 360
 QHCSDSQRTS SAMSQHSRSF ISRELKBISS TSQTLLFDLS LFDLSENGLG GRNLLPGVPG 420
 MGLAQEDTTS LRTLRISETS DSSQGQDSES VLLVDEAGGS GRAGPAPKGS SLQVTFPSET 480
 LNLSEKCI 488

15 Seq ID NO: C379 Protein Sequence
 Protein Accession #: NP_002650.1

1 11 21 31 41 51
 20 MGHPPILLPL LLLHTCVPAS WGLRCMQCKT NGDCRVEECA LGQDLCRTTI VRLWEEGEEEL 60
 ELWEKSCTHS EKNRNLTSR TGLKITSLTE VVCGLDLCNQ GNSGRAVITYS RSRYLECISC 120
 GSSDMSCERG RHQSLQCRSP EEQCLDVVTH WIQEGEEGRP KDDRHLRGCG YLPGCPGSGNG 180
 FHNNDTFHFL KCCNTTKCNE GPILLELENLF QNGRCQYSCK GNSTHGCSSE ETPFLIDCRGP 240
 MNQCLVATGT HEPKNQSYMV RGCATASMCQ HAHLGDAFPM NHIDVSCCTK SGCNHPDLVD 300
 25 QYRSGAAPQP GPAHLSTLIT LLMTARLWGG TLLWT 335

25 Seq ID NO: C380 Protein Sequence
 Protein Accession #: BAB55406.1

1 11 21 31 41 51
 30 MDFSQGVDP LASVILPPNL LENLSPEDSV LVRRQAQTPF NKTGLFQDVG PQRKTLVSIV 60
 MACSIGNITI QNLKDPVQIK IKHTRTQEVH HPICAPWDLN KNKSPGGWNT SGCVAHRDSD 120
 ASETVCLCNH FTFPGVLMDL PRSASQLDAR NTKVLTPISY ICGISAIPS AATLLTYVAF 180
 35 EKLRRDYPK ILMLLSTALL FLNLLFLLDG WITSFNVDGL CIAVAVLLHF PLLATFTWNG 240
 LEAHHMYIAL VKVFNTRYIR YILKFCIIGW GLPALVVSVV LASRNNNEVY GKESYKKEKG 300
 DEFCWIDQPF IFYVTCAGYF GVMFFLNIAF FIVVMVQICQ RNRKRSNRTL REEVLRNLRS 360
 VSLTFLLLGM TWGFAFPWAG PLNIPFMYLF SIFNSLQGLF IFIFHCAMKE NVQKQWRRLH 420
 COGRFLADN SDWSKTATNI IKKSSDNLGK SLSSSSIGSN STYLTSSKSKS SSTTYFKRNS 480
 40 HTDNVSYEHS FNRKSGSLRQC FHGQVIVKTG PC 512

40 Seq ID NO: C381 Protein Sequence
 Protein Accession #: NP_000565.1

1 11 21 31 41 51
 45 MTVARPSVPA ALPLLGELPR LLLLVLCLP AVNGDCGLPP DVFNQAQPALE GRTSFPEDTV 60
 ITRYCESFV KIPGKDSVI CLKGSQWSDI EEPFNRSCEV PTRLNSASLK QPYITQNYFP 120
 VGTVVEYECR PGYRRPESLS PKLTCLQNLK WSTAVEFCKK KSCPNFGEIR NGQIDVPGGI 180
 50 LFQATISFSC NTGYKLPGST SSFCLISGSS VQWSDPLPEC REIYCPAPPQ IDNGIIOGER 240
 DHYGYRQSVT YACNKGPTMI GEHSIYCTVN NDEGEWSGPP PECRGKSLTS KVPPTVQKPT 300
 TVNVPTTEVS PTSQKTTTIT TFPNAQATRS TPVSRITKHP HETTPNKGSG TTSQTTRLLS 360
 GHTCFTLTGL LGTLVTMGLL T 381

55 Seq ID NO: C382 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 60 MDTSLRGVLL SLFVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKQAF TGLYSLKVLN 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCFSG LHSRLHLWLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240
 LNYNNLEDEP TAIRTLNMLK ELHFYDNPQ FVGRSAFQHL PELRTLTLNG ASQITEFPDL 300
 65 TGTANLESST LTGAQISLSP QTVCNQLENL QVLDLSYNLL EDLPSFSVCQ KLQKIDLRHN 360
 EIYEIKVDTF QQLLSRLSN LAMNKIAIHH FNAFSTLPSL IKLDLSSNLL SSFPITGLHO 420
 LTHLKLGNH ALQSLISSN FPELKVIEP YAYQCCAFV CENAYKISNQ WNKGDSSMD 480
 DLHKDAGMF QAQDERDLED FLDFEEDLK ALHSVQCSPS PGPFKPCBHL LDGWLIRIGV 540
 WTIAYALATC NALVTSTVFR SPLYISPIKL LGIVIAAVNM LTGVSSAVLA GVDAPTFGSF 600
 70 ARHGAWWENG VGCHVIGPLS IFASESSVPL LTLAALERGF SVKYSAKPET KAPFSSLKVI 660
 ILLCALLALT MAAPVLGGS KYGASPLCLP LPFGEPSTWG YMVALILNS LCPLAMTIAY 720
 TKLYCNLDKG DLENINDCSM VKHIALLLFT NCILNCFVAF LSFSSILNLT FISPEVIKFI 780
 LLVVVPLPAC LNPLLYILFN PHFKEDLVSL RKQTYVWTRS KHPSLMSINS DDVEKQSCDS 840
 TQALVTFTSS SIYDLPSSS VPSPAYFVTE SCHLSSVAFV PCL 888

75 Seq ID NO: C383 Protein Sequence
 Protein Accession #: NP_003658.1

1 11 21 31 41 51
 80 MDTSLRGVLL SLPVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSVFTSY LDLSMNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKQAF TGLYSLKVLN 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCFSG LHSRLHLWLD DNALTEIPVQ 180
 AFRSLALQA MTLALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLETLD 240
 LNYNNLEDEP TAIRTLNMLK BLGFSNNIR SIPEKAFVGN PSLITIHFPD NPIQFVGRSA 300

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FOHLPELRTL TLNGASQITE FFDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360
YNLLEDLPSP SVQCKLQKID LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHPNAPST 420
LPSLIKLDLS SNLLSGFPIT GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480
AFGVCEENAYK ISNQWKNQDN SSMDDLHKKD AGMFOAQDER DLEDPLDPE EDLKALHSVQ 540
CSPSPGPFKP CEHLDLGWL I RIGVMTI AVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA 600
AVNMLTGVSS AVLAGVDAFT PGSFARHGAW WENGVCCHVI GFLSIFASES SVFLTLAAL 660
ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEF 720
STMGYMAVAL LLNSLCFLMM TIAYTKLYCN LDKGDLENIN DCSMVKHIAL LLPTNCILNC 780
PVAFLSPSSL INLTFISPEV IKFILLVVVP LPACLNPLLY ILFNPFPKED LVSLRKQTYV 840
WTRSKHPSLM SINSDDVEKQ SCDSTQALVT PTSSSITYDL PPSVVPSPAY PVTESCHLSS 900
VAFVPCL 907

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Seq ID NO: C384 Protein Sequence
Protein Accession #: NP_003497.1

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1 11 21 31 41 51
MEMFTLLTLC IFLPLLRGHS LFTCEPITVP RCMKAMAYNMT FFPNLMGHYD QSIAAEMEH 60
FLPLANLECS FNLETFLCKA FVPTCIEQIH VPPPCRKLCE KVSQDCKLI DTFGIRWPEE 120
LECDRLQYCD ETVPVTFDPH TFLGPGQKKT EQVQRDIGFW CPRHLKTSQG QGYKFLGIDQ 180
CAPPCPNMYP KSDLELEFAKS FIGTVSIFCL CATLFTPLTF LIDVRRFRYP ERPILYYSV 240
YSIVSLMYPI GFLLDGSTAC NKADEKLELG DTVVLGSQNK ACTVLFMLLY FETMAGTVWW 300
VILTITWFLA AGRKWSCEAI EQKAVWFHAV AWGTGFLTV MLLALNKVEG DNISGVCVVG 360
LYDLASRYF VLLPLCLCVF VGLSLLLAGI ISLNHVRQVI QHDGRNQEK KKFIRIGVFP 420
SGLYLVPVLT LLGCVVYEQV NRITWEITWV SDHCRQYHIP CPYQAKAKAR PELALFMIKY 480
LMTLIVGISA VFWVGSKKTC TEWAGFPKRN RKRDPISESR RVLQESCEFF LKHNSKVHKH 540
KKHYKPSHK LKVISKSMGT STGATANHGT SAVAITSHDY LQETLTLEIQ TSPETSMREV 600
KADGASTPRL REQDCGEPAS PAASISRLSG EQVDGKGQAG SVSESARSEG RISPKSDITD 660
TGLAQSNLQ VSSSESPSL KGSSTLLVHP VSGVRKEQGG GCHSDT 706

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Seq ID NO: C385 Protein Sequence
Protein Accession #: NP_000573

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1 11 21 31 41 51
MRIAIVICFL LGITCAIPVK QADSGSSEK QLYNKYPDAV ATWLNPDPSQ KQNLAPQTL 60
PSKSNESHDH MDDMDDEDD DHVDSQDSID SNDSDDVDDT DDSHQSDSH HSDEDELVT 120
DFPTDLPAE VFTPVVPTVD TYDGRGDSV YGLRSKSKFP RRPDIQYPA TDEDITSHME 180
SEELNGAYKA IPVAGDLNAP SDWDSRGKDS YETSQLDQGS AETHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREPH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDASASSEVN 300

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Seq ID NO: C386 Protein Sequence
Protein Accession #: NP_002812

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1 11 21 31 41 51
MGAARGSPAR PRLPLLSVL LPLLLGGTQT AIVFIKQPS QDALQGRAL LRCEVEAPGP 60
VHVYNLLDGA PQQDTERRA QGSSLSFAAV DRLQDSGTQ CVARDDVTGE EARSANASFN 120
IKWIEAGFVV LKHPASEAEI QPQTQVTLRC HIDGHPRTY QWFRDGTPLS DGQSNHTVSS 180
KERNLTLRPA GPESHSGLYC CAHSAGQAC SSQNFTLSIA DESFARVLA PQDVVVARYE 240
EAMFHQCPFA QPPPSLQWLF EDETPITNRS RPPHLRRATV FANGSLLLTQ VRPRNAGIYR 300
CIGQGQRPFP ILEATLHLA BIEDMPLFEP RVFTAGSEER VTCLPPKGLF EPSVWWEHAG 360
VRLPTHGRVY QKGHELVLAN IASDAGVYT CHAANLAGQR RQDVNITVAT VPSWLKPKQD 420
SQLBEGKPGY LDCLTQATPK PTVVYRNQM LISEDSRFEV FKNGTLRINS VEVDGTWYR 480
CMSSTPAGSI EAQARVQVLE KLKFTPPPQF QOCMEFDKEA TVPCSATGRE KPTIKWERAD 540
GSSLPEWVD NAGTLHFARV TRDDAGNYTC IASNGPQQI RAHVQLTVAV FITPKVEPER 600
TTYVQHTAL LQCEAQGDFK FLIQWKGKDR ILDPKLGPR MHIFQNGSLV IHDVAPEDSG 660
RYTCIAGNSC NIKHTEAPLY VVDKVPPEES EGPSPFPYK MIQTIGLSVG AAVAYIIAVL 720
GLMFYCKKRC KARKLQKPE GEPEMECLN GGPLQNGQPS AEIQEEVALT SLGSGPAATN 780
KRHSTSDKM PPRSSLPQIT TLGKSEFGEV FLAKAQGLEB GVAETLVLVK SLQTKDEQQQ 840
LDFRRELEMP GKLNHANVVR LLGLCREAEP HYMVLEYVDL GDLLKQFLRIS KSKDEKLKSO 900
PLSTKQKVAL CTQVALGMEH LSNNRFVHKD LAARNCLVSA QRQVKVSALG LSKDVYNSEY 960
YHFRQAWVPL RMWSPEAILE GDFSTKSDVN AFGVLMWEVP THGEMPHGGQ ADDEVLDLQ 1020
AGKARLPQPE GCPSKLYRLM QRCHALSPKD RPSFSEIASA LGDSTVDSKP 1070

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Seq ID NO: C387 Protein Sequence
Protein Accession #: NP_002300.1

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1 11 21 31 41 51
MKVLAAGVVP LLLVLHWHG AGSPLPITPV NATCAIRHPC HNNLMNQIRS QLAQLNGSAN 60
ALFIIYTTAQ GEPFPNNLDK LCGPNVTDFF PFHANGTEKA KLVELYRIV YLGTSLGNIT 120
RDQKILNPBA LSLHSLKNAT ADILRGLLSN VLCRLCSKYH VGHVDVITYG DTSGKDVPOK 180
KKLGCCQLGK YKQIIAVLAQ AF 202

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Seq ID NO: C388 Protein Sequence
Protein Accession #: XP_097508

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1 11 21 31 41 51
MGRPRLTLC HVSIIISARD LSMNNLTELO PGLFHHLRFL EELRLSGNHL SHIPGQAFSG 60
LYSLKILMLQ NNQLGGIPAS ALWELPSLQS LRLDANLISL VPERSFEGLS SLRHLWLDN 120
ALTEIPVRAL NNLPAQAMT LALNRISHIP DYAPQNLTSL VVLHLHNNRI QHLGTHSFEG 180
LHNLLETDLN YNKLEPPVA IRTLGRLQEL GFHNNNIKAI PEKAPMGNPL LQTIHFYDNP 240

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5 IQFVGRSAFQ YLPKHLTSL NGAMDIQEFPP DLKGTTSLEI LTLTRAGIRL LPSGMCQQLP 300
 RLRVLELSHN QIBELPSLHR CQKLEELGLQ HNRWEIGAD TFSQLSSLQA LDLSMNAIRS 360
 IHPFAFSTLH SILVKLDLTDN QLTTLPLAGL GGLMHLKLG NLALSQAFSK DSFFKLRILE 420
 VFYAYQCCPY GMCASFYKAS GQWEAEDLHL DDEESSKRPL GLLARQAEH YDQDLDELQL 480
 EMEDSKPHPS VQCSPTTPGPF KPCEYLFESW GIRLAVWAIV LLSVLCNGLV LLTVFAGGPV 540
 PLPPVKFVVG AIAGANTLTG ISCGLLASVD ALTFQQFSEY GARWETGLGC RATGFLAVLG 600
 SEASVLLTL AAVQCSVSVS CVRAYGKSPS LGSVRAGVLG CLALAGLAAA LPLASVGEYG 660
 ASPLCLPYAP PEGQPAALGF TVALVMNSF CFLVVAGAYI KLYCDLPRGD FEAVWDCAMV 720
 10 RHVAWLIFAD GLLYCPVAFI SFASMLGLFP VTPEAVKSVL LVVLPPLACL NPLLYLLFNP 780
 HFRDDLRLRL PRAGDSGLA YAAAGELEKS SCDSTQALVA FSDVDLILEA SEAGRPPGLE 840
 TYGFFSVTLI SCQQPGAPRL EGSCHVEPEG NHFGNPQPSM DGEILLRAEG STPAGGGLSG 900
 GGGFQPSGLA FASHV 915

15 Seq ID NO: C389 Protein Sequence
 Protein Accession #: NP_570901

20 1 11 21 31 41 51
 MASLVSLEIG LLLAVLVVTA TASPPAGLLS LLTSGQGALD QEALGGLINT LADRVHCTNG 60
 PGCKCLSVED ALGLGEPGGS GLPPGPVLEA RYVARLSAAA VLYLSNPEGT CEDTRAGLWA 120
 SHADHLALL ESPKALTPGL SWLLQRMQAR AAGQTPKTAC VDIPQLLEA VGAGAPGSAG 180
 GVLAALLDHW RSQSCFHALP SPQYFVDFVP QQHSSEVPMT LAELSALMQR LGVGREAHSD 240
 HSHRHGASS RDPVPLISS NSSSVWDTVC LSARDVMAAY GLSEQAGVTP EAWAQLSPAL 300
 25 LQQLSGACT SQSRPPVQDQ LSQSERYLYG SLATLLICLC AVFGLLLTTC TGRGVAHYI 360
 LQTFSLAVG ALTGDVAHLV TPKVLGLHTH SEEGLSQPPT WRLLAMLACL YAPFLFENLF 420
 NLLLPDPED LEDGPCGHSS HSHGSHSHGV SLQLAPSELR QPKPFHEGSR ADLVAESPE 480
 LLNPEPRRLS PELRLPLVMI TLGDVAHNFA DGLAVGAFA SSWKTGLATS LAVFCHLPH 540
 ELGDFALLH AGLSVRQALL NLASALTAF AGLYVALAVG VSESEANIL AVATGLFLYV 600
 30 ALCDMLPAML KVRDPRPWL FLHNVGLLG GWTVLLLSL YEDDITF 648

35 Seq ID NO: C390 Protein Sequence
 Protein Accession #: NP_061844

40 1 11 21 31 41 51
 MANASEPGGS GGGEEAALGL KLATLSLLLC VSLAGNVLFA LLIVRERSLH RAPPYLLLDL 60
 CLADGLRALA CLPAVLAAR RAAAAAGAPP GALGCKLAF LAALFCFHA FLLLVGVVTR 120
 YLAIAHHRPY AERLAGWPCA AMLVCAAWAL ALAAAPFPVL DGGGDEEDAP CALEQRPDGA 180
 PGALGPLLLL AVVVGATHLV YLRLLPFIHD RRMKRPRLV PAVSHDWTFF GPGATGQAAA 240
 45 NWTAGFGRGP TFPALVGIRP AGPGRGARRL LVLEEFKTEK RLCKMFPYAVT LLFLLWGPY 300
 VVASYLRLV RPGAPOQAYL TASVWLTFQA AGINEVVCPL FNRELRDCFR AQFPCCQSPR 360
 TTQATHPCDL KGIGL 375

50 Seq ID NO: C391 Protein Sequence
 Protein Accession #: NP_005622

55 1 11 21 31 41 51
 MAAARPARG ELPLLGLLLL LLLGDPGRGA ASSGNATGPG PRSAGGSARR SAAVTGPPPP 60
 LSHCGRAAPC EPLRYNVLG SVLPYGATST LLAGDSDSQE EAHGKLVLWS GLRNAPRCWA 120
 VIQPLLCAVY MPKCENDRVE LPSRTLQAT RGPCAIVERE RGWPDFLRCT PDRFPEGCTN 180
 EVQNIKFNS QQCEVPLVRT DNPKSWYEDV ECGGIQQQNP LPTAEHQDM HSIIAIFGAV 240
 TGLCTLFTLA TPAVDMRNSN RYPAVILFYV NACFPVGSIG WLAQFMDGAR REIVCRADGT 300
 60 MRLGPTSLFV TSCVIFVY VYALMAGVV WFPVLTIAWH TSFKALGTTY QPLSGKTSYF 360
 HLLTWSLFPV LTVAILAVAQ VDGDSSVSGIC FVGKYNRYR AGFVLAPIGL VLIVGGYFLI 420
 RGVMTLPSIK NMHPGLLSEK AASKINETML RLGIQFLAP GFVLITFSCH FYDFFNQAEM 480
 ERSFRDYVLC QANVTIGLPT KQPIPDCEIK NRPSLLVEKI NLPAMFGTOI AMSTWVWTKA 540
 TLLIWRRTWC RLTGQSDDEP KRKKSKMIA KAFSKRHLL QNPQGLSEFS MHTVSHDGFV 600
 65 AGLAFDLNEP SADVSSAWAQ HVTKMVARRG AILPQDISVT PVATPVPPPEE QANLWLVEAE 660
 ISPELQKRLG RKKKRRKKK EVCPLAPPE LHPPAPAPST IPRLPQLPRQ KCLVAAGAWG 720
 AGDSCRQAG TLVSNFPCPE PSPPQDPFLP SAPAPVAWAH GRRQGLGPIH SRTNLADTEL 780
 MDADSDP 788

70 Seq ID NO: C392 Protein Sequence
 Protein Accession #: BAC04382

75 1 11 21 31 41 51
 MGARSGARGA LLLALLLCWD PRLSQAGRKR SGEVLPDSFP SAPAEPLPYF LQEPQDAYIV 60
 KNKPVELRCR APPATQIYFK CNGEWVSQND BVTQEGLEDA TLGARGGLRV REVQIEVSRQ 120
 QVEBLGLEED YNQCVAWSS AGTTKSRRAY VRIAYLRKNF DQEPGLKEVP LDHEVLLQCR 180
 PPEGVPVAEV EWLKNEVDID PTQDTNFLT IDENLIIRQA RLSDTANYTC VAKNIVAKRR 240
 STTATVIVVY NGGWSSWAEW SPCSNRQGRG WQKTRTRCTN PAPLNGGAFAC EGQAPOKTC 300
 80 TTICFVDGAW TEWSKWSACS TECAHWSRE CMAPPPQNGG RDCSGTLLDS KNCTDGLCMQ 360
 NKKTLSDPNS HLLASGDAA LYAGLVVAIF VVVAIIMAVG VVVYRNRCD FDTDTIDSSA 420
 ALTGQFPHVN FKTRAPSNPQ LLHPSVPFDL TASAGIYRGF VYALQDSTDK IPMTNSPLLD 480
 PLPSLKVEVY SSSTTSGSGP LADGADLLGV LPPGTYPDSF ARDTHFLHLR SASLGSQQLL 540
 GLPRDPGSSV SGTFGCLGGR LSIPGTGVS LVPNGAIPQG KPYEMYLIN KAESTLPLSE 600
 GTQTVLSPSV TCGPTGLLLC RPVILTMPHC AEVSARDWIF QLKTAHQGH WEEVVTLDDE 660
 TLNTPCYQAL EPRACHILLD QLGTVYFTGE SYGRSAVKRL QLAVFAPALC TSLEYSLRVY 720
 85 CLEDTFQVK EVLELERTLG GYLVEEPKPL MFKDSVHNLR LSLHDLPHAH WRSKLAKVY 780
 EIPFYHIWGS SQKALHCTFT LERHSLASTE LTCKICVRQV EGEGQIFQLH TTLAETPAGS 840
 LDTLCSAPGS TVTTQLGPYA FKIPLSIRQ ICNSLDAPNS RGNDRMLAQ KLSMDRYLNY 900
 FATKASPTGV ILDLWEALQQ DDGDLNLSAS ALEEMGKSEM LVAVATDGDG 950

Seq ID NO: C393 Protein Sequence
Protein Accession #: NP_004616

5	1	11	21	31	41	51	
	MNRKARRCLG	HLFLSLGMVY	LRIGGFSSVV	ALGASII CNK	IPGLAPRQRA	IQCSRPDAAI	60
	VIGEGSQMGL	DECQFQFRNG	RWNCSALGER	TVFGKELKVG	SREAAFTYAI	IAAGVAHAIT	120
10	AACTQGNLSD	CGCDKEKQGG	YHRDEGWKVG	GCSADIRYGI	GFPAKFVDAR	EIKQNARTLM	180
	NLHNNEAGRK	ILEENMKLEC	KCHGVSGSCT	TKTCWTTLPQ	FRELGYVLKD	KYNEAVHVEP	240
	VRASRNKRPT	FLKIKKPLSY	RKPMOTDLVY	IEKSPNYCES	DPVTGSGVTQ	GRACNKTAPO	300
	ASGCDLMCCG	RGYNTHQYAR	VWQNCCKFRW	CCYVKCNTCS	ERTEMYTCK		349

Seq ID NO: C394 Protein Sequence
Protein Accession #: NP_003777

15	1	11	21	31	41	51	
	MDALCGSGEL	GSKFWDNSLS	VHTENPDLTP	CPQNSLLAW	PCIYLWVALP	CYLLYLRRHC	60
20	RGYIILSHLS	KLKMWLVGLL	WCVSWADLFY	SPHGLVHGRA	PAPVFPVTPL	VVGVTMLLAT	120
	LLIQYERLQG	VQSSGVLIIIF	WFLCVVCAIV	PFRSKILLAK	AEGEISDPFR	FTTFYIHFAL	180
	VLSALILACP	REKPPPPSAK	NVDNPNYPET	SAGFLSLRFF	WWFTKMAIYG	YRHPLEEKDL	240
	WSLKEEDRSQ	MVVQQLLEAW	RKQEKQTARH	KASAAPGKNA	SGEDEVLLGA	RPRFRKPSFL	300
25	KALLATFGSS	FLISACFKLI	QDLLSFINPQ	LLSILIRFIS	NPMAPSWWGF	LVAGLMFLCS	360
	MMQSLILQHY	YHYIFVTGVK	FRTGIMGVII	RKALVITNSV	KRASTVGBIV	NLMSVDAQRF	420
	MDLAPFLNLL	WSAPLQIILA	IYFLNQNLGP	SVLAGVAFMV	LLIPLNGAVA	VKMRAPQVQK	480
	MKLKDSRIKL	MSHILNGIKV	LKLYAWEPSP	LKQVEGIRQG	ELQLRLTAAY	LHTTTTFTWM	540
	CSPFLVTLIT	LMVYVYVDPN	NVLDAEKAFV	SVSLFNILRL	PLNMLPQLIS	NLTQASVSLK	600
30	RIQQFLSQEE	LDPQSVBRKT	ISPGYAITIH	SGTFTWAQDL	PPTLHSLDIQ	VPGALVAVV	660
	GPVCGGKSSL	VSALLGEMEK	LEGKVHMKGS	VAYVPQAWI	QNCTLQENVL	FGKALNPKRY	720
	QQTLEACALL	ASLEMLPGGD	QTEIGEGGIN	LSGGQRQRVS	LARAVYSADAD	IFLLDDPLSA	780
	VDHVAKHIFP	DRVIGPEGVL	AGKTRVLVTH	GISFLPQTFD	IIVLADGQVS	EMGPYPALLQ	840
	RNGSFANFLC	NYAPDEDQGH	LEDSTALEG	AEDKEALLIE	DTLSNHTDLT	DNDPVTYVVO	900
35	KQFMRQLSAL	SSDGGGQGRP	VPRRHLPSE	KVQVTEAKAD	GALTQEEKAA	IGTVLSVFW	960
	DYAKAVGLCT	TLAICLLYVG	QSAALIGANV	WLSAWTNDAM	ADSRQNTSL	RLGVYAALGI	1020
	LQGFVLMLAA	MAMAAGGIIA	ARVLHQALLH	NKIRSPQSF	DTTFSGRILN	CFSKDIYVVD	1080
	EVLAPVILML	LASFNAIST	LVMIMASTEL	FTVVILELAV	LYTLVQRFYA	ATSRQLKRL	1140
	SVSRSPYISH	PSETVTGASV	IRAYNRSDP	EIISDTKVDA	NQRSCYPYII	SNRWLSIGVE	1200
40	PVGNVVLFA	ALFAVIGRSS	LNPGLVGLSV	SYSLQVTFAL	NWMIRMMSDL	ESNIVAVERV	1260
	KEYSTETEA	PWVVGSRPP	EGWPPRGEVE	FRNYSVRYRP	GLDLVLRLDS	LHVHGGEKVG	1320
	IVGRTGAGKS	SMTLCFLRIL	BAKGEIRID	GLNVADIGLH	DLRSQLTIIIP	QDPILFSGTL	1380
	RMNLDPFGSY	SEEDIWALE	LSHLHTFVSS	QPAGLDFFQCS	EGGENLSVGQ	RQLVCLARAL	1440
	LKRSRLVLD	EATAAIDLET	DNLIQATIRT	QFDTCVTLTI	ABRLNTIMDY	TRVLVLDKGV	1500
45	VAEPDSFANL	IAARGIFYGM	ARDAGLA				1527

Seq ID NO: C395 Protein Sequence
Protein Accession #: NP_004617

50	1	11	21	31	41	51	
	MRARPQVCEA	LLFALALQTG	VCYGIKWAL	SKTPSALALN	QTQHCQLEG	LVSQVQLCR	60
	SNLELMHTVV	HAAREVMKAC	RRAPADMWRN	CSSIELAFNY	LLDLERGTR	SAPVYALSAA	120
	AISHAIARAC	TSGDLPGCSG	GPVPGEGPGP	GNRWGGCADN	LSYGLLMGAK	PSDAPMKVKK	180
55	TGSQAKLMR	LHNSEVGRQA	LRASLEMKCK	CHGVSGSCSI	RTCWKGLQEL	QDVAADLKTR	240
	YLSATKVVRH	PMGTRKHLVP	KDLDIRPVKD	SELVYLQSSP	DFCMKNEKVG	SHGTQDRQCN	300
	KTSNGSDSDC	LMCCGRGYNP	YTRVVERCH	CKYHWCCYVT	CRCERTVER	YVCK	354

Seq ID NO: C396 Protein Sequence
Protein Accession #: NP_114072

60	1	11	21	31	41	51	
	MEWGYLLEVT	SLLAALALLQ	RSSGAAAASA	KELACQETIV	PLCKGIGYNY	TYMPNQFNHD	60
	TQDEAGLEVH	QFWPLVEIQ	SPDLKFFLCS	MYTPICLEDY	KKPLPPCRSV	CERAKAGCAP	120
65	LMRQYGFANP	DRMRCDRLPE	QGNPDTLCMD	YNRTDLTTAA	PSFPRLPPP	PPGEQPPSGS	180
	GHGRPPGARF	PHRGGRGGG	GGDAAAPPAR	GGGGGKARP	PGGGAAPCEP	GQCRAPMVS	240
	VSSERHPLYN	RVKTGQIANC	ALPCHNPFFS	QDERAFTVFW	IGLWSVLCFV	STFATVSTFL	300
	IDMERFKYPE	RPIIFLSACY	LPVSVGYLVR	LVAGHEKVAC	SGGAPGAGGA	GGAGGAAAGA	360
	GAGAGAGAGP	GGRGYEELG	AVEQHVRYET	TGPALCTVVF	LLVYFFGMAS	SIWWVILSLT	420
70	WFLAAGMKWG	NEAIAGSQY	PHLAAMLVPS	VKSI AVLALS	SVGDGPFVAGI	CVVGNQSLDN	480
	LRGFVLAPLV	IYLFIGTMPL	LAFVSLFRIR	RSVIKQDGP	TKTHKLEKLM	IRLGLEFVLY	540
	TVPAAVVAC	LFYEQHNRPR	WEATHNCPCL	RDLQPDQARR	FDYAVFMLKY	FMCLVVGITS	600
	GVVWNSGKTL	ESWRSCLTRC	CWASKGAAVG	GGAGATAAGG	GGGPGGGGGG	GGGPGGGPGG	660
75	GGGLYSDDVS	TGLTWSGTA	SSVSYPKQMP	LSQV			694

Seq ID NO: C397 Protein Sequence
Protein Accession #: XP_050625

80	1	11	21	31	41	51	
	MLQPGSLLI	LFLASHCCLG	SARGLEFLPGQ	PDFSYKRSNC	KPIPANILQC	HGIEYQNMRL	60
	PNLLGHETMK	EVLEQAGAWI	PLVMKQCHFD	TKKFLCSLFA	FVCLDDLDLT	IQPCHSLCVQ	120
	VKORCAPVMS	APGFPWDM	ECORFPQDND	LCIPLASSDH	LLPATEEAPK	VCEACKNKND	180
	DDNDIMETLC	KNDPALKIKV	KEITYINRDT	KIILETKSRT	IYKINGVSR	DLKKSVLNLK	240

DSLQCTCEEM NDINAPYLVM GQKQGGELVI TSVKRWQKGQ RSFKRISRSI RKLQC 295

Seq ID NO: C398 Protein Sequence
Protein Accession #: NP_001297.1

5
10
1 11 21 31 41 51
MSMGLEITGT ALAVLGLWLT IVCCALPMWR VSAFIGSNII TSQNIWEGLN MNCVVQSTGQ 60
MQCKVYDSLL ALPODLQAAI ALIVVAILLA AFGLLVALVG AQCTNCVQDD TAKAKITIVA 120
GVLPLLAALL TLVPVWSAN TIIRDYFNFV VPEAQKREMG AGLYVGWAAA ALQLLGGALL 180
CCSCPPREKK YTATKVYVSA PRSTGPGASL GTGYDRKDYV 220

Seq ID NO: C399 Protein Sequence
Protein Accession #: NP_036581.1

15
20
1 11 21 31 41 51
MESRKDITNQ EELWKMKPRR NLEEDDYLHK DTGETSMLKR PVLLHLHQTA HADEFDCPSE 60
LQHTQELFPQ WLPKIKLAAI IASLTFLYTL LREVIHPLAT SHQQYFYKIP ILVINKVLPM 120
VSITLLALVY LPGVIAAIVQ LHNQTKYKKP PHWLDKMWLT RKQFGLLSFP FAVLHAIYSL 180
SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVWRMEIYV SLGIVGLAIL ALLAVTSIPS 240
VSDSLTWREF HYIQSLGIV SLLGTIHAL JFAWNKIDI KQFVWYTPPT FMAVFLPIV 300
VLIFKSILFL PCLRKILKI RHGWEDVTKI NKTEICSQL 339

Seq ID NO: C400 Protein Sequence
Protein Accession #: NP_001766.1

25
30
1 11 21 31 41 51
MANCFSPFVS GDKPCCLSR RAQLCLGVSI LVLILVVVLA VVVPWRQW SGPQTTKRFP 60
ETVLARCVKY TEIHPMRHV DCQSVWDAFK GAFISKHPCN ITEEDYQPLM KLGTTQTVPCN 120
KILLWSRIKD LAHQPTQVQR DMPTLEDTL GYLADDLTWC GEFNTSKINY QSCPDWRKDC 180
SNPFVSFWK TVSRRFABEA CDVVHVMLNG SRSKIFDKNS TFGSVEVHNL QPEKVQTLA 240
WVIHGGREDS RDLCDQPTIK ELESISKRN IQFSCKNYR PDKFLQCVKN PEDSSCTSEI 300

Seq ID NO: C401 Protein Sequence
Protein Accession #: XP_120513.2

35
40
1 11 21 31 41 51
MVSCFSGPL RETNENVKKF YALRAFMRM SSEAAMLGES RTPKPRKHRA TTRAKIFKRF 60
FSEGSSESNR LVEELAVIHT YSDDPAFTTS PSSVQPREFG VMQGAPRARF GSRTFPAAAE 120
ASSPHLGIGE AACQSGARAA APRAGARRCO PQRQAAAAA TAQTHTLPHA RTRADPAGRR 180
RRHPRSPAPG GEGTCSEGA PRRRMEEMQ PAEEGSPVVK IYQKRSYVS LKTFPSKRPA 240
LAKRYERPTL VELPHGLHRT PAQPPASPAA ASSSSPAAV VRLGAPPRPP RRGFRARGTI 300
PILLPAPGVA GTLLPPPTSS SPPSPRPRPW HAAAPRGTS HTHMWSQST LPGSDTMVSV 360
FGLMAQRRWQ HRSLLKQFEWG ILGSGWTWPC QGDWLEKEGQ VAVLLPRSEG NTAPKKSRI 420
LDFAQQCSR VLSSLNCGSK LLDNHSQSOM ISCVKQEGSS YNERQEHCHI KGKGVHSQTS 480
NVDIEMQYMQ RKQQTSAFLR VFTDSLQNYL LSGSFPTFNP SSASEYGHLA DVDPLSTSPV 540
HTLENISLDS TASLCKSRHL SREPFVKSDP PNPLQALAG GASRPFSGAQ QSIAYRVNSE 600
LEDGIRSPVP LSCGALEMDL TSLGSKQLLN NYPVYITSKQ WDEAVNSSKK DGRRLRLYLI 660
RFVPTTDELK YSCGLGKRKR SVQSGETGPE RRPLDPVKVT CLRGTASPRS VSFSPVISPHR 720
IGGSPRTSV QPSVF 735

Seq ID NO: C402 Protein Sequence
Protein Accession #: BAA92562.1

55
60
1 11 21 31 41 51
METTVLSGIN FEYKGMIGWE VAGDHIYTAA GASDNDPMIL TLVVPGRFP QSVMDTENK 60
EVARITFVPE TLCVNCELY FMVGVNSRTN TPVETWKGSK GKQSYTYIIE EMTTTSFTWA 120
FQRTTPEBAS RKYTNDVAKI YSINVTNVMN GVASYCRPCA LEASDVGSCS TSCPAGYYID 180
RDSQTCRSCP PNTILKAHQF YGVQACVPCG PGTKNNKIHS LCYNDCTFSR NTPTRTFNYN 240
PSALANTVTL AGGSPSTSKG LKYFHHPTLS LCGNQGRKMS VCTDNVTDLR IPEGESGFSK 300
SITAYVCQAV IIPPEVTGYK AGVSSQPVSL ADRLIGVITD MTLDGITSPA ELFHLESIGI 360
PDVIFPYRSN DVTQSCSSGR STTIRVRCSP QKTVPGSLLL PGTCSDGTCD GCMFHPLWES 420
AAACPLCSVA DYHAIIVSSCV AGIQKTTYVW REPKLCSGGI SLPEQRVTIC KTIDFWLKV 480
ISAGTCTAIL LTVLTCYFWK KNQKLEYKYS KLVNATLKD CDLPADSCA IMEGEDVEDD 540
LIPTSKKSLF GKIKSFTSKQ PAPVTISLSE DS 572

Seq ID NO: C403 Protein Sequence
Protein Accession #: NP_055139.1

75
80
1 11 21 31 41 51
MALQGISVVE LSGLAPGRXC AMVLADFGAR VVRVDRPGSR YDVSRLGRGX RSLVLDLKQP 60
REPRAAASVQ AVGCAAGALP PRCHGETPAG PRDSAAGKSK AYLCQAEWIM PVQESPCRLA 120
GHDINYLALS VGLSKIGRSG ENFYAPLNLV ADFAGGGLMC ALGIIMAFED RTRTDKGQVI 180
DANMVEGTAY LSSPLWKTQK SSLWEAPRGQ NMLDGGAPPY TTYRTADGEP MAVGAIEPQF 240
YELLIKGLGL KSDLPNQMS TDDWPEMKKK FADVFAKRTK AEWCQIFDGT DACVTPVLTP 300
EEVVHHDHMK ERGSPFITSE QDVSPLAPL LIANTPAIPSS KGDPFIGERT EEILEEFGPS 360
REBIYQNSD KIIESNKVKA SL 382

Seq ID NO: C404 Protein Sequence

Protein Accession #: XP_091332.1

	1	11	21	31	41	51	
5	MQRWTLWAAA	FLTLHSAQAF	PQTDISISPA	LPFLPLPSLC	PLFWMEFKGH	CYRFPPLNKT	60
	WAEADLYCSE	FSVGRKSARK	ASIHSEENV	FVYDLVNSCV	PGIPADVWGT	LHDHRQEGQP	120
	EWTDGSSYDY	SYWDGSDPDD	GVHADPEED	CVQINRYPTS	EQLOAPEPQL	PLSISEATDV	180
	YLPEDFPAEP	KLMDQSWVSR	KSLKPSKSHL	MEPPTPVAKH	QKAKTRHRS	RGVWVPSGKA	240
10	GSWKERMNAD	YGRKRSAFPR	QEGRLRCRER	RLRAASGQGR	PEGQRKQROQ	ERQERGWEE	300
	GGVSPMRGAQ	AMQHGLGAGS	QRGAAPCEGE	NHQAPELGST	WRGQRLOPQT	AALCHPALRK	360
	LPGNAHGLAA	AFVQPALQVQ	EEKNNRTRFS	GAYFTMSDPT	CDQDSKEQSL	RRHGREAED	420
	GPYRLVKKKR	GPVACPSSFE	LQSGGEVCLD	FFVELRAGTW	IAREPP		466

Seq ID NO: C405 Protein Sequence
Protein Accession #: XP_054869.2

	1	11	21	31	41	51	
20	MHTCCPFVTL	BQDLHRKQMS	WMLQTLFAV	TSLVLSCAET	IDYVGEICDN	ACPCEEKDOI	60
	LTVSCENRGI	ISLSEISPPR	PPIYHLLLSG	NLNLRLYPNE	FVNYTGASIL	HLGNSVIQDI	120
	ETGAFHGLRG	LRLHLNNK	LELLRDTDFL	GLENLLEYLQV	DYNYISVIEP	NAPGKLHLQ	180
	VLILNDNLLS	SLPNNLFRFV	PLTHLDLRGN	RLKLLPYVGL	LQHMDKVVEL	QLEENPNWCS	240
	CELISLKDWL	DSISYSALVG	DVVCETPFRL	HGRDLDEVSK	QELCPRLIS	DYEMRPQTPL	300
	STGYLHTTP	ASVNSVATSS	SAVYKPLKLP	PKGTRQPNKP	RVRPTSRQPS	KDLGYSNYGP	360
25	SIAYQTKSPV	PLECPTACSC	MLQISDLGLN	VNCQERKIES	IAELQPKFYN	PKKMYLTENY	420
	IAVVRRTDFL	BATGLDLHL	GNNRISMIQD	RAPGDLTNLR	RLYLNGNRIE	RLSPFLFYGL	480
	QSLQYLFLQY	NLIREIQSGT	FDPVPNLQLL	FLNNMLLQAM	PSGVFSGLTL	LRNLRLSNHF	540
	TSLFVSGVLD	QLKSLIQIDL	HDNFDCTCD	IVGMKLWVEQ	LKVGVLVDE	ICKAPKKFAE	600
30	TDNRSKSEL	LCPDYSVVV	STPTPSSIQV	PARTSAVTPA	VRNLSTGAPA	SLGAGGGASS	660
	VPLSVLILSL	LLVFIMSVFV	AAGLFVLVMK	RRKGNQSDHT	STNNSDVSSF	NMQYSVYGGG	720
	GGTGGPHLPH	VHHRGPAKPK	VKTPAGHVYE	YIPHLGHMC	KNPIYRSREG	NSVEDYKDLH	780
	ELKVITYSSNH	HLQQQQQPPF	PPQQPQQQPP	PQLQLQPGE	ERRESHLRS	PAYSVSTIEP	840
	REDLSPVQD	ADRFYRGILE	PDKHCSTTPA	GNSLPEYKPK	PCSPAAYTFS	PNYDLRRPHQ	900
35	YLHPGAGDSR	LREPVLYSPF	SAVPVEPNRN	EYLELKAKLN	VEPDYLEVLE	KQTTFSQP	958

Seq ID NO: C406 Protein Sequence
Protein Accession #: NP_000784.2

	1	11	21	31	41	51	
40	MGILSVDLII	TLQILPVFFS	NCLFLALYDS	VILLKHVVLL	LSRSKSTRGE	WRRMLTSEGL	60
	RCVWKFLLD	AYKQVLKGED	APNSSVVHVS	STEGGDNDSN	GTQEKIABGA	TCHLLDFASP	120
	ERPLVNFQGS	ATUPPFTSQL	PAPRKLVEEP	SSVADFLVY	IDEAHFSDGN	AIPGDSLSL	180
45	EVKKHQHQED	RCAAAQQLLE	RPSLPPQCRV	VADRMNNAN	IAYGVAFERV	CIVQRQKIAY	240
	LGKGPPFTYN	LQEVHMLEK	NFSKRUKKTR	LAG			273

Seq ID NO: C407 Protein Sequence
Protein Accession #: NP_006540.2

	1	11	21	31	41	51	
50	MSSCVSSQPS	SNRAAPQDEL	GGRGSSSSSES	QKPCALRGL	SSLSIHLGME	SFIVVTECEP	60
	GCAVDLGLAR	DRPLEADGQE	VPLDSSGSQA	RPHLSGRKLS	LQRSQGGLA	AGGSLDMNGR	120
55	CICPSLPYSP	VSSPQSSPRL	PRRPVESHSH	VSITGMQDCV	QLNQYTLKDE	IGKGSYGVVK	180
	LAYNENDNTY	YAMKVLKSKK	LIRQAGPFR	PPRGTRPAP	GGCIQPRGPI	EQVYQBIAIL	240
	KKLDHNPVVK	LVEVLDDPNE	DHLYMVPELV	NQGFVMEVPT	LKPLSEDQAR	FYFQDLIKGI	300
	EYLHYQKIIH	RDIKPSNLLV	GEDGHIKIAD	FQVSNEFKGS	DALLSNTVGT	PAFMAPESL	360
	ETRKIPSGKA	LDVWAMGVTL	YCFVFGQCP	MDERIMCLHS	KIKSQALEFP	DQPDIAEDLK	420
60	DLITRMLDKN	PESRIVVPEI	KLHPVWTRHG	AEPLSEDEN	CTLVEVTEEE	VENSVKIHPS	480
	LATVILVKIM	IRKRSPGNPF	EGSRREERSL	SAPGNLLTKK	PTRECESSLE	LKEARQRRQP	540
	PGHRPAPRGG	GGGSLVRGSP	CVESCWAPAP	GSPARMHLPR	PEEAMEFE		588

Seq ID NO: C408 Protein Sequence
Protein Accession #: NP_061116.2

	1	11	21	31	41	51	
65	MGLSLPKEKG	LILCLWSKFC	RWFQRRRESWA	QSRDEQNLLQ	QKRIWESPLL	LAAKONDVQA	60
	LNKLLKYEDC	KVHQRGAMGE	TALHIAALYD	NLEAAMVLME	AAPELVFEP	TSELYEGQTA	120
70	LHIAVNVQNM	NLVRALLARR	ASVSARATGT	AFRRSPCNLI	YFGEHPLSFA	ACVNSEIIVR	180
	LLIEHGADIR	AQDSLGNLTV	HILILQPNKT	FACQMYNLL	SYDRHGDHLQ	PLDLVPNHQ	240
	LTPPKLAGVE	GNTVMPQHL	QKRKHTQWTY	GPLTSTLYDL	TEIDSSGDEQ	SLLELIITTK	300
	KREARQILDQ	TPVKELVSLK	WKRYGRPYFC	MLGAIYLLYI	ICPTMCCTIYR	PLKPRTNNT	360
	SPRNTLLQQ	KLQRAYMTP	KDDIRLVGEL	VTIGAIIL	LVEVPDIFRM	GVTRFPQT	420
75	LGPPFHLVII	TYAPMLVVTM	VMRLISASGE	VVPMSPALVL	GWCNVMYFAR	GFQMLGPFIT	480
	MIQKMI PGDL	MRPCWLMMAV	ILGFASAFYI	IFQTEDEPEL	GHPYDYPMAL	FSTFEFLTI	540
	IDGPANYND	LPPMYSITYA	APAIATLTM	LNLLIAMMGD	THWRVAHERD	ELWRAQIVAT	600
	TVMLERKLPR	CLWPRSGICG	REYGLGDRWF	LRVEDRQDLN	RQRIQRYAQA	FHTRGSEDL	660
80	KDSVEKLELG	CPFSPLSLP	MPSVSRSTSR	SSANWERLRQ	GTLARDLRGI	INRGLEDGES	720
	WEYQI						725

Seq ID NO: C409 Protein Sequence
Protein Accession #: NP_068710.1

1 11 21 31 41 51
 1 MQKVTGLGLLV FLAGPPVLDL NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSEW 60
 5 RSSGEQAGRG WGSPPPLTQL SPTGAKCKCK FGQKSGHHPG ETPPLITPGS AQS 113

Seq ID NO: C410 Protein Sequence
 Protein Accession #: NP_005962.1

1 11 21 31 41 51
 10 1 MQKVTGLGLLV FLAGPPVLDL NDLEDKNSPF YYDWHSLQVG GLICAGVLCA MGIIIVMSAK 60
 CKCKFGQKSG HHPGETPLI TPESAQS 87

Seq ID NO: C411 Protein Sequence
 Protein Accession #: NP_004952.1

1 11 21 31 41 51
 20 1 MLSKVLPLLL GILLILQSRV EGPQTESKNE ASSRDVVYGP QPQPLENQLL SEETKSTETE 60
 TGSRVGKLE ASRILNTILS NYDHKLRLPGI GEKPTVVTV E IAVNSLGPLS ILDMEYITDI 120
 IPSQTWYDER LCYNDTFESL VLNQNVVSQ L WIPDTFFRNS KRTHHEITM PNQMVRIYKD 180
 GVLVLTIRMT IDAGCSLHML RFPMDSHSCP LSPSSFSYPE NEMIKWENF KLEINEKNSW 240
 KLFQDFDTGV SNKTEIITP VGDFVMVITF FNVSRFRGYV AFQNYVPSV TMLSWVSPW 300
 25 IKTESAPART SLGITSVLTM TLTGTFSRKN FPRVSITAL DFYIAICVPF CFCALLEFAV 360
 LNFLIYNQTK AHASPKLRHP RINSRAHART RARSACARQ HQEAFVCQIV TTEGSDGEER 420
 PSCSAQQPPS PGSPGPRSL CSKLACCENC KRPKKYFCMV PDCGSTWQQ GRLCIHVYRL 480
 DNYSRVVPFV TFFFFNVLYW LVCLNL 506

Seq ID NO: C412 Protein Sequence
 Protein Accession #: NP_068819.1

1 11 21 31 41 51
 35 1 MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQWLIP DTFPRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSP SSFSYPENEM IYKWNPKLE 120
 INEKNWKLFP QLDFTGVSNK TEIITTFVGD FMVMTIFFNV SRRPGYVAFQ NYVPSSVTM 180
 LSWVSWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240
 ALLEPAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVQIVTTE 300
 40 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCENCKRF KKYFCMVPCD EGSTWQQARL 360
 CIHVYRLDNY SRVVPFVTFP FPNVLYWLVCL LNL 393

Seq ID NO: C413 Protein Sequence
 Protein Accession #: NP_068822.1

1 11 21 31 41 51
 45 1 MEYTIIDIFS QTWNSKRTHS HEITMPNQMV RIYKDGKVLV TIRMTIDAGC SLHMLRFPMD 60
 SHSCPLSPGS PSYPENEMIV KWNFKLEIN EKNSWKLQPF DFTGVSNKTE IITTFVGDPM 120
 50 VMTIFFNVSR RFGYVAFQNY VPSSVTMMLS WVSFWIKTES APARTSLGIT SVLTMTTLGT 180
 FSRKNFPRVS YITALDFYIA ICFVFCFCAL LEFAVLNFI YNQTAKHASP KLRHPRINSR 240
 AHARTRARS ACARQHQEAF VQIVTTEGS DGEERPSCSA QQPPSPGSPE GPRSLCSKLA 300
 CCENCKRFFK YFCMVPCDG STWQQGRLCI HVYRLDNYSR VVPFVTFPP NVLYWLVCLN 360
 L 361

Seq ID NO: C414 Protein Sequence
 Protein Accession #: NP_068830.1

1 11 21 31 41 51
 60 1 MEYTIIDIFS QTWYDERLCY NDTFESLVLN GNVVSQWLIP DTFPRNSKRT HEHEITMPNQ 60
 MVRIYKDGKV LYTIRMTIDA GCSLHMLRFP MDSHSCPLSP SSFSYPENEM IYKWNPKLE 120
 INEKNWKLFP QDFTGVSNK TEIITTFVGD FMVMTIFFNV SRRPGYVAFQ NYVPSSVTM 180
 LSWVSWIKT ESAPARTSLG ITSVLMTTL GTFSRKNFPR VSYITALDFY IACFVFCFC 240
 65 ALLEPAVLNF LIYNQTKAHA SPKLRHPRIN SRAHARTRAR SRACARQHQE AFVQIVTTE 300
 GSDGEERPSC SAQQPPSPGS PEGPRSLCSK LACCENCKRF KKYFCMVPCD EGSTWQQARL 360
 CIHVYRLDNY SRVVPFVTFP FPNVLYWLVCL LNL 393

Seq ID NO: C415 Protein Sequence
 Protein Accession #: NP_068591.1

1 11 21 31 41 51
 70 1 MPAVSGPGPL FCLLLLLLDP HSPETGCPPL RPEYKLSFK GPRLALPGAG IPFNSHGDGA 60
 ILGLEEVRLT PSMNRNSGAV WSRASVPPSA WEVEVQMRVT GLGRRGANGM AVWYTRGRGH 120
 75 VGSVLGLAS WDQIGIFPDS PASDTQDSPA IRVLASDGIH PSEQPGDGAS QGLGSGCHMD 180
 RNRPHFRAR IYWGQRLRM SLNSQLTPSD PGEFCVDVGP LLLVPGGFFG VSAATGTLD 240
 DHDVLSFLT SLSESPSEVP PQPFLEMQL RLAQLGLEGLW ARLGLGTRED VTPKSDSEAG 300
 GEGERLFDLE ETLGRHRRIL QALRGLSKQL AQAEQWKKQ LGPPGQARPD GGWALDASCO 360
 80 IPSTPGRGGH LMSLNKDSA KVGALLHGQW TLLQALQEMR DAAVRMAAEA QVSYPVVGIE 420
 HHFLDLHIL GLLQEELRGP AKAAAKAPRP PGQPPRASSC LQPGIFLYL LIQTVGPFY 480
 VHFRLQELNKS LQECSTGSL PLGPAHTFR ALGILRRQPL PASMPA 526

Seq ID NO: C416 Protein Sequence
 Protein Accession #: XP_117036.1

1 11 21 31 41 51
 5 MERRTRGALG SRRPPPPPLPA LRHLCTGLQA AGMAWPGLTW RHTCQGRAXA AEGPWGLFRP 60
 HRCPREAGQA FVGSPETQG VAHVCSRARV SVDREPGGG AYAMHVTPRW KGCHRHSGRT 120
 VRGSVSWKRP EQAAPETGRG PAVARGSGDG NECGWG 156

Seq ID NO: C417 Protein Sequence
 Protein Accession #: XP_167803.2

1 11 21 31 41 51
 10 MPGKQQRKTA TNKPGGLPGA PGVGIGGHCL YVLECKCPK NKTKTHHHKK KNFAAKRNEE 60
 15 KKKKKKKQEK KNTKFFPHHT YPLSQQDFLP AKSYFCGNGP CFLWQGLF 108

Seq ID NO: C418 Protein Sequence
 Protein Accession #: NP_079056.1

1 11 21 31 41 51
 20 MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLMNT VALSGEECWE TLIGQDIYRL 60
 LLMDFVPSLV NSFPLGEFLRR IIGMQLITSL GLQEPDIARN VLELIYAQTL VWIGIFFCPL 120
 LPPIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFP IFLFFPSPT GVLCTLAITI 180
 25 WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVVW IYRNIGSVH FFFILTLIVL 240
 IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP SSVLVERREV 300
 EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 330

Seq ID NO: C419 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 30 MLSDDHVNEI IIQVENVSSG VQSHPSNNOI POEKVLLDSS INMVLISIEDI DVIDSQTVSK 60
 RNDQKGNQVL RFSTSLNESM SQTLSLSECM GIDTPGSSHE TVQGKLIAS LIPMTSRDRI 120
 35 KAIRNQPRTM EEKRNLRKIV DKEKSKQTHR ILQNLCCIQC LNSISRAYRR SKNSLSEILN 180
 SISLWQKTLK IIGGKPGTSV LSYFNFLRWL LKFNIPSPIL NPSFIIIPQF TVAKGNTLQF 240
 TGLEPFTGVG YPRDTVMYVG FYTNSTIQHG NSGASYNMQL AYIFTIGACL TTCFFSLLFS 300
 MAKYPRNNFI NPHIYSGGIT KLIFCWDFTV THEKAVKLKQ KNLSTEIREN LSELREQENSK 360
 40 LTFNQLLTFR SAYMVAVVVS TGVAIACCA VYLAENYLE PLKTHSNPGA VLLLPFVVSC 420
 INLAVPCIYS MFRLVERYEM PRHEVYVLLI RNIFLKISII GILCYWLMNT VALSGEECWE 480
 TLIGQDIYRL LLMDFVPSLV NSFPLGEFLRR IIGMQLITSL GLQEPDIARN VLELIYAQTL 540
 VWIGIFFCPL LPPIQMIMLF IMFYSKNISL MMNFQPPSKA WRASQMMTFP IFLFFPSPT 600
 GVLCTLAITI WRLKPSADCG PFRGLPLFIH SIYSWIDTSL TRPGYLWVVW IYRNIGSVH 660
 45 FFFILTLIVL IITYLYWQIT EGRKIMIRLL HEQIINEGKD KMFLIEKLIK LQDMEKKANP 720
 SSVLVERREV EQQGFHLHGE HDGSLDLRSR RSVQEGNPRA 760

Seq ID NO: C420 Protein Sequence
 Protein Accession #: NP_002241.1

1 11 21 31 41 51
 50 MGGDLVLGLG ALRRRKRLLE QEKSLAGWAL VLAGTGIGLM VLHAEMLWFG GCSWALYLFL 60
 VKCTISISTF LLLCLIVAFH AKEVQLFMTD NGLRDWRVAL TGRQAAQIVL ELVVCGLHPA 120
 55 PVRGPPCVDQ LGAPLTSPOQ WPGPLGQGBA LLSLAMLRL YLVPRAVLLR SGVLLNASYR 180
 SIGALNQVRF RHWFVAKLYM NTHPGRLLLG LTLGLWLTTA WVLSVAERQA VNATGHLSDT 240
 LWLIPITFIT IGYGDVVPQT MWGKIVCLCT GVMGVCCIAL LVAVVARKLE FNKAKEVHN 300
 FMDIQTYTE MKESAARVLQ EAMMFYKHTR RKESHAARRH QRKLLAALNA PRQVRLKHKR 360
 60 LREQVNSMVD ISKQHMILYD LQONLSSSHR ALEKQIDTLA GKLDALTELL STALGPRQLP 420
 EPSQQSK 427

Seq ID NO: C421 Protein Sequence
 Protein Accession #: NP_079533.1

1 11 21 31 41 51
 65 MGGQRDEDD EAYGKPKYD PSFRGPIKNR SCTDVICCVL FLLFILGYIV VGIVAWLYGD 60
 PRQVLYPRNS TGAYCGMGEN KDKPYLLYPN IFSCILSNI ISVAENGLQC PTPQVCVSSC 120
 PEDFWTVGKN EFSQTVGEVF YTKNRNFCPL GVPWNMTVIT SLQQLCPSP LLSAPALGR 180
 70 CFPWNTITPP ALPGITNDTT IQQGISGLID SLNARDISVK IFEDPAQSWY WILVALGVAL 240
 VLSLLFILLL RLIVAGPLVLV LILGVLGVLA YGIYCWEEY RVLDRKGASI SQLGFTTNLS 300
 AYQSVQETWL AALIVLAVLE AILLLVLIFL RQRIRIAIAL LKEASKAVGQ MMSTMFYPLV 360
 TFWLLLCIA YWAMTALYPL PTQPATLGYV LWASNISSPG CEKVPTINTSC NPTAHLVNSS 420
 75 CPGLMCFVQG YSSKGLIQRS VFNLIYGVV GLFWTLNWL ALGCQVLGA FASFYWAFHK 480
 PQDIPTFPLI SAFIRTLRYH TQSLAPGALI LTLVQIARVI LEYIDHKLKG VQNPVARCIM 540
 CCPKCLWLCL EKFIKFLNRN AYIMIAIYK NPCVSARNAP MLMRNIVRV VVLDKVTDL 600
 LPPGKLLVVG GVGVLSPFFP SGRIPLGKD PKSPHLNYYW LPIMTSILGA YVIASGFFSV 660
 FGMVCDTLFL CFLDLERNW GSLDRPYYS KSLKILGKK NEAPPDNKKR KK 712

Seq ID NO: C422 Protein Sequence
 Protein Accession #: NP_057264.1

1 11 21 31 41 51
 80 MGSNSGQAGR HIYKSLADDG PFDSVEPPKR PTERLIMHSM AMFGREFCYA VEAAYVTPVL 60

5 LSVGLPSSLY SIVWFLSPIL GFLQLQFVVG ASDHCRSRWG RRRPYILTLG VMMLVGMALY 120
 LAGATVVAAL IANPRRLVW AISVTMIGVV LFDFAADPID GPIKAYLFDV CSHQDKKEGL 180
 HYHALFTGFG GALGYLLGAI DWAHLELGR LGEFQVMFF PSALVLTLCF TVHLCSISEA 240
 PLTEVAKGIP PQOTPODPPL SSDGMYEYGS IEKVNGYVN PELAMQGAON KNHAEQTRRA 300
 MTLKSLRLAL VNMPPHYRYL CISHLIGWTA FLNMLFPTD FMQIVYRGD PYSAHNSTEF 360
 LIYERGVEVG CNGPCINSVF SSLYSYFQKV LVSYIGLKGL YFTGYLLPGL GTGFIGLFPN 420
 VYSTLVLCSL PGVMSSTLYT VPFNLITEYH REEEKERQQA PGDPPDNSVR GKGMDCATLT 480
 CMVQLAQILV GGGGLFLVNT AGTVVVVVIT ASAVALIGCC FVALFVRYVD 530

10 Seq ID NO: C423 Protein Sequence
 Protein Accession #: NP_003264.1

15 1 11 21 31 41 51
 | | | | | |
 MEGFGGVGGR GTRGFAAKGV WRGRAEEGPV LGAAERGFMV STGSRRRVFE GPGGGGLRWT 60
 PGKGTGRQGR AMGPRAEDGV RRRTLGMPRG SRRDVRAPCG PAGSWGARGG RRRDGPSSRR 120
 RGSATAAARH HVPPAPGGPF GPRAPAGSTR VPARAGGAVE PTGAAAVARL ARPAGGALPT 180
 AGAQAGAPAR GRSGGGSEWA RRGKGRPGFY QSPLGPAVAE GQELKDKSRL RYPINGFOAL 240
 20 VLTALLVQLG MSAGLPLQAL PEMLLPLAFV ATLTAFIGSL FLYMKAQVAP VSALAPGGNS 300
 GNPIYDFPLG RBLNPRICFP DFYFCELRP GLIGWVLINL ALLMKEAEIR GSPSLAMWL 360
 NGFQLLYVGD ALWHEEAVLT TMDITHDGF FMLAFGDMAN VPTYSLQAG FLWHHPQPLG 420
 LPMASVICLI NATGYIIFRG ANSQKNTFRK NPSPDRVAGL ETISTATGRK LLVSGWNGMV 480
 RHPNYLGLDI MALAWSLPCG VSHLLPYFYL LYPTALLVHR EARDERSACR STAWPGRSTA 540
 25 GVCLTASCPT STEAAPPPQV GHVPTHPPAH PGPGASTHLG LKGLHPTQP 589

Seq ID NO: C424 Protein Sequence
 Protein Accession #: NP_056535.1

30 1 11 21 31 41 51
 | | | | | |
 MGRLLRAARL PPLLSPLLL LVGGAFLGAC VAGSDEPGPE GLTSTSLDL LLPTGLEPLD 60
 SEEPSETMGL GAGLGAPGSG FPEENEESR ILQPPQYFWE EEEELNDSSL DLGPTADYVF 120
 PDLTEKAGSI EOTSGAQELP NLSPLEKMN LVEPPWHMPP EEEEEEEEE EEREKEEVEK 180
 35 QEEEEEEELL PVNGSQEAK PQVRDFSLTS SSQTPGATKS RHEDSGDQAS SGVEVESSMG 240
 SELLPLSPVP TTVTPGDQDS TSQEAETVL PAAGLGVEFE APQBASEAT AGAAGLSGQH 300
 EEVPALPSFF QTTAPSGAEH PDEDPLGSR SASSPLAPGD MELTPSSATL QGEDLNQQLL 360
 EQAAEAQSR IPWDSTQVIC KDNWNLAKN YIILNMTENI DCEVFRQHRG PQLLALVEEV 420
 LPRHSGHHG AMHISLSKPS EKEQHLLMTL VGEQGVVPTQ DVLMLGDIR RSLEBIGION 480
 40 YSTTSSQAR ASQVRSDYGT LFVVLVIGA ICIIIALGL LYNCWQRRLP KLKHVSHGEE 540
 LRFVENGCHD NPTLDVADS QSEMQEKHPS LGGGALNGP GSWGALMGK RDPEDSDVFE 600
 EDTHL 605

Seq ID NO: C425 Protein Sequence
 Protein Accession #: NP_001188.1

45 1 11 21 31 41 51
 | | | | | |
 MSEVRPLSRD ILMETLLYEQ LLEPPTMEVL GMTDSEEDLD PMEDFDSLEC MEGSDALALR 60
 LACIGDEMIV SLRAPRLAQL SEVAMHSLGL APIYDQTEDI RDVLRSPMDG FTTLKENIMR 120
 50 FNRSPNPGSW VSCBQVLLAL LLLALLLPL LSGGLHLLK 160

Seq ID NO: C426 Protein Sequence
 Protein Accession #: AAF76225.1

55 1 11 21 31 41 51
 | | | | | |
 MATPLPPSP RHLRLRLRL LSGVLGAALR GAAAGHPDVA ACPGSLDCAL KRRARCPPGA 60
 HACGPCLQPF QEDQQLCVP RMRRPPGGGR PQPRLEDEID FLAQELARKE SQGSTPPLPK 120
 DRQLKEPAT LGFSARQQL ELGLPSTPGT PTPPTHTSLG SPVSSDFVHM SPLPRGGQG 180
 60 DGLALVLILA PCVAGAAALS VASLCWCRLQ REIRLTQKAD YATAKAPGSP AAPRISPGDQ 240
 RLQAQSAEMTH YQHQRQQLC LERHKEPFKE LDTASSDEEN EDGDFTVYEC PGLAPTGE 300
 VRNPLFDHAA LSAPLPAPSS PPALP 325

65 Seq ID NO: C427 Protein Sequence
 Protein Accession #: NP_004436.1

70 1 11 21 31 41 51
 | | | | | |
 MVCSLWVLL VSSVLALBEV LLDTTGETSE IGWLYPPGG WDEVSVLDDQ RRLTRTFEAC 60
 EVAGAPPGTG QDNWLQTHFV ERRGAQRAHI RLHFSVRACS SLGVSGGTGR ETFTLYYRQA 120
 BEPDSFDSVS SWHLKRNTHV DTIAADESFP SSSSSSSSS SAAWAVGPHG AGQRAQLQLN 180
 VKERSFGPLT QRGFYVAFQD TGACIALVAV RLPSYTCPAV LRSFASFPET QASGAGGASL 240
 75 VAAVGTCAVA AEPEEDGVGG QAGGSPPRLH CNGEGKMVA VGGCRQPGY QPARGDKACQ 300
 ACPRGLYKGS AGNAPCSPCP ARSHAPNPAA FVPCLEGFY RASDDPPRAP CTGPPSAPQE 360
 LWFEVQSGAL MLHWRLPREL GGRGDLLFN VCKECEGRQE PASGGGGTCH RCRDEVHFD 420
 RORGLTESRV LVGGLRAHVP YILEVQAVNG VSELSDFPQ AAANVSTSH EVPSAVPVVH 480
 QVSRASNSIT VSWPQPDQTN GNILDYQLRY YDQAEDESHS FTLTSTNTA TVTQLSPGHI 540
 YGFQVART AAGHPYGGKV YFTLPGQEL SSQPERLSL VIGSILGALA FLLAAITVL 600
 80 AVVFQRKRG TGYTEQLQY SSPGLGVKYY IDPSTYEDPC QAIRELAREV DPAYIKIEV 660
 IGTGSGFEVR QRLQPRGR EQTVAIQALW AGGASLQMT FLGRAAVLQ FQHPNILLR 720
 GVTKSRPLM VITEFMELGP LDSFLRQREG QFSSLQLVAM QRGVAAAMQY LSSFAFVHRS 780
 LSAHSVILNS HLVCKVARLG HSPQGPSCLL RNAAPEVIAH GKHTTSDVW SPGLMWEVM 840
 SYGERPYWDM SEQEVNLNIE QEFRLPPFP CPGHLHLLM DTWQKDRAR PHFDQLVAAP 900
 DKMIRKPDTL QAGSDPGERP SQALLTFVAL DFPCLDSPA WLSAIGLEY QDNFSKFGLC 960

TFSDVAQLSL EDLPALGITL AGHQKLLHH IQLLQHLRQ QGSVEV

1006

Seq ID NO: C428 Protein Sequence
Protein Accession #: XP_043340.2

5

1	11	21	31	41	51	
MPDFRRFDI	YRKVPKDLTQ	PTYTGAIISI	CCCLFILFLF	LSELTGFITT	BVNVELYVDD	60
PDKDSGGKID	VSLNISLFLN	HCELVLGLDIQ	DEMGRHEVGH	IDNSMKIPLN	NGAGCRFEGQ	120
FSINKVPGNF	HVSTHSATAQ	PQNPDMTNVI	HKLSFGDTLQ	VQNIHGAFNA	LGGADRLLTSN	180
PLASHDYILK	IVPTVYEDKS	GKQRYSYQYT	VANKEYVAYS	HTGRIIPAIN	FRYDLSPITV	240
KYTERRQPLY	RFITTICAI	GGTFTVAGIL	DSCIPTASEA	WKKIQLGKMH		290

15

Seq ID NO: C429 Protein Sequence
Protein Accession #: NP_002142.1

20

1	11	21	31	41	51	
MAQKEGGRTV	PCCSRPKVAA	LTAGTLLLLT	AIGAASWAIV	AVLLRSQDEP	LYPVQVSSAD	60
ARLMVFDKTE	GTWRILCSSR	SNARVAGLSC	EEMGFLRALT	HSELDVRTAG	ANGTSGFFCV	120
DEGRLPHTQR	LLEVISVCDG	PRGRFLAAIC	QDCGRRLKLV	DRIVGGRDTS	LGRWPWQVSL	180
RYDGAHLCCG	SLLSGDWILT	AAHCFPERNR	VLSRWRVFAG	AVAQASPHGL	QLGVQAVVYH	240
GGYLFRRDPN	SEENSNDIAL	VHLSSPLPLT	EYIQPVCLPA	AGQALVDGKI	CTVTGWGNTQ	300
YYGQAGVLO	EARVPIISND	VCNGADFYGN	QIKPKMFCAG	YPEGCGIDACQ	GDSGGPFVCE	360
DSISRTPRWR	LCGIVSMGTG	CALAQKPGVY	TKVSDFRENI	FQAIKTHSEA	SGMVTQL	417

25

Seq ID NO: C430 Protein Sequence
Protein Accession #: BAA92562.1

30

1	11	21	31	41	51	
METTIVLSGIN	FEYKGMTGWE	VAGDHIYTAA	GASDNDFMIL	TLVVPGRFRP	QSVMAATENK	60
EVARITVFEE	TLCSVNCRLY	FMVGVNSRTN	TFVETWKGSK	GKQSYTYIIE	ENTTTSPTWA	120
PQRTTFHEAS	KYTTNDVAKI	YSINVTNVMN	GVASYCRPCA	LEASDVGSSC	TSCPAGYYID	180
RDSGTCHSCP	PNTILKAHQF	YGVQACVPCG	PGTKNNKIHS	LCYNDCTFSR	NTPTRTFNYN	240
FSALANTVTL	AGGPFSTSKG	LKYFHHFTLS	LCGNQGRKMS	VCTDNVTDLR	IPEGESGFSK	300
SITAVVCAV	IIEPVEVTGY	AGVSSQFVSL	ADRLIGVTTD	MTLDGITSFA	ELFHLESGLI	360
PDVIFFYRSN	DVTQSCSSGR	STTIRVRCSP	QKTVPGLLL	PGTCSGDTCD	GCFHFLWES	420
AAACPLCSVA	DYHAIVSSCV	AGIKKITYVM	REPCLCSGGI	SLPEQRVTIC	KTIDFWLKVQ	480
ISAGTCTAIL	LTVLTCYFWK	KNQKLEYKYS	KLVMNATLKD	CDLPAADSCA	IMEGEDVEDD	540
LIFTSKSLF	GKIKSFTSKQ	PAPVTISLSE	DS			572

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Seq ID NO: C431 Protein Sequence
Protein Accession #: NP_004855.1

45

1	11	21	31	41	51	
MPGQELRTVN	GSQMLLVLLV	LSWLPHGGAL	SLAEASRAS	PGPSELHSED	SRPRELRKRY	60
EDLLTLRLAN	QSWEDSNTDL	VPAPAVRILT	PEVRLGSGGH	LHLRISRAAL	PEGLPEASRL	120
HRALFRLSPT	ASRSWDVTRF	LRRQLSLARP	QAPALHLRLS	PPPSQSDQLL	AESSSARPLQ	180
ELHLRPAAR	GRRRARARNG	DDCPLGPGRC	CRHHTVRASL	EDLGWADWVL	SPREVQVTMC	240
IGACPSQFRA	ANMHAQIKTS	LHRLKPTBTP	APCCVPASYN	PMVLIQKTD	GVSLQTYDDL	300
LAKDCHCI						308

50

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Seq ID NO: C433 Protein Sequence
Protein Accession #: NP_443090.1

60

1	11	21	31	41	51	
MEDPSGAREP	RARPRERDPG	RRPHPDQGR	HDRPRDRPGD	PRRKRSSDGN	RRRDGDRDPK	60
RDQERDGNRD	RNRDRERERE	RERDPDRGPR	RDTHRDAGFR	AGEHGVWEKP	RQSRTRDGAR	120
GLTWDAAPP	GPAPWEAPEP	PQPQRKGDPG	RRRPESRPFS	ERYLPSTPRP	GREEVEYYQS	180
EAEGLECHK	CKYLCTGRAC	CQMLEVLNL	LILACSSVSY	SSTGGYTGIT	SLGGIYYYQF	240
GGAYSGFDGA	DGEKAQQLDV	QFYQLKLPV	TVAMACSGAL	TALCCLFVAM	GVLRVPMHCP	300
LLLVTEGLLD	MLIAGGYIPA	LYFYFHYLSA	AYGSPVCKER	QALYQSKGYS	GFGCSFHGAD	360
IGAGIFAALG	IVVPALGAVL	AIKGYRKVRK	LKEKPAEMFE	P		401

65

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Seq ID NO: C435 Protein Sequence
Protein Accession #: Eos sequence

75

1	11	21	31	41	51	
MGAAGRQDFL	FKAMLTISWL	TLTCFFGATS	TVAAGCPDQS	PELQPNWPGH	DQDHHVHIGQ	60
GKTLTLLTSSA	TVYSIHISEG	GKLVIKDHDE	PIVLRTRHIL	IDNGGELHAG	SALCPFGQNF	120
TIILYGRADE	GIQDPFYIYL	KYIGVGKGGG	LELHGQKKLS	WTFPLNKTLP	GGMAEGGYFF	180
ERSWGHKGI	VHVIDPKSGT	VIHSDRFDY	RSKKSERLV	QYLNAVDPGR	ILSVAVNDEG	240
SENLDMMARK	AMTKLGSKHP	LHLGFRHPWS	FLTVKGNPSS	SVEDHIEYHG	HRGSAARVP	300
KLPQTEHGEY	FNVSLSSEWV	QDVWTEWFD	HDKVSQTKGG	EKISDLWKAH	PGKICNRPID	360
IQATTMDGVN	LSTEVVYKKG	QDYRFACYDR	GRACRSYVR	PLCGKFVRPK	LTVTIDTNVN	420
STILNLEDNV	QSWKPGDTLV	IASTDYSMYQ	AEFQVLPSCR	SCAFNQVQVA	GKPMYHLIGE	480
EIDGDMRAE	VGLLSRNIIV	MGEMEDKCYF	YRNHICNFFD	PDTFGGHIFP	ALGFKAAHLE	540
GTCLKHMGQ	LVGQYPIHPH	LAGDVDERGG	YDPPTYIRDL	SIHHTFSRCV	TVHGSNGLLI	600
KDVVGYNISG	HCFPTEDGPE	ERNTFDHCLG	LLVKSGLTLP	SDRDSKMKCM	ITEDSYPGYI	660
PKPRQDCNAV	STFWMANPNN	NLINCAAAGS	EETGFWFIFP	HVPTGPSVGM	YSPGYSEHIP	720

80

LGKPYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGGD	VMILDSCHFRG	EAQEGFLLTG	MKAGGILLGG	DEAASGMAQG	840
FSPPCRCLK	LVTGSPFAH	VSLAHS				866

5

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication, accession number, or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1 1. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%
3 identical to a sequence as described in Tables 2A-80 in a biological sample from said patient,
4 thereby determining the presence or absence of said pathological cell.

1 2. The method of Claim 1, wherein:
2 a) said pathology is described in Table 1, including a cancer; and/or
3 b) said biological sample comprises isolated nucleic acids.

1 3. The method of Claim 1, wherein said biological sample is tissue from an organ
2 which is affected by said pathology of Table 1, including a cancer.

1 4. The method of Claim 2, wherein said nucleic acids are mRNA

1 5. The method of Claim 2:
2 a) further comprising a step of amplifying nucleic acids before said step of detecting
3 said nucleic acid; or
4 b) where said detecting is of a protein encoded by said nucleic acid.

1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as
2 described in Tables 2A-80.

1 7. The method of Claim 2, wherein:
2 a) said detecting step is carried out by:
3 i) using a labeled nucleic acid probe;
4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence
5 as described in Tables 2A-80; or
6 iii) detecting a polypeptide encoded by said nucleic acid; or
7 b) said patient is:
8 i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
9 ii) is suspected of having said pathology or cancer.

1 8. An isolated nucleic acid molecule comprising a sequence as described in
2 Tables 2A-80.

- 1 9. The nucleic acid molecule of Claim 8, which is labeled.
- 1 10. An expression vector comprising the nucleic acid of Claim 8.
- 1 11. A host cell comprising the expression vector of Claim 10.
- 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule
2 comprising a sequence as described in Tables 2A-80.
- 1 13. An antibody that specifically binds a polypeptide of Claim 12.
- 1 14. The antibody of Claim 13:
2 a) conjugated to an effector component;
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a
4 cytotoxic chemical;
5 c) which is an antibody fragment; or
6 d) which is a humanized antibody.
- 1 15. A method for specifically targeting a compound to a pathological cell in a
2 patient, said method comprising administering to said patient an antibody of Claim 13,
3 thereby providing said targeting.
- 1 16. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1 17. The method of Claim 16, wherein:
2 a) said antibody is conjugated to:
3 i) an effector component; or
4 ii) a fluorescent label; or
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1 18. A method for identifying a compound that modulates a pathology-associated
2 polypeptide, said method comprising the steps of:

- 3 a) contacting said compound with a pathology-associated polypeptide, said
4 polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence
5 at least 80% identical to a sequence as described in Tables 2A-80; and
6 b) determining the functional effect of said compound upon said polypeptide.

1 19. A drug screening assay comprising the steps of:

- 2 a) administering a test compound to a mammal having a pathology of Table 1 or a
3 cell isolated therefrom; and
4 b) comparing the level of gene expression of a polynucleotide that selectively
5 hybridizes to a sequence at least 80% identical to a sequence as described in
6 Tables 2A-80 in a treated cell or mammal with the level of gene expression of said
7 polynucleotide in a control cell or mammal, wherein a test compound that
8 modulates said level of expression of the polynucleotide is a candidate for the
9 treatment of said pathology.

10

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
22 May 2003 (22.05.2003)

PCT

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60/356,714	13 February 2002 (13.02.2002)	US
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60/368,809	29 March 2002 (29.03.2002)	US
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60/372,246	12 April 2002 (12.04.2002)	US
60/386,614	5 June 2002 (05.06.2002)	US
60/396,839	16 July 2002 (16.07.2002)	US
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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/02, 21/04

US CL : 435/6; 536/23.1, 24.3

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6; 536/23.1, 24.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WEST, PubMed**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	SATO, H. et al., Cloning and Expression of a Plasma Membrane Cystine/Glutamate Exchange Transporter Composed of Two Distinct Proteins, J. Biol. Chem. 23 April 1999, Vol. 247, No. 17, pp. 11455-11458.	1-7
A	KIM, J. Y. et al., Human cystine/glutamate transporter: cDNA cloning and upregulation by oxidative stress in glioma cells, B.B. Acta. June 2001, Vol. 1512, pp. 335-344.	1-7



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"Z" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/36810

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-7, SEQ ID NO: 19

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-7, drawn to a special technical feature of a method for determining presence or absence of a pathological cell in a patient, said method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from said patient, thereby determining the presence or absence of said pathological cell.

Group II, claim(s) 8-11, drawn to a special technical feature of an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, expression vector comprising the nucleic acid and a host cell comprising the expression vector.

Group III, claim(s) 12, drawn to a special technical feature of an isolated polypeptide which is encoded by an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80.

Group IV, claim(s) 13, 14, drawn to a special technical feature of an antibody which specifically binds to polypeptide of claim 12.

Group V, claim(s) 15, drawn to a special technical feature of a method for specifically targeting a compound to a pathological cell in a patient, comprising administering to a patient an antibody of claim 13.

Group VI, claim(s) 16, 17, drawn to a special technical feature of a method for determining the presence or absence of a pathological cell in a patient, comprising contacting a biological sample with an antibody of claim 13.

Group VII, claim(s) 18, drawn to a special technical feature of a method for identifying a compound that modulates a pathology-associated polypeptide by contacting the compound with a pathology-associated polypeptide encoded by a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 and determining the functional effect of the compound on the polypeptide.

Group VIII, claim(s) 19, drawn to a special technical feature of a drug screening assay comprising the steps of: administering a test compound to a mammal having pathology of Table 1 or a cell isolated therefrom; comparing the level of gene expression of a polynucleotide which selectively hybridizes to a sequence at least 80% identical to a sequence described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal.

The inventions listed as Groups I-VIII do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: claim 8 is anticipated by a sequence with accession No. BE440042 (Table 2A, first entry) (July 25, 2000), therefore there is no contribution of claim 8 over prior art.

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